GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:33:29 ; Search time 4260.27 Seconds
(without alignments)
4210.361 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 187
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size: 1

Total number of hits satisfying chosen parameters: 12722138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110449_27523/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rge -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss08
-USER=US10821670_@CGN_1_1_6646_@runat_07062006_110449_27523 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	187	100.0	561	2	AR596007	AR596007 Sequence
c	2	187	100.0	561	2	AR596008	AR596008 Sequence
	3	187	100.0	591	2	AR595954	AR595954 Sequence
c	4	187	100.0	591	2	AR595955	AR595955 Sequence
	5	187	100.0	666	2	AR595952	AR595952 Sequence
c	6	187	100.0	666	2	AR595953	AR595953 Sequence
	7	187	100.0	669	14	FCIL12P35	Y07761 Felis catus
	8	187	100.0	1533	2	AR595959	AR595959 Sequence
c	9	187	100.0	1533	2	AR595960	AR595960 Sequence
	10	187	100.0	1599	2	AR595956	AR595956 Sequence
c	11	187	100.0	1599	2	AR595957	AR595957 Sequence
	12	185	98.9	591	2	AR242439	AR242439 Sequence
	13	185	98.9	591	2	AR280207	AR280207 Sequence
	14	185	98.9	591	2	AR322422	AR322422 Sequence
	15	185	98.9	689	2	AR242451	AR242451 Sequence
	16	185	98.9	689	2	AR280219	AR280219 Sequence
	17	185	98.9	689	2	AR322434	AR322434 Sequence
	18	185	98.9	1441	2	AR242438	AR242438 Sequence
	19	185	98.9	1441	2	AR280206	AR280206 Sequence
	20	185	98.9	1441	2	AR322421	AR322421 Sequence
	21	154	82.4	669	14	FCU83185	U83185 Felis catus
	22	84	44.9	285	14	AF054605	AF054605 Felis cat
	23	59	31.6	660	2	AX154615	AX154615 Sequence
	24	59	31.6	660	2	AX154619	AX154619 Sequence
	25	59	31.6	660	2	AX154620	AX154620 Sequence
	26	56	29.9	660	2	AX154616	AX154616 Sequence
	27	54	28.9	669	2	AX076201	AX076201 Sequence
	28	54	28.9	669	2	AX076483	AX076483 Sequence
	29	54	28.9	4201	2	AX076477	AX076477 Sequence
	30	52	27.8	591	2	BD171284	BD171284 Novel can
	31	52	27.8	591	2	AR595963	AR595963 Sequence
c	32	52	27.8	591	2	AR595964	AR595964 Sequence
	33	52	27.8	666	2	AR595961	AR595961 Sequence
c	34	52	27.8	666	2	AR595962	AR595962 Sequence
	35	52	27.8	669	2	AR151062	AR151062 Sequence
	36	52	27.8	669	2	AR151072	AR151072 Sequence
	37	52	27.8	669	2	BD014654	BD014654 Process f
	38	52	27.8	669	2	BD014664	BD014664 Process f
	39	52	27.8	669	2	E15018	E15018 Canine mRNA
	40	52	27.8	669	2	AR316461	AR316461 Sequence
	41	52	27.8	669	2	AR316471	AR316471 Sequence
	42	52	27.8	1282	2	BD171283	BD171283 Novel can
	43	52	27.8	1455	2	AR596009	AR596009 Sequence
c	44	52	27.8	1455	2	AR596010	AR596010 Sequence
	45	52	27.8	1533	2	AR595973	AR595973 Sequence
c	46	52	27.8	1533	2	AR595974	AR595974 Sequence
	47	52	27.8	1599	2	AR595971	AR595971 Sequence
c	48	52	27.8	1599	2	AR595972	AR595972 Sequence
	49	50	26.7	669	14	CFU49085	U49085 Canis famil
	50	43	23.0	666	2	AX154613	AX154613 Sequence
	51	42	22.5	618	14	AY603407	AY603407 Capra hir
	52	42	22.5	666	14	AF173557	AF173557 Ovis arie
	53	42	22.5	666	14	AY232819	AY232819 Bubalus b
	54	42	22.5	690	14	AB246272	AB246272 Bubalus c
	55	42	22.5	690	14	AB246352	AB246352 Bubalus b
	56	42	22.5	690	14	AB246359	AB246359 Bubalus b
	57	42	22.5	690	14	AF003542	AF003542 Capra hir
	58	42	22.5	690	14	BTU14416	U14416 Bos taurus
	59	40	21.4	666	14	CEU57751	U57751 Cervus elap
	60	40	21.4	669	14	AB107653	AB107653 Lama glam
	61	40	21.4	669	14	AB246672	AB246672 Camelus b
	62	40	21.4	703	2	E35793	E35793 Process for
	63	39	20.9	657	8	AY191828	AY191828 Synthetic
	64	39	20.9	660	2	AX154614	AX154614 Sequence
	65	39	20.9	660	2	AX154617	AX154617 Sequence
	66	39	20.9	660	2	AX154621	AX154621 Sequence
	67	37	19.8	660	2	AX154618	AX154618 Sequence
	68	34	18.2	1426	14	PIGIL12PSU	L35765 Sus scrofa
	69	31	16.6	666	2	AX154612	AX154612 Sequence
	70	30	16.0	669	14	ECIL12P35	Y11130 Equus cabal
	71	30	16.0	1626	8	AF401989	AF401989 Synthetic
	72	29	15.5	660	2	AR008951	AR008951 Sequence
	73	29	15.5	660	2	BD007071	BD007071 IL-12 gen
	74	29	15.5	660	2	BD007079	BD007079 Gene expr
	75	29	15.5	660	2	BD007080	BD007080 Gene expr

76	29	15.5	660	2	BD007081	BD007081 Gene expr
77	29	15.5	660	2	BD136037	BD136037 Interfero
78	29	15.5	660	2	BD136038	BD136038 Interfero
79	29	15.5	660	2	BD136039	BD136039 Interfero
80	29	15.5	660	2	I28592	I28592 Sequence 3
81	29	15.5	660	2	AX154634	AX154634 Sequence
82	29	15.5	702	2	CQ829447	CQ829447 Sequence
83	29	15.5	721	2	AR052862	AR052862 Sequence
84	29	15.5	721	2	AR288174	AR288174 Sequence
85	29	15.5	721	2	AR567161	AR567161 Sequence
86	29	15.5	762	2	BD105971	BD105971 Animal mo
87	29	15.5	762	2	CQ803343	CQ803343 Sequence
88	29	15.5	762	2	AR533401	AR533401 Sequence
89	29	15.5	762	5	AF101062	AF101062 Homo sapi
90	29	15.5	780	5	MMU19842	U19842 Macaca mula
91	29	15.5	823	5	AF180562	AF180562 Homo sapi
92	29	15.5	856	2	BD165801	BD165801 Antibody
93	29	15.5	1020	2	CQ716168	CQ716168 Sequence
94	29	15.5	1021	5	BC104982	BC104982 Homo sapi
95	29	15.5	1021	5	BC104984	BC104984 Homo sapi
96	29	15.5	1026	2	AR091390	AR091390 Sequence
97	29	15.5	1026	2	AR380496	AR380496 Sequence
98	29	15.5	1026	5	HUMCLMF35	M65271 Human cytot
99	29	15.5	1287	2	AR393790	AR393790 Sequence
100	29	15.5	1287	2	AX084108	AX084108 Sequence
101	29	15.5	1316	2	AR050785	AR050785 Sequence
102	29	15.5	1316	2	AR212036	AR212036 Sequence
103	29	15.5	1316	5	HUMNKSFP35	M65291 Human natur
104	29	15.5	1364	2	AR082685	AR082685 Sequence
105	29	15.5	1364	2	AR122961	AR122961 Sequence
106	29	15.5	1364	2	I28326	I28326 Sequence 3
107	29	15.5	1364	2	I89771	I89771 Sequence 3
108	29	15.5	1395	2	AR309637	AR309637 Sequence
109	29	15.5	1444	2	CS032085	CS032085 Sequence
110	29	15.5	1444	2	CS041037	CS041037 Sequence
111	29	15.5	1444	2	CS143811	CS143811 Sequence
112	29	15.5	1560	2	AR091395	AR091395 Sequence
113	29	15.5	1623	2	AR091394	AR091394 Sequence
114	29	15.5	1645	2	A92078	A92078 Sequence 2
115	29	15.5	1645	2	AR230689	AR230689 Sequence
116	29	15.5	3205	2	CS131489	CS131489 Sequence
117	29	15.5	5686	2	BD136048	BD136048 Interfero
118	29	15.5	6139	2	AR091393	AR091393 Sequence
119	29	15.5	11792	5	AF404773	AF404773 Homo sapi
120	29	15.5	157079	5	AC010370	AC010370 Homo sapi
121	29	15.5	176108	5	AC026118	AC026118 Homo sapi
122	29	15.5	300140	12	AC129109	AC129109 Homo sapi
123	27	14.4	785	5	AY234219	AY234219 Papio anu
124	27	14.4	786	5	CTU19835	U19835 Cercocebus
125	26	13.9	79	2	AR242449	AR242449 Sequence
126	26	13.9	79	2	AR280217	AR280217 Sequence
127	26	13.9	79	2	AR322432	AR322432 Sequence
128	26	13.9	817	14	AY686642	AY686642 Equus cab
129	23	12.3	71	2	AX076207	AX076207 Sequence
130	21	11.2	711	14	BTA271034	AJ271034 Bos tauru
131	21	11.2	714	14	OAR271035	AJ271035 Ovis arie
c 132	18	9.6	76	2	AX076205	AX076205 Sequence
c 133	18	9.6	76	2	AX076208	AX076208 Sequence
134	16	8.6	666	6	AB025723	AB025723 Cavia por
135	15	8.0	827	6	AF421396	AF421396 Sigmodon
c 136	14	7.5	559	7	BV429425	BV429425 S237P6482
137	14	7.5	1239	6	AB085791	AB085791 Mesocrice
138	13	7.0	60	2	CQ542775	CQ542775 Sequence
139	13	7.0	660	2	BD136054	BD136054 Interfero
c 140	12	6.4	36	2	AR242450	AR242450 Sequence
c 141	12	6.4	36	2	AR280218	AR280218 Sequence
c 142	12	6.4	36	2	AR322433	AR322433 Sequence
c 143	12	6.4	144	14	AY388980S3	AY388982 Sus scrof
144	12	6.4	1119	6	AF288849	AF288849 Meriones
145	11	5.9	672	6	AF288520	AF288520 Marmota m
146	11	5.9	672	6	MMIL12P35	X97018 M.monax mRN
147	10	5.3	39	2	AR595997	AR595997 Sequence
• 148	10	5.3	146	14	AY575615	AY575615 Ovis arie
149	10	5.3	146	14	AY575616	AY575616 Ovis arie
c 150	10	5.3	322	7	BV094414	BV094414 RPAMMSEQ0
c 151	10	5.3	483	7	BV300932	BV300932 S239P60FH
152	10	5.3	582	2	AR393785	AR393785 Sequence
153	10	5.3	582	2	AX084103	AX084103 Sequence
154	10	5.3	660	2	E26662	E26662 Improved me
155	10	5.3	700	6	S82412S4	S82418 interleukin
156	10	5.3	713	2	AR069652	AR069652 Sequence
157	10	5.3	713	6	AF128212	AF128212 Mus muscu
158	10	5.3	713	6	AF128213	AF128213 Mus muscu
159	10	5.3	786	6	AF128210	AF128210 Mus muscu
160	10	5.3	786	6	AF128211	AF128211 Mus muscu
161	10	5.3	793	6	AF177031	AF177031 Rattus no
162	10	5.3	1265	6	MUSIL35A	M86672 Mus musculu
163	10	5.3	1278	2	AR393789	AR393789 Sequence
164	10	5.3	1278	2	AX084107	AX084107 Sequence
165	10	5.3	1569	2	AR393796	AR393796 Sequence
166	10	5.3	1569	2	AX084114	AX084114 Sequence
167	10	5.3	1669	8	AF411293	AF411293 Synthetic
168	10	5.3	2013	2	AR393795	AR393795 Sequence
169	10	5.3	2013	2	AX084113	AX084113 Sequence
170	10	5.3	2438	2	CQ812173	CQ812173 Sequence
171	10	5.3	2709	2	AR393797	AR393797 Sequence
172	10	5.3	2709	2	AX084115	AX084115 Sequence
173	10	5.3	5252	2	CQ803341	CQ803341 Sequence
174	10	5.3	5966	2	BD136050	BD136050 Interfero
175	10	5.3	9049	2	CQ803350	CQ803350 Sequence
176	10	5.3	10633	2	CQ803349	CQ803349 Sequence
177	10	5.3	11746	2	CQ803348	CQ803348 Sequence
178	10	5.3	38246	2	CQ803351	CQ803351 Sequence
c 179	10	5.3	195059	6	AC121306	AC121306 Mus muscu
c 180	10	5.3	215198	6	AC113180	AC113180 Mus muscu
c 181	10	5.3	223879	12	AC111877	AC111877 Rattus no
c 182	10	5.3	256720	6	AC110241	AC110241 Mus muscu
c 183	9	4.8	51	2	AR596002	AR596002 Sequence
184	9	4.8	282	2	AX308844	AX308844 Sequence
185	9	4.8	1200	6	S82412S5	S82419 interleukin
c 186	9	4.8	1641	15	DQ302585	DQ302585 Listeria
187	9	4.8	68903	5	HS92M18	Z73359 Human DNA s
188	9	4.8	79506	5	AL137247	AL137247 Human DNA
189	9	4.8	96244	6	AL807794	AL807794 Mouse DNA
c 190	9	4.8	110000	15	CP000155_34	Continuation (35 o
191	9	4.8	123414	12	AC164019	AC164019 Bos tauru
c 192	9	4.8	127362	12	AC010014	AC010014 Drosophil
193	9	4.8	134844	12	AC142020	AC142020 Rattus no
c 194	9	4.8	140221	12	AC141992	AC141992 Rattus no
c 195	9	4.8	142997	11	CR391924	CR391924 Zebrafish
196	9	4.8	153791	12	AC119629	AC119629 Rattus no
197	9	4.8	169735	13	AC010006	AC010006 Drosophil
198	9	4.8	170365	6	AC102834	AC102834 Mus muscu
c 199	9	4.8	170810	12	CT025599	CT025599 Mus muscu
200	9	4.8	171697	13	AC093548	AC093548 Drosophil

ALIGNMENTS

RESULT 1
AR596007
LOCUS AR596007 561 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 101 from patent US 6818444.
ACCESSION AR596007
VERSION AR596007.1 GI:56646988
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 561)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 101 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .561

```
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                4.37e-192      Length:          561
Score:                    187.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR596007 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 2
AR596008/c
LOCUS       AR596008                561 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 103 from patent US 6818444.
ACCESSION   AR596008
VERSION     AR596008.1  GI:56646989
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 103 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                4.37e-192      Length:          561
Score:                    187.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR596008 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 3
AR595954
LOCUS       AR595954                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 35 from patent US 6818444.
ACCESSION   AR595954
VERSION     AR595954.1  GI:56646935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 35 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

```
lignment Scores:
red. No.:              4.55e-192      Length:        591
core:                  187.00         Matches:       187
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-102 (1-187) x AR595954 (1-591)

y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

y          21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

y          41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

y          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

y          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

y          101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

y          121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

y          141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

y          161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

y          181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
b        571 ATGAGCTATCTGAATGCTTCC 591

ESULT 4
R595955/c
OCUS       AR595955                591 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 37 from patent US 6818444.
CCESSION   AR595955
ERSION     AR595955.1  GI:56646936
EYWORDS    .
OURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
EFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 37 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
     source         1. .591
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
red. No.:              4.55e-192      Length:        591
Score:                 187.00         Matches:       187
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           100.0%         Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-102 (1-187) x AR595955 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy          21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy          41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy         141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy         161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy         181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 5
AR595952
LOCUS       AR595952                666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 32 from patent US 6818444.
ACCESSION   AR595952
VERSION     AR595952.1  GI:56646933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 32 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:             4.98e-192      Length:        666
Score:                 187.00         Matches:       187
Percent Similarity:    100.0%         Conservative:  0
```

```
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595952 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666

RESULT 6
AR595953/c
LOCUS       AR595953                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.98e-192       Length:         666
Score:                  187.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595953 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 7
FCIL12P35
LOCUS       FCIL12P35                669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
```

```
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="GOA:O02743"
                     /db_xref="InterPro:IPR004281"
                     /db_xref="InterPro:IPR009079"
                     /db_xref="UniProtKB/Swiss-Prot:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNAS"
ORIGIN

Alignment Scores:
Pred. No.:                5e-192          Length:         669
Score:                    187.00          Matches:        187
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-102 (1-187) x FCIL12P35 (1-669)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666

RESULT 8
AR595959
LOCUS       AR595959                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                9.4e-192        Length:         1533
Score:                    187.00          Matches:        187
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595959 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533

RESULT 9
AR595960/c
LOCUS       AR595960                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
```

```
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                9.4e-192      Length:          1533
Score:                    187.00        Matches:         187
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              100.0%        Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-102 (1-187) x AR595960 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 10
AR595956
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                9.7e-192      Length:          1599
Score:                    187.00        Matches:         187
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              100.0%        Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-102 (1-187) x AR595956 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599

RESULT 11
AR595957/c
LOCUS       AR595957                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
```

```
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              9.7e-192        Length:         1599
Score:                  187.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595957 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 12
AR242439
LOCUS       AR242439                 591 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6472509.
ACCESSION   AR242439
VERSION     AR242439.1  GI:27288856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.58e-190       Length:         591
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR242439 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsn 185
              ||||||||||||||||
Db        571 ATGAGCTACCTGAAT 585

RESULT 13
AR280207
LOCUS       AR280207                 591 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6518045.
ACCESSION   AR280207
VERSION     AR280207.1  GI:29715597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 9 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.58e-190       Length:         591
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR280207 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        571 ATGAGCTACCTGAAT 585

RESULT 14
AR322422
LOCUS       AR322422                 591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.58e-190       Length:         591
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR322422 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        571 ATGAGCTACCTGAAT 585

RESULT 15
AR242451
LOCUS       AR242451                 689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.39e-190       Length:         689
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR242451 (1-689)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        652 ATGAGCTACCTGAAT 666

RESULT 16
AR280219
LOCUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6518045.
ACCESSION   AR280219
VERSION     AR280219.1  GI:29715609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.39e-190       Length:         689
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR280219 (1-689)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        652 ATGAGCTACCTGAAT 666

RESULT 17
AR322434
LOCUS       AR322434                689 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 26 from patent US 6566097.
ACCESSION   AR322434
VERSION     AR322434.1  GI:33708187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 26 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                7.39e-190      Length:          689
Score:                    185.00         Matches:         185
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              98.9%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR322434 (1-689)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        652 ATGAGCTACCTGAAT 666

RESULT 18
AR242438
LOCUS       AR242438               1441 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6472509.
ACCESSION   AR242438
VERSION     AR242438.1  GI:27288855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.

REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.3e-189       Length:          1441
Score:                    185.00         Matches:         185
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              98.9%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR242438 (1-1441)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 427

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 487

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 547

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 607

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 667

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 727

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 787

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        788 ATGAGCTACCTGAAT 802

RESULT 19
AR280206
LOCUS       AR280206               1441 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518045.
ACCESSION   AR280206
VERSION     AR280206.1  GI:29715596
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 8 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.3e-189        Length:         1441
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR280206 (1-1441)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 427

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 487

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 547

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 607

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 667

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 727

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 787

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        788 ATGAGCTACCTGAAT 802

RESULT 20
AR322421
LOCUS       AR322421               1441 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6566097.
ACCESSION   AR322421
VERSION     AR322421.1  GI:33708174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 8 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.3e-189        Length:         1441
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR322421 (1-1441)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 427

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 487

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 547

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 607

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 667

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 727

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 787

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        788 ATGAGCTACCTGAAT 802

RESULT 21
FCU83185
LOCUS       FCU83185               669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNSS"
ORIGIN

Alignment Scores:
Pred. No.:              2.21e-156       Length:         669
Score:                  154.00          Matches:        154
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            82.4%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x FCU83185 (1-669)

Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 258

Qy         52 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

Qy         72 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCys 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGC 378

Qy         92 LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAla 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 438

Qy        112 LysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 498

Qy        132 AspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeu 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTG 558

Qy        152 GluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArg 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618

Qy        172 IleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 185
              |||||||||||||||||||||||||||||||||||||||||||
Db        619 ATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

RESULT 22
AF054605
LOCUS       AF054605                 285 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION   AF054605
VERSION     AF054605.1  GI:3126818
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
REFERENCE   2  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>285
                     /codon_start=3
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAC15978.1"
                     /db_xref="GI:3126819"
                     /translation="LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLP
                     LELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE"
ORIGIN

Alignment Scores:
Pred. No.:              4.74e-81        Length:         285
Score:                  84.00           Matches:        84
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            44.9%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x AF054605 (1-285)

Qy         22 LysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAsp 41
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 92

Qy         42 IleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsn 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 152

Qy         62 GluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 212

Qy         82 ArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMet 101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 272

Qy        102 TyrGlnValGlu 105
              ||||||||||||
```

```
Db        273 TACCAGGTGGAG 284

RESULT 23
AX154615
LOCUS       AX154615                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 19 from Patent WO0140257.
ACCESSION   AX154615
VERSION     AX154615.1  GI:14536190
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 19 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

ORIGIN

Alignment Scores:
Pred. No.:              9.09e-54        Length:         660
Score:                  59.00           Matches:        59
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            31.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX154615 (1-660)

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 89
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

Qy          90 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 109
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 CTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy         110 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 24
AX154619
LOCUS       AX154619                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 23 from Patent WO0140257.
ACCESSION   AX154619
VERSION     AX154619.1  GI:14536194
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

ORIGIN

Alignment Scores:
Pred. No.:              9.09e-54        Length:         660
Score:                  59.00           Matches:        59
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            31.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX154619 (1-660)

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 89
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACAACC 363

Qy          90 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 109
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy         110 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 25
AX154620
LOCUS       AX154620                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 24 from Patent WO0140257.
ACCESSION   AX154620
VERSION     AX154620.1  GI:14536195
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 24 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              9.09e-54        Length:         660
Score:                  59.00           Matches:        59
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            31.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX154620 (1-660)

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 89
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

Qy          90 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 109
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy         110 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 AATGCAAAGCTGTTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 26
AX154616
LOCUS       AX154616                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 20 from Patent WO0140257.
ACCESSION   AX154616
VERSION     AX154616.1  GI:14536191
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
```

```
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 20 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              1.58e-50        Length:         660
Score:                  56.00           Matches:        56
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            29.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX154616 (1-660)

Qy          73 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu 92
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         313 ATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTT 372

Qy          93 SerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLys 112
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         373 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 432

Qy         113 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 128
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         433 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 27
AX076201
LOCUS       AX076201                669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-48        Length:         669
Score:                  54.00           Matches:        54
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            28.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX076201 (1-669)

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
               ||||||||||||||||||||||||||||||||||||||||||
Db         466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507

RESULT 28
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-48        Length:         669
Score:                  54.00           Matches:        54
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            28.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX076483 (1-669)

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
               ||||||||||||||||||||||||||||||||||||||||||
Db         466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507

RESULT 29
AX076477
LOCUS       AX076477                4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
```

```
          Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
ORIGIN

Alignment Scores:
Pred. No.:              9.37e-48       Length:        4201
Score:                  54.00          Matches:       54
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            28.9%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x AX076477 (1-4201)

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3392 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 3451

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3452 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 3511

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
              ||||||||||||||||||||||||||||||||||||||||||
Db       3512 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 3553

RESULT 30
BD171284
LOCUS       BD171284                 591 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171284
VERSION     BD171284.1  GI:28412574
KEYWORDS    JP 2002241398-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 4 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/4
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              3.04e-46       Length:        591
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x BD171284 (1-591)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              ||||||||||||||||||||||||||||||||||||
Db        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 31
AR595963
LOCUS       AR595963                 591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 49 from patent US 6818444.
ACCESSION   AR595963
VERSION     AR595963.1  GI:56646944
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 49 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.04e-46       Length:        591
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x AR595963 (1-591)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              ||||||||||||||||||||||||||||||||||||
Db        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 32
AR595964/c
LOCUS       AR595964                 591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 51 from patent US 6818444.
ACCESSION   AR595964
VERSION     AR595964.1  GI:56646945
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 51 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
```

```
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.04e-46        Length:         591
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595964 (1-591)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 33
AR595961
LOCUS       AR595961                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 46 from patent US 6818444.
ACCESSION   AR595961
VERSION     AR595961.1  GI:56646942
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 46 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.33e-46        Length:         666
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595961 (1-666)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 34
AR595962/c
LOCUS       AR595962                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 48 from patent US 6818444.
ACCESSION   AR595962
VERSION     AR595962.1  GI:56646943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 48 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.33e-46        Length:         666
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595962 (1-666)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 35
AR151062
LOCUS       AR151062                 669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-46        Length:         669
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR151062 (1-669)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252
```

```
Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 36
AR151072
LOCUS       AR151072                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6231850.
ACCESSION   AR151072
VERSION     AR151072.1  GI:15117122
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 12 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-46       Length:        669
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x AR151072 (1-669)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 37
BD014654
LOCUS       BD014654                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014654
VERSION     BD014654.1  GI:22555437
KEYWORDS    JP 2001161378-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 2 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/2
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-46       Length:        669
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x BD014654 (1-669)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 38
BD014664
LOCUS       BD014664                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014664
VERSION     BD014664.1  GI:22555447
KEYWORDS    JP 2001161378-A/12.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 12 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/12
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
```

```
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                       protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                       immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="Canis sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-46        Length:         669
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x BD014664 (1-669)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 39
E15018
LOCUS       E15018                  669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="Canis sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-46        Length:         669
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x E15018 (1-669)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 40
AR316461
LOCUS       AR316461                669 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 2 from patent US 6562334.
ACCESSION   AR316461
VERSION     AR316461.1  GI:33695289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 2 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="unknown"
                      /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-46        Length:         669
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR316461 (1-669)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
```

```
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 41
AR316471
LOCUS       AR316471                669 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6562334.
ACCESSION   AR316471
VERSION     AR316471.1  GI:33695299
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 12 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-46       Length:        669
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x AR316471 (1-669)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 42
BD171283
LOCUS       BD171283                1282 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171283
VERSION     BD171283.1  GI:28412573
KEYWORDS    JP 2002241398-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1282)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 3 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/3
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1282
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              5.49e-46       Length:        1282
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x BD171283 (1-1282)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 317

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 377

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        378 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 413

RESULT 43
AR596009
LOCUS       AR596009                1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 104 from patent US 6818444.
ACCESSION   AR596009
VERSION     AR596009.1  GI:56646990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 104 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1455
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.04e-46       Length:        1455
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x AR596009 (1-1455)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

RESULT 44
AR596010/c
```

```
LOCUS       AR596010                1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 106 from patent US 6818444.
ACCESSION   AR596010
VERSION     AR596010.1  GI:56646991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 106 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1455
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                6.04e-46       Length:          1455
Score:                    52.00          Matches:         52
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              27.8%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR596010 (1-1455)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

RESULT 45
AR595973
LOCUS       AR595973                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                6.29e-46       Length:          1533
Score:                    52.00          Matches:         52
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              27.8%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR595973 (1-1533)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db        1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 46
AR595974/c
LOCUS       AR595974                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                6.29e-46       Length:          1533
Score:                    52.00          Matches:         52
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              27.8%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR595974 (1-1533)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 47
AR595971
LOCUS       AR595971                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
```

```
ORIGIN

Alignment Scores:
Pred. No.:              6.49e-46        Length:         1599
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595971 (1-1599)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
Db       1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 48
AR595972/c
LOCUS       AR595972                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.49e-46        Length:         1599
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR595972 (1-1599)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 49
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LNSS"
ORIGIN

Alignment Scores:
Pred. No.:              4.84e-44        Length:         669
Score:                  50.00           Matches:        50
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x CFU49085 (1-669)

Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAG 258

Qy         52 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

Qy         72 LeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||
Db        319 TTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 50
AX154613
LOCUS       AX154613                666 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 17 from Patent WO0140257.
ACCESSION   AX154613
VERSION     AX154613.1  GI:14536188
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 17 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="synthetic construct"
```

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

ORIGIN

Alignment Scores:

Pred. No.:	1.76e-36	Length:	666
Score:	43.00	Matches:	43
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.0%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-102 (1-187) x AX154613 (1-666)

```
Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAG 402

Qy        101 MetTyrGln 103
              |||||||||
Db        403 ATGTACCAG 411
```

RESULT 51
AY603407
LOCUS AY603407 618 bp mRNA linear MAM 18-JUL-2004
DEFINITION Capra hircus interleukin 12 p35 subunit precursor, mRNA, partial cds.
ACCESSION AY603407
VERSION AY603407.1 GI:50261481
KEYWORDS .
SOURCE Capra hircus (goat)
ORGANISM Capra hircus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Capra.
REFERENCE 1 (bases 1 to 618)
AUTHORS Rasool,T.J., Shebannavar,S., Hosamani,M., Sreekumar,E., George,A.A. and Premraj,A.
TITLE cloning and sequencing of goat cytokines
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 618)
AUTHORS Rasool,T.J., Shebannavar,S., Hosamani,M., Sreekumar,E., George,A.A. and Premraj,A.
TITLE Direct Submission
JOURNAL Submitted (20-APR-2004) Division of Virology, Indian Veterinary Research Institute, Mukteswar, Nainital, Uttaranchal 263138, India
FEATURES Location/Qualifiers
source 1. .618
/organism="Capra hircus"
/mol_type="mRNA"
/isolation_source="peripheral blood mononuclear cells stimulated with Concanavalin A"
/db_xref="taxon:9925"
/note="breed: Pashmina"
CDS <1. .618
/codon_start=1
/product="interleukin 12 p35 subunit precursor"
/protein_id="AAT72317.1"
/db_xref="GI:50261482"
/translation="HHLPHLSLGRSLPTTTAGPGRSCLDYSQNLLRAVSNTLQKARQT
LEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRETSLITNGHCLASGKT
SFMTTLCLRSIYKDLKMYHMEFQAMNAKLLMDPKRQVSLDQNMLAAIAELMQALNFDS
ETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYLSSS"

ORIGIN

Alignment Scores:

Pred. No.:	2e-35	Length:	618
Score:	42.00	Matches:	42
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	22.5%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-102 (1-187) x AY603407 (1-618)

```
Qy         17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 162

Qy         37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 222

Qy         57 GluLeu 58
              ||||||
Db        223 GAATTA 228
```

RESULT 52
AF173557
LOCUS AF173557 666 bp mRNA linear MAM 13-NOV-2000
DEFINITION Ovis aries interleukin-12 p35 subunit precursor, mRNA, complete cds.
ACCESSION AF173557
VERSION AF173557.1 GI:5805389
KEYWORDS .
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 666)
AUTHORS Swinburne,S.J., Russ,G.R. and Krishnan,R.
TITLE Ovine interleukin 12 has biological activity on ovine and human activated peripheral blood mononuclear cells
JOURNAL Cytokine 12 (10), 1546-1552 (2000)
PUBMED 11023671
REFERENCE 2 (bases 1 to 666)
AUTHORS Swinburne,S.J., Russ,G.R. and Krishnan,R.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1999) Transplantation Immunology Laboratory, The Queen Elizabeth Hospital, Woodville Road, Adelaide, South Australia 5011, Australia
FEATURES Location/Qualifiers
source 1. .666
/organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
/tissue_type="inflammed renal tissue"
CDS 1. .666
/note="Il-12; cytokine"
/codon_start=1
/product="interleukin-12 p35 subunit precursor"
/protein_id="AAD51976.1"
/db_xref="GI:5805390"
/translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTAGPGTSCLDYSQ
NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
ETSLITNGHCLSSGKTSFMTTLCLRSIYKDLKMYHMEFQAMNAKLLMDPKRQVFLDQN
MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
SSS"
sig_peptide 1. .75
mat_peptide 76. .663
/product="interleukin-12 p35 subunit"

ORIGIN

Alignment Scores:

Pred. No.:	2.11e-35	Length:	666
Score:	42.00	Matches:	42
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	22.5%	Indels:	0
DB:	14	Gaps:	0

```
US-10-821-670A-102 (1-187) x AF173557 (1-666)

Qy         17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy         37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy         57 GluLeu 58
              ||||||
Db        271 GAATTA 276

RESULT 53
AY232819
LOCUS       AY232819                 666 bp    mRNA    linear   MAM 09-JUN-2005
DEFINITION  Bubalus bubalis interleukin-12 p35 subunit precursor, mRNA,
            complete cds.
ACCESSION   AY232819
VERSION     AY232819.1  GI:31322541
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
  TITLE     Interleukin-12 subunits p35 and p40 of Indian water buffalo
            (Bubalus bubalis) maintain high sequence homology with those of
            other ruminants
  JOURNAL   Eur. J. Immunogenet. 32 (3), 179-186 (2005)
REFERENCE   2  (bases 1 to 666)
  AUTHORS   Premraj,A., Sreekumar,E. and Rasool,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-FEB-2003) Animal Biotechnology, Rajiv Gandhi Centre
            for Biotechnology, Jagathy, Trivandrum, Kerala 695014, India
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
                     /cell_type="concanavalin A stimulated splenocytes"
     CDS             1. .666
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit precursor"
                     /protein_id="AAO61417.1"
                     /db_xref="GI:31322542"
                     /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                     NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                     ETSFITNGRCLASGKTSFMTTLCLKSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                     MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
ORIGIN

Alignment Scores:
Pred. No.:              2.11e-35        Length:         666
Score:                  42.00           Matches:        42
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            22.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x AY232819 (1-666)

Qy         17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy         37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy         57 GluLeu 58
              ||||||
Db        271 GAATTA 276

RESULT 54
AB246272
LOCUS       AB246272                 690 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus carabanensis IL-12p35 mRNA for interleukin-12p35, complete
            cds.
ACCESSION   AB246272
VERSION     AB246272.1  GI:84871693
KEYWORDS    .
SOURCE      Bubalus carabanensis
  ORGANISM  Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:346063"
                     /sex="female"
                     /cell_type="PBMC"
     gene            1. .690
                     /gene="IL-12p35"
     CDS             1. .666
                     /gene="IL-12p35"
                     /codon_start=1
                     /product="interleukin-12p35"
                     /protein_id="BAE75849.1"
                     /db_xref="GI:84871694"
                     /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                     NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                     ETSFITNGRCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                     MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
ORIGIN

Alignment Scores:
Pred. No.:              2.17e-35        Length:         690
Score:                  42.00           Matches:        42
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            22.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x AB246272 (1-690)

Qy         17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy         37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270
```

```
Qy          57 GluLeu 58
               ||||||
Db         271 GAACTA 276

RESULT 55
AB246352
LOCUS       AB246352                690 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus bubalis IL-12p35 mRNA for interleukin-12p35, complete cds.
ACCESSION   AB246352
VERSION     AB246352.1  GI:84871715
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
                     /sex="female"
                     /cell_type="PBMC"
                     /note="Bulgarian Murrah buffalo - crossbreed between
                     Mediterranean and Indian buffalo both are Riverine type
                     water buffalo"
     gene            1. .690
                     /gene="IL-12p35"
     CDS             1. .666
                     /gene="IL-12p35"
                     /codon_start=1
                     /product="interleukin-12p35"
                     /protein_id="BAE75857.1"
                     /db_xref="GI:84871716"
                     /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                     NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                     ETSFITNGRCLASGKTSYMTTLCLKSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                     MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
ORIGIN

Alignment Scores:
Pred. No.:              2.17e-35        Length:         690
Score:                  42.00           Matches:        42
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            22.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x AB246352 (1-690)

Qy          17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy          37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270
```

```
Qy          57 GluLeu 58
               ||||||
Db         271 GAATTA 276

RESULT 56
AB246359
LOCUS       AB246359                690 bp    mRNA    linear   MAM 14-JAN-2006
DEFINITION  Bubalus bubalis x Bubalus carabanensis IL-12p35 mRNA for
            interleukin-12p35, complete cds.
ACCESSION   AB246359
VERSION     AB246359.1  GI:84875358
KEYWORDS    .
SOURCE      Bubalus bubalis x Bubalus carabanensis
  ORGANISM  Bubalus bubalis x Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Bubalus bubalis x Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:365610"
                     /sex="female"
                     /cell_type="PBMC"
                     /note="Philippine carabao crossbreed (CB) - crossbreed
                     between Philippine carabao (Swamp type water buffalo) and
                     Indian Murrah buffalo (Riverine type water buffalo)"
     gene            1. .690
                     /gene="IL-12p35"
     CDS             1. .666
                     /gene="IL-12p35"
                     /codon_start=1
                     /product="interleukin-12p35"
                     /protein_id="BAE75893.1"
                     /db_xref="GI:84875359"
                     /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                     NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                     ETSFITNGHCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                     MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
ORIGIN

Alignment Scores:
Pred. No.:              2.17e-35        Length:         690
Score:                  42.00           Matches:        42
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            22.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x AB246359 (1-690)

Qy          17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy          37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy         57 GluLeu 58
              ||||||
Db        271 GAATTA 276

RESULT 57
AF003542
LOCUS       AF003542                690 bp    mRNA    linear   MAM 17-JUN-1997
DEFINITION  Capra hircus interleukin 12 35kD subunit mRNA, complete cds.
ACCESSION   AF003542
VERSION     AF003542.1  GI:2197070
KEYWORDS    .
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Beyer,J.C., Kumpula-McWhirter,N.M. and Cheevers,W.P.
  TITLE     Caprine Interleukin 12 35kD subunit
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Beyer,J.C., Kumpula-McWhirter,N.M. and Cheevers,W.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-1997) Veterinary Microbiology and Pathology,
            Washington State University, P.O Box 647040, Pullman, WA
            99164-7040, USA
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Capra hircus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9925"
                     /cell_type="LPS stimulated caprine microglial cells"
     CDS             1. .666
                     /codon_start=1
                     /product="interleukin 12 35kD subunit"
                     /protein_id="AAB61287.1"
                     /db_xref="GI:2197071"
                     /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPITTAGPGRSCLDYSQ
                     NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                     ETSLITNGHCLASGKTSFMTTLCLRSIYKDLKMYHMEFQAINAKLLMDPKRQVSLDQN
                     MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
ORIGIN

Alignment Scores:
Pred. No.:              2.17e-35        Length:         690
Score:                  42.00           Matches:        42
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            22.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x AF003542 (1-690)

Qy         17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy         37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy         57 GluLeu 58
              ||||||
Db        271 GAATTA 276

RESULT 58
BTU14416
LOCUS       BTU14416                690 bp    mRNA    linear   MAM 27-JAN-1996
DEFINITION  Bos taurus interleukin 12 35 kDa subunit mRNA, complete cds.
ACCESSION   U14416
VERSION     U14416.1  GI:555917
KEYWORDS    .
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Zarlenga,D.S., Canals,A., Aschenbrenner,R.A. and Gasbarre,L.C.
  TITLE     Enzymatic amplification and molecular cloning of cDNA encoding the
            small and large subunits of bovine interleukin 12
  JOURNAL   Biochim. Biophys. Acta 1270 (2-3), 215-217 (1995)
  PUBMED    7727547
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Zarlenga,D.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-SEP-1994) Dante S. Zarlenga, U.S. Department of
            Agriculture, ARS, LPSI, PIL, Beltsville, MD 20705, USA
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="BIL12 35"
                     /sex="male"
                     /cell_type="lymphocytes and macrophages"
                     /tissue_type="lymphoid"
     CDS             1. .666
                     /codon_start=1
                     /product="interleukin 12 35 kDa subunit"
                     /protein_id="AAA85810.1"
                     /db_xref="GI:555918"
                     /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                     NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                     ETSFITNGHCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQN
                     MLAAIAELMQALNFDSETVPQKPSLKELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
ORIGIN

Alignment Scores:
Pred. No.:              2.17e-35        Length:         690
Score:                  42.00           Matches:        42
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            22.5%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x BTU14416 (1-690)

Qy         17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy         37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy         57 GluLeu 58
              ||||||
Db        271 GAATTA 276

RESULT 59
CEU57751
LOCUS       CEU57751                666 bp    mRNA    linear   MAM 28-OCT-1999
DEFINITION  Cervus elaphus interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U57751
VERSION     U57751.1  GI:1373385
KEYWORDS    .
SOURCE      Cervus elaphus (red deer)
  ORGANISM  Cervus elaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
```

```
            Pecora; Cervidae; Cervinae; Cervus.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Lockhart,E., Slobbe,L. and Buchan,G.
  TITLE     The characterisation of a cervine immunoregulatory cytokine,
            interleukin 12
  JOURNAL   DNA Seq. 10 (2), 139-148 (1999)
   PUBMED   10376218
REFERENCE   2  (bases 1 to 666)
  AUTHORS   Lockhart,E.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAY-1996) Euan A. Lockhart, Microbiology, University
            of Otago, Cumberland St, Dunedin, New Zealand
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Cervus elaphus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9860"
                     /cell_type="peripheral blood mononuclear cells"
     CDS             1. .666
                     /note="IL-12 p35 subunit"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB02257.1"
                     /db_xref="GI:1373386"
                     /translation="MCPLRSLLLLSTLVLLHHLPHLSLGRSLPPTTAGPGRSCLNYSQ
                     NLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLVSR
                     ETSLITHGSCLASGKTSFMTTLCLKSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQN
                     MLAAIAELMQALNFNSETVPQKPSLEEMDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
     primer_bind     1. .17
     primer_bind     complement(658. .666)
ORIGIN

Alignment Scores:
Pred. No.:                3.06e-33        Length:         666
Score:                    40.00           Matches:        40
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              21.4%           Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-102 (1-187) x CEU57751 (1-666)

Qy          19 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 38
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         157 ACACTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 216

Qy          39 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         217 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 276

RESULT 60
AB107653
LOCUS       AB107653                669 bp    mRNA    linear   MAM 29-APR-2004
DEFINITION  Lama glama IL-12 p35 mRNA for interleukin 12 p35 subunit, complete
            cds.
ACCESSION   AB107653
VERSION     AB107653.1  GI:29603616
KEYWORDS    .
SOURCE      Lama glama (llama)
  ORGANISM  Lama glama
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
            Camelidae; Lama.
REFERENCE   1
  AUTHORS   Odbileg,R., Lee,S.I., Yoshida,R., Chang,K.S., Ohashi,K.,
            Sugimoto,C. and Onuma,M.
  TITLE     Cloning and sequence analysis of llama cytokines related to
            cell-mediated immunity
  JOURNAL   Vet. Immunol. Immunopathol. 99 (1-2), 1-10 (2004)
   PUBMED   15113649
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Ohashi,K., Raadan,O. and Lee,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2003) Kazuhiko Ohashi, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control; Kita-ku Kita 18 Nishi 9, Sapporo, Hokkaido 060-0818, Japan
            (E-mail:okazu@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
            Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Lama glama"
                     /mol_type="mRNA"
                     /db_xref="taxon:9844"
                     /sex="Female"
                     /cell_type="PBMC"
                     /country="Japan"
     gene            1. .669
                     /gene="IL-12 p35"
     CDS             1. .669
                     /gene="IL-12 p35"
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="BAC75390.1"
                     /db_xref="GI:29603617"
                     /translation="MCPLRSLFLMATLVFLNHLDHLSLARSLPTTTAGPGMFQCLSHS
                     QNLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLAS
                     RETSLITHGSCLASGKTSFMTTLCLSSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQ
                     NMLVAIAELMQALNVSGETVPQKPSLEEPDFYKTKVKLCILLHAFRIRAVTIDRMMSY
                     LSSS"
ORIGIN

Alignment Scores:
Pred. No.:                3.07e-33        Length:         669
Score:                    40.00           Matches:        40
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              21.4%           Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-102 (1-187) x AB107653 (1-669)

Qy          19 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 38
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 ACACTTCAGAAGGCCAGACAAACCCTAGAATTTTACTCTTGCACTTCTGAAGAGATTGAC 219

Qy          39 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

RESULT 61
AB246672
LOCUS       AB246672                669 bp    mRNA    linear   MAM 12-JAN-2006
DEFINITION  Camelus bactrianus IL-12p35 mRNA for interleukin-12p35, complete
            cds.
ACCESSION   AB246672
VERSION     AB246672.1  GI:84794455
KEYWORDS    .
SOURCE      Camelus bactrianus (Bactrian camel)
  ORGANISM  Camelus bactrianus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
            Camelidae; Camelus.
REFERENCE   1
  AUTHORS   Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Molecular cloning and sequence analysis of Th1 and Th2 cytokine
            cDNAs from the bactrian camel (Camelus bactrianus)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-2006) Odbileg Raadan, Graduate School of
            Veterinary Medicine, Hokkaido University, Disease Control,
            Laboratory of Infectious Disease; Kita ku, Kita-18, Nishi-9,
            Sapporo, Hokkaido 060-0818, Japan
            (E-mail:odbileg@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
```

```
          Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Camelus bactrianus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9837"
                     /sex="female"
                     /cell_type="PBMC"
                     /country="Japan"
     gene            1. .669
                     /gene="IL-12p35"
     CDS             1. .669
                     /gene="IL-12p35"
                     /codon_start=1
                     /product="interleukin-12p35"
                     /protein_id="BAE75803.1"
                     /db_xref="GI:84794456"
                     /translation="MCPLRSLFLMATLVFLIHLDHLSLARSLPTTTAGPGMFQCLSHS
                     QNLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLAS
                     RETSLITHGSCLASGKTPFMTTLCLSSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQ
                     NMLVAIAELMQALNVSSETVPQKPSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LSSS"
ORIGIN

Alignment Scores:
Pred. No.:              3.07e-33        Length:         669
Score:                  40.00           Matches:        40
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            21.4%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x AB246672 (1-669)

Qy         19 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 38
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ACGCTTCAGAAGGCCAGACAAACCCTAGAATTTTACTCTTGCACTTCTGAAGAGATTGAC 219

Qy         39 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

RESULT 62
E35793
LOCUS       E35793                  703 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Process for producing interleukin 12.
ACCESSION   E35793
VERSION     E35793.1  GI:18624617
KEYWORDS    JP 2000157274-A/5.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 703)
  AUTHORS   Nakamura,M., Takehara,K. and Ohara,E.
  TITLE     Process for producing interleukin 12
  JOURNAL   Patent: JP 2000157274-A 5 13-JUN-2000;
            DAI ICHI SEIYAKU CO LTD
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2000157274-A/5
            PD   13-JUN-2000
            PF   20-NOV-1998 JP 1998331052
            PR
            PI   MASAYUKI NAKAMURA,KAZUAKI TAKEHARA,EIJI OHARA PC
            C12N15/09,C07K14/54,C12N5/10,C12P21/02//(C12N15/09,C12R1:91), PC
            (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC
            (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .703
            FT                   /organism='Bos sp. (bovine)'.
FEATURES             Location/Qualifiers
     source          1. .703
                     /organism="Bos sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:29061"
ORIGIN

Alignment Scores:
Pred. No.:              3.18e-33        Length:         703
Score:                  40.00           Matches:        40
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            21.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x E35793 (1-703)

Qy         19 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 38
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 ACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 227

Qy         39 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 287

RESULT 63
AY191828
LOCUS       AY191828                657 bp    mRNA    linear   SYN 04-FEB-2003
DEFINITION  Synthetic construct evolved IL-12 p35 precursor, mRNA, partial cds.
ACCESSION   AY191828
VERSION     AY191828.1  GI:27729523
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Optimized expression and specific activity of IL-12 by directed
            molecular evolution
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
   PUBMED   12529500
REFERENCE   2  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
            Drive, Redwood City, CA 94063, USA
FEATURES             Location/Qualifiers
     source          1. .657
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .>657
                     /codon_start=1
                     /transl_table=11
                     /product="evolved IL-12 p35 precursor"
                     /protein_id="AAO19111.1"
                     /db_xref="GI:27729524"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRGI
                     SLITNGSCLASRKTSFMTTLCLGSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNML
                     TAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS
                     S"
     sig_peptide     1. .66
     mat_peptide     67. .657
                     /product="evolved IL-12 p35"
ORIGIN

Alignment Scores:
Pred. No.:              3.64e-32        Length:         657
Score:                  39.00           Matches:        39
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
```

```
Query Match:            20.9%       Indels:        0
DB:                     8           Gaps:          0

US-10-821-670A-102 (1-187) x AY191828 (1-657)

Qy         20 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 39
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 270

RESULT 64
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              3.65e-32    Length:        660
Score:                  39.00       Matches:       39
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            20.9%       Indels:        0
DB:                     2           Gaps:          0

US-10-821-670A-102 (1-187) x AX154614 (1-660)

Qy         20 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 39
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

RESULT 65
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              3.65e-32    Length:        660
Score:                  39.00       Matches:       39
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            20.9%       Indels:        0
DB:                     2           Gaps:          0

US-10-821-670A-102 (1-187) x AX154617 (1-660)

Qy         20 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 39
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

RESULT 66
AX154621
LOCUS       AX154621                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              3.65e-32    Length:        660
Score:                  39.00       Matches:       39
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            20.9%       Indels:        0
DB:                     2           Gaps:          0

US-10-821-670A-102 (1-187) x AX154621 (1-660)

Qy         20 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 39
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

RESULT 67
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
```

```
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              5.28e-30        Length:         660
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            19.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX154618 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 185
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

RESULT 68
PIGIL12PSU
LOCUS       PIGIL12PSU              1426 bp    mRNA    linear   MAM 09-JUL-2001
DEFINITION  Sus scrofa interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   L35765
VERSION     L35765.1  GI:927204
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 1426)
  AUTHORS   Foss,D.L. and Murtaugh,M.P.
  TITLE     Molecular cloning and mRNA expression of porcine interleukin-12
  JOURNAL   Vet. Immunol. Immunopathol. 57 (1-2), 121-134 (1997)
   PUBMED   9239844
COMMENT     On Aug 2, 1995 this sequence version replaced gi:755667.
FEATURES             Location/Qualifiers
     source          1. .1426
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /cell_type="mononuclear"
                     /tissue_type="peripheral blood"
     CDS             108. .878
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAA73897.1"
                     /db_xref="GI:927205"
                     /translation="MCSPGFGLQTSDLTCDVHPSASSRRLAVTAAPLSMCPLRNLLLV
                     ATLVLLNHLDHLSLGRSLPATTAGPGMFKCLNHSQNLLKAVSNTLQKAKQTLEFYSCT
                     SEEIDHEDITKDKTSTVEACLPLELATNESCLAARETSLITNGNCLTSGKTSFMTTLC
                     LSSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQNMLTAITELMQALNFNSETVPQKP
                     SLEELDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS"
     primer_bind     196. .216
     primer_bind     complement(859. .878)
     polyA_site      1426
ORIGIN

Alignment Scores:
Pred. No.:              1.65e-26        Length:         1426
Score:                  34.00           Matches:        34
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            18.2%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x PIGIL12PSU (1-1426)

Qy         25 GlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLys 44
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CAAACCCTAGAATTTTACTCCTGCACTTCAGAAGAGATCGATCATGAAGATATCACCAAA 446

Qy         45 AspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
              |||||||||||||||||||||||||||||||||||||||||||
Db        447 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTTGAACTA 488

RESULT 69
AX154612
LOCUS       AX154612                666 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 16 from Patent WO0140257.
ACCESSION   AX154612
VERSION     AX154612.1  GI:14536187
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 16 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              1.61e-23        Length:         666
Score:                  31.00           Matches:        31
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            16.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX154612 (1-666)

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

Qy         81 SerArgLysThrSerPheMetThrThrLeuCys 91
              |||||||||||||||||||||||||||||||
Db        343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGC 375

RESULT 70
ECIL12P35
LOCUS       ECIL12P35               669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Equus caballus mRNA for interleukin 12 p35 subunit.
ACCESSION   Y11130
VERSION     Y11130.1  GI:5441624
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1
  AUTHORS   Nicolson,L., Penha-Goncalves,M.N., Keanie,J.L., Logan,N.A.,
            Argyle,D.J. and Onions,D.E.
  TITLE     Cloning and sequencing of horse interleukin-12 and interleukin-18
            cDNAs
```

```
  JOURNAL   Immunogenetics 50 (1-2), 94-97 (1999)
   PUBMED   10541814
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-FEB-1997) L. Nicolson, Dept. of Vet. Pathology,
            University of Glasgow Vet. School, Bearsden Rd., Glasgow G61 1QH,
            UK
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Equus caballus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9796"
                     /cell_line="LPS-stimulated alveolar macrophages"
                     /cell_type="alveolar macrophages"
     gene            1. .669
                     /gene="IL-12 p35"
     CDS             1. .669
                     /gene="IL-12 p35"
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="CAA72012.1"
                     /db_xref="GI:5441625"
                     /db_xref="GOA:Q9XSQ6"
                     /db_xref="InterPro:IPR004281"
                     /db_xref="InterPro:IPR009079"
                     /db_xref="UniProtKB/Swiss-Prot:Q9XSQ6"
                     /translation="MCPPRGLLLVAILVLLNHLDHLSLARNLPTATPGPGMFQCLNHS
                     QNLLRTVSNTLQKARQTLEFYSCTSEEIDHEDITKDKSSTVAACLPLELAPNESCLAS
                     REISFITNGSCLTPGKASSMMTLCLSSIYEDLKMYQVEFKAMNAKLLIDPQRQIFLDE
                     NMLTAIDKLMQALNFNSETVPQKPSLEGLDFYKTKVKLCILLHAFRIRAVTINRMMGY
                     LNAS"
     sig_peptide     1. .69
                     /gene="IL-12 p35"
     misc_feature    1. .16
                     /gene="IL-12 p35"
                     /note="primer-derived sequence"
     misc_feature    651. .669
                     /gene="IL-12 p35"
                     /note="primer-derived sequence"
ORIGIN

Alignment Scores:
Pred. No.:              1.94e-22        Length:         669
Score:                  30.00           Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            16.0%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x ECIL12P35 (1-669)

Qy         17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 AGCAACACGCTTCAGAAGGCCAGGCAAACCCTAGAATTCTACTCCTGCACTTCTGAAGAG 213

Qy         37 IleAspHisGluAspIleThrLysAspLys 46
              ||||||||||||||||||||||||||||||
Db        214 ATCGATCATGAGGATATCACAAAAGACAAG 243

RESULT 71
AF401989
LOCUS       AF401989                1626 bp    mRNA    linear   SYN 14-FEB-2002
DEFINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION   AF401989
VERSION     AF401989.1  GI:18656516
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1626)
  AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
            Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
            Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
     source          1. .1626
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .1626
                     /note="derived from Equus caballus; N-terminal p40 subunit
                     linked by (Gly4Ser)3 linker to signal-peptide deleted p35
                     subunit"
                     /codon_start=1
                     /transl_table=11
                     /product="single chain interleukin-12"
                     /protein_id="AAL77817.1"
                     /db_xref="GI:18656517"
                     /translation="MGHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
                     MVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHL
                     LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                     LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
                     QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCSGGGGS
                     GGGGSGGGGSRNLPTATPGPGMFQCLNHSQNLLRTVSNTLQKARQTLEFYSCTSEEID
                     HEDITKDKSSTVAACLPLELAPNESCLASREISFITNGSCLTPGKASSMMTLCLSSIY
                     EDLKMYQVEFKAMNAKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETVPQKPSLEGL
                     DFYKTKVKLCILLHAFRIRAVTINRMMGYLNAS"
     primer_bind     1. .14
     misc_feature    15. .987
                     /note="interleukin-12 p40 sequence"
     misc_feature    988. .1032
                     /note="linker"
     misc_feature    1033. .1611
                     /note="interleukin-12 p35 sequence"
     primer_bind     complement(1612. .1626)
ORIGIN

Alignment Scores:
Pred. No.:              3.82e-22        Length:         1626
Score:                  30.00           Matches:        30
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            16.0%           Indels:         0
DB:                     8               Gaps:           0

US-10-821-670A-102 (1-187) x AF401989 (1-1626)

Qy         17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 AGCAACACGCTTCAGAAGGCCAGGCAAACCCTAGAATTCTACTCCTGCACTTCTGAAGAG 1170

Qy         37 IleAspHisGluAspIleThrLysAspLys 46
              ||||||||||||||||||||||||||||||
Db       1171 ATCGATCATGAGGATATCACAAAAGACAAG 1200

RESULT 72
AR008951
LOCUS       AR008951                660 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5756085.
ACCESSION   AR008951
VERSION     AR008951.1  GI:3967756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

```
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 3 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x AR008951 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 73
BD007071
LOCUS       BD007071                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007071
VERSION     BD007071.1  GI:18635442
KEYWORDS    JP 2001503257-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 2 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/2
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x BD007071 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 74
BD007079
LOCUS       BD007079                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007079
VERSION     BD007079.1  GI:18635450
KEYWORDS    JP 2001503258-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 4 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/4
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x BD007079 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 75
BD007080
LOCUS       BD007080                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007080
VERSION     BD007080.1  GI:18635451
KEYWORDS    JP 2001503258-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
```

```
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 5 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/5
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x BD007080 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

RESULT 76
BD007081
LOCUS       BD007081                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007081
VERSION     BD007081.1  GI:18635452
KEYWORDS    JP 2001503258-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 6 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/6
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x BD007081 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGGGCCGTGACCATC 627

RESULT 77
BD136037
LOCUS       BD136037                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136037
VERSION     BD136037.1  GI:23230982
KEYWORDS    JP 2002506647-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 4 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506647-A/4
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                 preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0
```

```
JS-10-821-670A-102 (1-187) x BD136037 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 78
BD136038
LOCUS       BD136038                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136038
VERSION     BD136038.1  GI:23230983
KEYWORDS    JP 2002506647-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 5 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/5
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: all optimized codons
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

JS-10-821-670A-102 (1-187) x BD136038 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

RESULT 79
BD136039
LOCUS       BD136039                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136039
VERSION     BD136039.1  GI:23230984
KEYWORDS    JP 2002506647-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 6 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/6
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: most codons optimized
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x BD136039 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGGGCCGTGACCATC 627

RESULT 80
I28592
LOCUS       I28592                  660 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5573764.
ACCESSION   I28592
VERSION     I28592.1  GI:1819368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 3 12-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
```

```
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x I28592 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 81
AX154634
LOCUS       AX154634                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 38 from Patent WO0140257.
ACCESSION   AX154634
VERSION     AX154634.1  GI:14536198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 38 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-21        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX154634 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 82
CQ829447
LOCUS       CQ829447                702 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 6 from Patent WO2004052929.
ACCESSION   CQ829447
VERSION     CQ829447.1  GI:49732783
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 6 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES             Location/Qualifiers
     source          1. .702
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="cDNA for alpha chain of IL-12"
ORIGIN

Alignment Scores:
Pred. No.:              2.42e-21        Length:         702
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x CQ829447 (1-702)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 615

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        616 GCTTTCAGAATTCGGGCAGTGACTATT 642

RESULT 83
AR052862
LOCUS       AR052862                721 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 199 from patent US 5833975.
ACCESSION   AR052862
VERSION     AR052862.1  GI:5977724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 199 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.47e-21        Length:         721
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR052862 (1-721)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 84
AR288174
LOCUS       AR288174                721 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 199 from patent US 6537594.
ACCESSION   AR288174
VERSION     AR288174.1  GI:31675453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
            genes
  JOURNAL   Patent: US 6537594-A 199 25-MAR-2003;
            Virogenetics Corporation; Troy, NY
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.47e-21       Length:         721
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            15.5%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-102 (1-187) x AR288174 (1-721)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 85
AR567161
LOCUS       AR567161                721 bp    mRNA    linear   PAT 08-OCT-2004
DEFINITION  Sequence 199 from patent US 6780407.
ACCESSION   AR567161
VERSION     AR567161.1  GI:53984803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 199 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.47e-21       Length:         721
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            15.5%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-102 (1-187) x AR567161 (1-721)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 86
BD105971
LOCUS       BD105971                762 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Animal model for evaluation of vaccines.
ACCESSION   BD105971
VERSION     BD105971.1  GI:23200789
KEYWORDS    JP 2002501375-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 21 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/21
            PD   15-JAN-2002
            PF   09-APR-1998 JP 1998543062
            PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
            09-DEC-1997 US    60/069163
            PI   LUNG JI CHANG
            PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
              C12N7/04,
            PC   A61K39/21
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              2.58e-21       Length:         762
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            15.5%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-102 (1-187) x BD105971 (1-762)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 87
CQ803343
LOCUS       CQ803343                762 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 3 from Patent WO2004035799.
ACCESSION   CQ803343
VERSION     CQ803343.1  GI:47110209
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 3 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
```

```
Alignment Scores:
Pred. No.:                2.58e-21        Length:         762
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x CQ803343 (1-762)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 88
AR533401
LOCUS       AR533401                 762 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 21 from patent US 6730512.
ACCESSION   AR533401
VERSION     AR533401.1  GI:53923067
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.-J.
  TITLE     Combination immunogene therapy
  JOURNAL   Patent: US 6730512-A 21 04-MAY-2004;
            Amdl, Inc.; Tustin, CA
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.58e-21        Length:         762
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x AR533401 (1-762)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 89
AF101062
LOCUS       AF101062                 762 bp    mRNA    linear   PRI 03-MAR-1999
DEFINITION  Homo sapiens interleukin 12 mRNA, complete cds.
ACCESSION   AF101062
VERSION     AF101062.1  GI:4323578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Liu,y., Guo,Y. and Wu,M.
  TITLE     Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
            Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Liu,Y., Guo,Y. and Wu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1998) Molecular Biology Department, Cancer
            Institute of Second Military Medical University, 800 XianYin Road,
            Shanghai 200433, P.R. China
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /map="3p12-q13.2"
                     /cell_line="lymphoblastoid B-cell line NC37"
                     /note="cells induced by phorbol 12-myristate 13 acetate
                     (PMA) and ionophore A23187"
     CDS             1. .762
                     /note="natural killer cell stimulatory factor; cytotoxic
                     lymphocyte maturation factor 35kDa subunit; p35"
                     /codon_start=1
                     /product="interleukin 12"
                     /protein_id="AAD16432.1"
                     /db_xref="GI:4323579"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
     variation       132
                     /replace="c"
     variation       732
                     /replace="c"
     variation       740
                     /replace="c"
ORIGIN

Alignment Scores:
Pred. No.:                2.58e-21        Length:         762
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       5               Gaps:           0

US-10-821-670A-102 (1-187) x AF101062 (1-762)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 90
MMU19842
LOCUS       MMU19842                 780 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Macaca mulatta interleukin-12 beta p35 subunit (IL-12b) mRNA,
            complete cds.
ACCESSION   U19842
VERSION     U19842.1  GI:644801
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
```

```
   PUBMED   7561102
REFERENCE   2  (bases 1 to 780)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /clone="RNc IL-12b"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .780
                     /gene="IL-12b"
     CDS             10. .771
                     /gene="IL-12b"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 beta p35 subunit"
                     /protein_id="AAA86707.1"
                     /db_xref="GI:644802"
                     /translation="MWPPGSASQPPPSPATATGLHPAARPEPPQCRLSMCPARSLLLV
                     ATLVLLDYLSLARNLSVATPGPEMFPCLHHSQNLLKAASNTLQKARQILEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTSFMMALCLRS
                     IYEDLKMYQVEFKTMNAKLLRDPKRQIFLDQNILGVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

Alignment Scores:
Pred. No.:                2.63e-21       Length:          780
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       5              Gaps:            0

US-10-821-670A-102 (1-187) x MMU19842 (1-780)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 711

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        712 GCTTTCAGAATTCGGGCAGTGACTATT 738

RESULT 91
AF180562
LOCUS       AF180562                 823 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P35 mRNA, complete cds.
ACCESSION   AF180562
VERSION     AF180562.1  GI:5923852
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
     source          1. .823
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /map="3p12-q13.2"
                     /cell_type="peripheral mononuclear"
     CDS             60. .821
                     /note="NKSF/CLMF; IL12p35; 35kD"
                     /codon_start=1
                     /product="interleukin 12, P35"
                     /protein_id="AAD56385.1"
                     /db_xref="GI:5923853"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

Alignment Scores:
Pred. No.:                2.74e-21       Length:          823
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       5              Gaps:            0

US-10-821-670A-102 (1-187) x AF180562 (1-823)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 761

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        762 GCTTTCAGAATTCGGGCAGTGACTATT 788

RESULT 92
BD165801
LOCUS       BD165801                 856 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165801
VERSION     BD165801.1  GI:27871613
KEYWORDS    JP 2002167400-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
  TITLE     Antibody against cytotoxic lymphocyte maturing factors
  JOURNAL   Patent: JP 2002167400-A 2 11-JUN-2002;
            PROTEIN DESIGN LABS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002167400-A/2
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
            PI   GUBLER,
            PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
            PI   ALVIN SETH STERN
            PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
              Antibody against cytotoxic lymphocyte maturing factors FH   Key
                    Location/Qualifiers
            FT   CDS              (170). .(826).
FEATURES             Location/Qualifiers
     source          1. .856
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
```

```
Pred. No.:              2.82e-21        Length:         856
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x BD165801 (1-856)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 93
CQ716168
LOCUS       CQ716168                1020 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 2102 from Patent WO02068579.
ACCESSION   CQ716168
VERSION     CQ716168.1  GI:42277025
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 2102 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1020
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              3.22e-21        Length:         1020
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x CQ716168 (1-1020)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 762

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        763 GCTTTCAGAATTCGGGCAGTGACTATT 789

RESULT 94
BC104982
LOCUS       BC104982                1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132642 IMAGE:8143985), complete cds.
ACCESSION   BC104982
VERSION     BC104982.1  GI:85397857
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRCB Plate: 3 Row: j Column: 15.
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:132642 IMAGE:8143985"
                     /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                     /clone_lib="NIH_MGC_287"
                     /note="Vector: pCR4-TOPO with reversed insert; Clone
                     identification sequence tag: TCGTTGCT"
     gene            1. .1021
                     /gene="IL12A"
                     /note="synonyms: IL-12A, NFSK, CLMF"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
     CDS             154. .915
                     /gene="IL12A"
```

```
                     /codon_start=1
                     /product="interleukin 12A, precursor"
                     /protein_id="AAI04983.1"
                     /db_xref="GI:85397858"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

Alignment Scores:
Pred. No.:                3.23e-21       Length:          1021
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       5              Gaps:            0

US-10-821-670A-102 (1-187) x BC104982 (1-1021)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 855

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        856 GCTTTCAGAATTCGGGCAGTGACTATT 882

RESULT 95
BC104984
LOCUS       BC104984                1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132644 IMAGE:8143987), complete cds.
ACCESSION   BC104984
VERSION     BC104984.1  GI:85397860
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRCB Plate: 3 Row: j Column: 17.
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:132644 IMAGE:8143987"
                     /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                     /clone_lib="NIH_MGC_287"
                     /note="Vector: pCR4-TOPO with reversed insert; Clone
                     identification sequence tag: AAATAGCC"
     gene            1. .1021
                     /gene="IL12A"
                     /note="synonyms: IL-12A, NFSK, CLMF"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
     CDS             154. .915
                     /gene="IL12A"
                     /codon_start=1
                     /product="interleukin 12A, precursor"
                     /protein_id="AAI04985.1"
                     /db_xref="GI:85397861"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

Alignment Scores:
Pred. No.:                3.23e-21       Length:          1021
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       5              Gaps:            0

US-10-821-670A-102 (1-187) x BC104984 (1-1021)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 855
```

```
Qy        169 AlaPheArgIleArgAlaValThrIle 177
              ||||||||||||||||||||||||||||
Db        856 GCTTTCAGAATTCGGGCAGTGACTATT 882

RESULT 96
AR091390
LOCUS       AR091390                1026 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5994104.
ACCESSION   AR091390
VERSION     AR091390.1  GI:10018145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 1 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.24e-21       Length:          1026
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR091390 (1-1026)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              ||||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 97
AR380496
LOCUS       AR380496                1026 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1041 from patent US 6607879.
ACCESSION   AR380496
VERSION     AR380496.1  GI:40088130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1041 19-AUG-2003;
            Incyte Corporation; Palo Alto, CA
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                3.24e-21       Length:          1026
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR380496 (1-1026)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              ||||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 98
HUMCLMF35
LOCUS       HUMCLMF35               1026 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human cytotoxic lymphocyte maturation factor 35 kDa subunit mRNA,
            complete cds.
ACCESSION   M65271 M38443
VERSION     M65271.1  GI:180623
KEYWORDS    cytotoxic lymphocyte maturation factor 35 kDa subunit; interleukin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
            Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
            and Gately,M.K.
  TITLE     Coexpression of two distinct genes is required to generate secreted
            bioactive cytotoxic lymphocyte maturation factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
   PUBMED   1674604
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             170. .829
                     /codon_start=1
                     /product="cytotoxic lymphocyte maturation factor 35 kDa
                     subunit"
                     /protein_id="AAA35694.1"
                     /db_xref="GI:180624"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
                     SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNML
                     AVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNA
                     S"
ORIGIN

Alignment Scores:
Pred. No.:                3.24e-21       Length:          1026
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       5              Gaps:            0

US-10-821-670A-102 (1-187) x HUMCLMF35 (1-1026)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              ||||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 99
AR393790
LOCUS       AR393790                1287 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6617135.
ACCESSION   AR393790
```

```
VERSION     AR393790.1  GI:40120794
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 6 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.85e-21        Length:         1287
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AR393790 (1-1287)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254

RESULT 100
AX084108
LOCUS       AX084108               1287 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 6 from Patent WO0110912.
ACCESSION   AX084108
VERSION     AX084108.1  GI:13185658
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 6 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="human Fc-p35 fusion protein coding sequence"
ORIGIN

Alignment Scores:
Pred. No.:              3.85e-21        Length:         1287
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AX084108 (1-1287)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254


Search completed: June 10, 2006, 12:08:41
Job time : 4268.27 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:43:45 ; Search time 106.602 Seconds
(without alignments)
4923.420 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 187
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2800942

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110458_27682/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rni
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05p
-USER=US10821670_@CGN_1_1_677_@runat_07062006_110458_27682 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	187	100.0	561	3	US-09-917-265A-101	Sequence 101, App
c	2	187	100.0	561	3	US-09-917-265A-103	Sequence 103, App
	3	187	100.0	591	3	US-09-917-265A-35	Sequence 35, Appl
c	4	187	100.0	591	3	US-09-917-265A-37	Sequence 37, Appl
	5	187	100.0	666	3	US-09-917-265A-32	Sequence 32, Appl
c	6	187	100.0	666	3	US-09-917-265A-34	Sequence 34, Appl
	7	187	100.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	8	187	100.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
	9	187	100.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	10	187	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
	11	185	98.9	591	3	US-09-011-143-9	Sequence 9, Appli
	12	185	98.9	591	3	US-09-302-495-9	Sequence 9, Appli
	13	185	98.9	591	3	US-10-079-616-9	Sequence 9, Appli
	14	185	98.9	689	3	US-09-011-143-26	Sequence 26, Appl
	15	185	98.9	689	3	US-09-302-495-26	Sequence 26, Appl
	16	185	98.9	689	3	US-10-079-616-26	Sequence 26, Appl
	17	185	98.9	1441	3	US-09-011-143-8	Sequence 8, Appli
	18	185	98.9	1441	3	US-09-302-495-8	Sequence 8, Appli
	19	185	98.9	1441	3	US-10-079-616-8	Sequence 8, Appli
	20	52	27.8	591	3	US-09-917-265A-49	Sequence 49, Appl
c	21	52	27.8	591	3	US-09-917-265A-51	Sequence 51, Appl
	22	52	27.8	666	3	US-09-917-265A-46	Sequence 46, Appl
c	23	52	27.8	666	3	US-09-917-265A-48	Sequence 48, Appl
	24	52	27.8	669	3	US-09-079-984A-2	Sequence 2, Appli
	25	52	27.8	669	3	US-09-079-984A-12	Sequence 12, Appl
	26	52	27.8	669	3	US-09-390-729-2	Sequence 2, Appli
	27	52	27.8	669	3	US-09-390-729-12	Sequence 12, Appl
	28	52	27.8	1455	3	US-09-917-265A-104	Sequence 104, App
c	29	52	27.8	1455	3	US-09-917-265A-106	Sequence 106, App
	30	52	27.8	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	31	52	27.8	1533	3	US-09-917-265A-68	Sequence 68, Appl
	32	52	27.8	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	33	52	27.8	1599	3	US-09-917-265A-63	Sequence 63, Appl
	34	29	15.5	601	3	US-09-949-016-20385	Sequence 20385, A
	35	29	15.5	601	3	US-09-949-016-87352	Sequence 87352, A
	36	29	15.5	660	2	US-08-186-529-3	Sequence 3, Appli
	37	29	15.5	660	2	US-08-640-386A-3	Sequence 3, Appli
	38	29	15.5	721	2	US-08-184-009-199	Sequence 199, App
	39	29	15.5	721	2	US-08-458-356-199	Sequence 199, App
	40	29	15.5	721	3	US-08-460-736-199	Sequence 199, App
	41	29	15.5	721	3	US-09-535-370-199	Sequence 199, App
	42	29	15.5	721	3	US-09-663-667-199	Sequence 199, App
	43	29	15.5	762	3	US-08-848-760B-21	Sequence 21, Appl
	44	29	15.5	762	3	US-09-826-025-21	Sequence 21, Appl
	45	29	15.5	762	5	US-09-543-679A-2890	Sequence 2890, Ap
	46	29	15.5	1019	3	US-09-949-016-2462	Sequence 2462, Ap
	47	29	15.5	1026	2	US-08-751-767A-1	Sequence 1, Appli
	48	29	15.5	1026	3	US-09-023-655-1041	Sequence 1041, Ap
	49	29	15.5	1026	3	US-09-949-016-130	Sequence 130, App
	50	29	15.5	1287	3	US-09-634-368-6	Sequence 6, Appli
	51	29	15.5	1316	2	US-08-684-687-3	Sequence 3, Appli
	52	29	15.5	1316	3	US-09-851-520-3	Sequence 3, Appli
	53	29	15.5	1364	2	US-08-265-087-3	Sequence 3, Appli
	54	29	15.5	1364	2	US-08-621-493-3	Sequence 3, Appli
	55	29	15.5	1364	2	US-08-965-688-3	Sequence 3, Appli
	56	29	15.5	1364	3	US-09-260-173-3	Sequence 3, Appli
	57	29	15.5	1395	3	US-09-924-703-5	Sequence 5, Appli
	58	29	15.5	1560	2	US-08-751-767A-11	Sequence 11, Appl
	59	29	15.5	1623	2	US-08-751-767A-9	Sequence 9, Appli
	60	29	15.5	1645	3	US-09-310-842-2	Sequence 2, Appli
	61	29	15.5	4521	5	US-09-543-679A-2893	Sequence 2893, Ap
	62	29	15.5	6139	2	US-08-751-767A-7	Sequence 7, Appli
	63	29	15.5	10764	3	US-09-949-016-11872	Sequence 11872, A
	64	29	15.5	10765	3	US-09-949-016-14204	Sequence 14204, A
	65	28	15.0	601	3	US-09-949-016-20381	Sequence 20381, A
	66	28	15.0	601	3	US-09-949-016-87348	Sequence 87348, A
	67	26	13.9	79	3	US-09-011-143-24	Sequence 24, Appl
	68	26	13.9	79	3	US-09-302-495-24	Sequence 24, Appl
	69	26	13.9	79	3	US-10-079-616-24	Sequence 24, Appl
c	70	12	6.4	36	3	US-09-011-143-25	Sequence 25, Appl
c	71	12	6.4	36	3	US-09-302-495-25	Sequence 25, Appl
c	72	12	6.4	36	3	US-10-079-616-25	Sequence 25, Appl
	73	10	5.3	39	3	US-09-917-265A-91	Sequence 91, Appl
	74	10	5.3	582	3	US-09-634-368-1	Sequence 1, Appli
	75	10	5.3	713	2	US-08-385-335A-10	Sequence 10, Appl
	76	10	5.3	1278	3	US-09-634-368-5	Sequence 5, Appli
	77	10	5.3	1569	3	US-09-634-368-12	Sequence 12, Appl
	78	10	5.3	2013	3	US-09-634-368-11	Sequence 11, Appl
	79	10	5.3	2709	3	US-09-634-368-13	Sequence 13, Appl
	80	10	5.3	6295	2	US-08-659-206A-4	Sequence 4, Appli

	81	10	5.3	7287	2	US-08-659-206A-1 Sequence 1, Appli
c	82	9	4.8	51	3	US-09-917-265A-96 Sequence 96, Appl
	83	8	4.3	25	3	US-09-396-196G-121547 Sequence 121547,
c	84	8	4.3	27	3	US-09-917-265A-90 Sequence 90, Appl
c	85	8	4.3	41	3	US-09-917-265A-92 Sequence 92, Appl
c	86	8	4.3	601	3	US-09-949-016-60737 Sequence 60737, A
c	87	8	4.3	601	3	US-09-949-016-60738 Sequence 60738, A
c	88	8	4.3	601	3	US-09-949-016-60739 Sequence 60739, A
	89	8	4.3	601	3	US-09-949-016-111391 Sequence 111391,
	90	8	4.3	601	3	US-09-949-016-111392 Sequence 111392,
c	91	8	4.3	601	3	US-09-949-016-154644 Sequence 154644,
c	92	8	4.3	601	3	US-09-949-016-154645 Sequence 154645,
	93	8	4.3	1380	3	US-09-134-000C-3234 Sequence 3234, Ap
c	94	8	4.3	1465	4	US-09-605-703B-525 Sequence 525, App
c	95	8	4.3	1570	4	US-09-605-703B-523 Sequence 523, App
c	96	8	4.3	1697	3	US-09-902-540-8882 Sequence 8882, Ap
	97	8	4.3	2792	3	US-10-104-047-458 Sequence 458, App
	98	8	4.3	2957	3	US-09-221-017B-775 Sequence 775, App
	99	8	4.3	3098	3	US-10-104-047-401 Sequence 401, App
	100	8	4.3	4447	3	US-09-949-016-15763 Sequence 15763, A
c	101	8	4.3	4623	3	US-09-949-016-15769 Sequence 15769, A
c	102	8	4.3	9937	3	US-09-902-540-946 Sequence 946, App
c	103	8	4.3	45086	3	US-09-949-016-14816 Sequence 14816, A
	104	8	4.3	275110	3	US-09-949-016-12706 Sequence 12706, A
	105	8	4.3	275110	3	US-09-949-016-16070 Sequence 16070, A
c	106	8	4.3	283538	3	US-09-949-016-13506 Sequence 13506, A
c	107	7	3.7	21	3	US-09-011-143-17 Sequence 17, Appl
c	108	7	3.7	21	3	US-09-011-143-18 Sequence 18, Appl
c	109	7	3.7	21	3	US-09-302-495-17 Sequence 17, Appl
c	110	7	3.7	21	3	US-09-302-495-18 Sequence 18, Appl
c	111	7	3.7	21	3	US-10-079-616-17 Sequence 17, Appl
c	112	7	3.7	21	3	US-10-079-616-18 Sequence 18, Appl
	113	7	3.7	32	2	US-08-859-998-383 Sequence 383, App
	114	7	3.7	32	3	US-09-225-928-383 Sequence 383, App
	115	7	3.7	32	3	US-09-225-201B-383 Sequence 383, App
c	116	7	3.7	39	3	US-09-079-984A-16 Sequence 16, Appl
c	117	7	3.7	39	3	US-09-390-729-16 Sequence 16, Appl
c	118	7	3.7	146	3	US-09-513-999C-35664 Sequence 35664, A
c	119	7	3.7	186	3	US-09-787-986A-8 Sequence 8, Appli
	120	7	3.7	225	2	US-08-073-807A-7 Sequence 7, Appli
	121	7	3.7	233	3	US-09-513-999C-35730 Sequence 35730, A
	122	7	3.7	235	3	US-09-009-156-9 Sequence 9, Appli
	123	7	3.7	235	3	US-09-372-154-9 Sequence 9, Appli
	124	7	3.7	235	3	US-09-950-688-9 Sequence 9, Appli
	125	7	3.7	270	3	US-09-248-796A-12538 Sequence 12538, A
c	126	7	3.7	271	3	US-09-313-294A-848 Sequence 848, App
	127	7	3.7	299	3	US-09-313-294A-786 Sequence 786, App
	128	7	3.7	301	3	US-09-270-767-2250 Sequence 2250, Ap
	129	7	3.7	301	3	US-09-270-767-17532 Sequence 17532, A
	130	7	3.7	323	3	US-09-009-156-8 Sequence 8, Appli
	131	7	3.7	323	3	US-09-372-154-8 Sequence 8, Appli
	132	7	3.7	323	3	US-09-392-184-25 Sequence 25, Appl
	133	7	3.7	323	3	US-09-950-688-8 Sequence 8, Appli
	134	7	3.7	326	3	US-09-673-395A-64 Sequence 64, Appl
c	135	7	3.7	332	3	US-09-513-999C-11474 Sequence 11474, A
c	136	7	3.7	375	3	US-09-601-198-91 Sequence 91, Appl
c	137	7	3.7	376	3	US-09-149-476-201 Sequence 201, App
	138	7	3.7	409	3	US-09-640-211A-1395 Sequence 1395, Ap
	139	7	3.7	419	3	US-09-533-559-2175 Sequence 2175, Ap
	140	7	3.7	435	3	US-09-328-352-1934 Sequence 1934, Ap
	141	7	3.7	441	3	US-09-252-991A-14937 Sequence 14937, A
	142	7	3.7	442	3	US-09-621-976-8885 Sequence 8885, Ap
	143	7	3.7	458	3	US-09-621-976-583 Sequence 583, App
	144	7	3.7	459	3	US-09-248-796A-3939 Sequence 3939, Ap
	145	7	3.7	520	3	US-09-621-976-1422 Sequence 1422, Ap
c	146	7	3.7	524	3	US-09-621-976-3041 Sequence 3041, Ap
c	147	7	3.7	550	3	US-09-149-476-19 Sequence 19, Appl
	148	7	3.7	564	3	US-09-270-767-3283 Sequence 3283, Ap
	149	7	3.7	564	3	US-09-270-767-18565 Sequence 18565, A
	150	7	3.7	576	3	US-09-134-000C-3119 Sequence 3119, Ap
	151	7	3.7	585	3	US-09-248-796A-4233 Sequence 4233, Ap
c	152	7	3.7	600	3	US-09-270-767-29877 Sequence 29877, A
	153	7	3.7	601	3	US-09-949-016-18467 Sequence 18467, A
	154	7	3.7	601	3	US-09-949-016-18612 Sequence 18612, A
c	155	7	3.7	601	3	US-09-949-016-22576 Sequence 22576, A
c	156	7	3.7	601	3	US-09-949-016-22577 Sequence 22577, A
c	157	7	3.7	601	3	US-09-949-016-31911 Sequence 31911, A
c	158	7	3.7	601	3	US-09-949-016-31912 Sequence 31912, A
c	159	7	3.7	601	3	US-09-949-016-31913 Sequence 31913, A
	160	7	3.7	601	3	US-09-949-016-51808 Sequence 51808, A
	161	7	3.7	601	3	US-09-949-016-52134 Sequence 52134, A
	162	7	3.7	601	3	US-09-949-016-52135 Sequence 52135, A
c	163	7	3.7	601	3	US-09-949-016-61639 Sequence 61639, A
c	164	7	3.7	601	3	US-09-949-016-61761 Sequence 61761, A
	165	7	3.7	601	3	US-09-949-016-65108 Sequence 65108, A
	166	7	3.7	601	3	US-09-949-016-66314 Sequence 66314, A
	167	7	3.7	601	3	US-09-949-016-66315 Sequence 66315, A
	168	7	3.7	601	3	US-09-949-016-81866 Sequence 81866, A
	169	7	3.7	601	3	US-09-949-016-81867 Sequence 81867, A
	170	7	3.7	601	3	US-09-949-016-87978 Sequence 87978, A
	171	7	3.7	601	3	US-09-949-016-92361 Sequence 92361, A
	172	7	3.7	601	3	US-09-949-016-92362 Sequence 92362, A
	173	7	3.7	601	3	US-09-949-016-92524 Sequence 92524, A
	174	7	3.7	601	3	US-09-949-016-108354 Sequence 108354,
	175	7	3.7	601	3	US-09-949-016-108355 Sequence 108355,
c	176	7	3.7	601	3	US-09-949-016-122052 Sequence 122052,
c	177	7	3.7	601	3	US-09-949-016-122053 Sequence 122053,
c	178	7	3.7	601	3	US-09-949-016-122054 Sequence 122054,
	179	7	3.7	601	3	US-09-949-016-122071 Sequence 122071,
	180	7	3.7	601	3	US-09-949-016-122080 Sequence 122080,
	181	7	3.7	601	3	US-09-949-016-124879 Sequence 124879,
c	182	7	3.7	601	3	US-09-949-016-128338 Sequence 128338,
	183	7	3.7	601	3	US-09-949-016-134767 Sequence 134767,
	184	7	3.7	601	3	US-09-949-016-134830 Sequence 134830,
c	185	7	3.7	601	3	US-09-949-016-145822 Sequence 145822,
c	186	7	3.7	601	3	US-09-949-016-146090 Sequence 146090,
c	187	7	3.7	601	3	US-09-949-016-146358 Sequence 146358,
c	188	7	3.7	601	3	US-09-949-016-151254 Sequence 151254,
c	189	7	3.7	601	3	US-09-949-016-151255 Sequence 151255,
c	190	7	3.7	601	3	US-09-949-016-163995 Sequence 163995,
c	191	7	3.7	601	3	US-09-949-016-163996 Sequence 163996,
c	192	7	3.7	601	3	US-09-949-016-163997 Sequence 163997,
c	193	7	3.7	601	3	US-09-949-016-163998 Sequence 163998,
	194	7	3.7	601	3	US-09-949-016-165814 Sequence 165814,
	195	7	3.7	601	3	US-09-949-016-169321 Sequence 169321,
c	196	7	3.7	601	3	US-09-949-016-171145 Sequence 171145,
c	197	7	3.7	601	3	US-09-949-016-171275 Sequence 171275,
c	198	7	3.7	601	3	US-09-949-016-173794 Sequence 173794,
c	199	7	3.7	601	3	US-09-949-016-173795 Sequence 173795,
c	200	7	3.7	601	3	US-09-949-016-187055 Sequence 187055,

ALIGNMENTS

```
RESULT 1
US-09-917-265A-101
; Sequence 101, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
```

; LOCATION: (1)..(561)
US-09-917-265A-101

Alignment Scores:

Pred. No.:	4.16e-185	Length:	561
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265A-101 (1-561)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
```

RESULT 2
US-09-917-265A-103/c
; Sequence 103, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus

US-09-917-265A-103

Alignment Scores:

Pred. No.:	4.16e-185	Length:	561
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265A-103 (1-561)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 3
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:

```
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
JS-09-917-265A-35

Alignment Scores:
Pred. No.:              4.37e-185       Length:         591
Score:                  187.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-35 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591

RESULT 4
JS-09-917-265A-37/c
; Sequence 37, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-37

Alignment Scores:
Pred. No.:              4.37e-185       Length:         591
Score:                  187.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-37 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
```

```
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-32

Alignment Scores:
Pred. No.:                4.89e-185       Length:         666
Score:                    187.00          Matches:        187
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-32 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666

RESULT 6
US-09-917-265A-34/c
; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

Alignment Scores:
Pred. No.:                4.89e-185       Length:         666
Score:                    187.00          Matches:        187
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-34 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 7
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
```

```
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1533)
/S-09-917-265A-43

Alignment Scores:
Pred. No.:              1.07e-184      Length:          1533
Score:                  187.00         Matches:         187
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-917-265A-43 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533

RESULT 8
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;  LENGTH: 1533
;  TYPE: DNA
;  ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.:              1.07e-184      Length:          1533
Score:                  187.00         Matches:         187
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-917-265A-45 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;  LENGTH: 1599
```

```
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:
Pred. No.:                1.12e-184       Length:         1599
Score:                    187.00          Matches:        187
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-38 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599

RESULT 10
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:                1.12e-184       Length:         1599
Score:                    187.00          Matches:        187
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-40 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 11
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
```

```
      COUNTRY:  USA
      ZIP:  20004
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/011,143
      FILING DATE:  04-FEB-1998
      CLASSIFICATION:  536
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  PCT/JP97/01824
      FILING DATE:  29-MAY-1997
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  JP 165249/1996
      FILING DATE:  04-JUN-1996
    ATTORNEY/AGENT INFORMATION:
      NAME:  BROWDY, Roger L.
      REGISTRATION NUMBER:  25,618
      REFERENCE/DOCKET NUMBER:  IMAMURA=1
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  202-628-5197
      TELEFAX:  202-737-3528
  INFORMATION FOR SEQ ID NO:  9:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  591 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
JS-09-011-143-9

Alignment Scores:
Pred. No.:              5.23e-183     Length:          591
Score:                  185.00        Matches:         185
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            98.9%         Indels:          0
DB:                     3             Gaps:            0

US-10-821-670A-102 (1-187) x US-09-011-143-9 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsn 185
              ||||||||||||||||
Db        571 ATGAGCTACCTGAAT 585

RESULT 12
US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

Alignment Scores:
Pred. No.:              5.23e-183     Length:          591
Score:                  185.00        Matches:         185
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            98.9%         Indels:          0
DB:                     3             Gaps:            0

US-10-821-670A-102 (1-187) x US-09-302-495-9 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsn 185
                |||||||||||||||
Db        571 ATGAGCTACCTGAAT 585

RESULT 13
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 591 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

Alignment Scores:
Pred. No.:                5.23e-183       Length:          591
Score:                    185.00          Matches:         185
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              98.9%           Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-102 (1-187) x US-10-079-616-9 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsn 185
                |||||||||||||||
Db        571 ATGAGCTACCTGAAT 585

RESULT 14
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
```

```
    APPLICANT:  IMAMURA, Takayuki
    APPLICANT:  MAEDA, Hiroaki
    APPLICANT:  FUJIYASU, Takeshi
    APPLICANT:  IMAGAWA, Yoshitaka
    APPLICANT:  TOKIYOSHI, Sachio
    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
    NUMBER OF SEQUENCES:  26
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  BROWDY AND NEIMARK
      STREET:  419 Seventh Street, N.W., Suite 300
      CITY:  Washington
      STATE:  D.C.
      COUNTRY:  USA
      ZIP:  20004
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/011,143
      FILING DATE:  04-FEB-1998
      CLASSIFICATION:  536
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  PCT/JP97/01824
      FILING DATE:  29-MAY-1997
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  JP 165249/1996
      FILING DATE:  04-JUN-1996
    ATTORNEY/AGENT INFORMATION:
      NAME:  BROWDY, Roger L.
      REGISTRATION NUMBER:  25,618
      REFERENCE/DOCKET NUMBER:  IMAMURA=1
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  202-628-5197
      TELEFAX:  202-737-3528
  INFORMATION FOR SEQ ID NO:  26:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  689 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
S-09-011-143-26

lignment Scores:
red. No.:              6.05e-183     Length:        689
core:                  185.00        Matches:       185
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            98.9%         Indels:        0
B:                     3             Gaps:          0

S-10-821-670A-102 (1-187) x US-09-011-143-26 (1-689)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        652 ATGAGCTACCTGAAT 666

RESULT 15
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26
```

```
Alignment Scores:
Pred. No.:                6.05e-183       Length:          689
Score:                    185.00          Matches:         185
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              98.9%           Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-102 (1-187) x US-09-302-495-26 (1-689)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        652 ATGAGCTACCTGAAT 666

RESULT 16
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

Alignment Scores:
Pred. No.:                6.05e-183       Length:          689
Score:                    185.00          Matches:         185
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              98.9%           Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-102 (1-187) x US-10-079-616-26 (1-689)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsn 185
                ||||||||||||||||
Db        652 ATGAGCTACCTGAAT 666

RESULT 17
US-09-011-143-8
  Sequence 8, Application US/09011143
  Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
     APPLICANT:  MAEDA, Hiroaki
     APPLICANT:  FUJIYASU, Takeshi
     APPLICANT:  IMAGAWA, Yoshitaka
     APPLICANT:  TOKIYOSHI, Sachio
     TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
     NUMBER OF SEQUENCES:  26
     CORRESPONDENCE ADDRESS:
       ADDRESSEE:  BROWDY AND NEIMARK
       STREET:  419 Seventh Street, N.W., Suite 300
       CITY:  Washington
       STATE:  D.C.
       COUNTRY:  USA
       ZIP:  20004
     COMPUTER READABLE FORM:
       MEDIUM TYPE:  Floppy disk
       COMPUTER:  IBM PC compatible
       OPERATING SYSTEM:  PC-DOS/MS-DOS
       SOFTWARE:  PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
       APPLICATION NUMBER:  US/09/011,143
       FILING DATE:  04-FEB-1998
       CLASSIFICATION:  536
     PRIOR APPLICATION DATA:
       APPLICATION NUMBER:  PCT/JP97/01824
       FILING DATE:  29-MAY-1997
     PRIOR APPLICATION DATA:
       APPLICATION NUMBER:  JP 165249/1996
       FILING DATE:  04-JUN-1996
     ATTORNEY/AGENT INFORMATION:
       NAME:  BROWDY, Roger L.
       REGISTRATION NUMBER:  25,618
       REFERENCE/DOCKET NUMBER:  IMAMURA=1
     TELECOMMUNICATION INFORMATION:
       TELEPHONE:  202-628-5197
       TELEFAX:  202-737-3528
   INFORMATION FOR SEQ ID NO:  8:
     SEQUENCE CHARACTERISTICS:
       LENGTH:  1441 base pairs
       TYPE:  nucleic acid
       STRANDEDNESS:  single
       TOPOLOGY:  linear
     MOLECULE TYPE:  cDNA
US-09-011-143-8

Alignment Scores:
Pred. No.:              1.21e-182       Length:         1441
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
FB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-011-143-8 (1-1441)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 427

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 487

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 547

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 607

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 667

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 727

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 787

Qy        181 MetSerTyrLeuAsn 185
                ||||||||||||||||
Db        788 ATGAGCTACCTGAAT 802

RESULT 18
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
```

```
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-302-495-8

Alignment Scores:
Pred. No.:              1.21e-182      Length:          1441
Score:                  185.00         Matches:         185
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            98.9%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-302-495-8 (1-1441)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 427

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 487

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 547

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 607

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 667

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 727

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 787

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        788 ATGAGCTACCTGAAT 802

RESULT 19
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

Alignment Scores:
Pred. No.:              1.21e-182      Length:          1441
Score:                  185.00         Matches:         185
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            98.9%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-102 (1-187) x US-10-079-616-8 (1-1441)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 427

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 487

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 547

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          548 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 607

y          121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          608 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 667

y          141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          668 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 727

y          161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          728 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 787

y          181 MetSerTyrLeuAsn 185
                ||||||||||||||||
b          788 ATGAGCTACCTGAAT 802

ESULT 20
S-09-917-265A-49
 Sequence 49, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 49
   LENGTH: 591
   TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(591)
S-09-917-265A-49

lignment Scores:
red. No.:              8.56e-45       Length:         591
core:                  52.00          Matches:        52
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            27.8%          Indels:         0
B:                     3              Gaps:           0

S-10-821-670A-102 (1-187) x US-09-917-265A-49 (1-591)

y           30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

y           50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

y           70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
b          238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

ESULT 21
S-09-917-265A-51/c
 Sequence 51, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 51
   LENGTH: 591
   TYPE: DNA
   ORGANISM: Canis familiaris
US-09-917-265A-51

Alignment Scores:
Pred. No.:              8.56e-45       Length:         591
Score:                  52.00          Matches:        52
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            27.8%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-51 (1-591)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 22
US-09-917-265A-46
; Sequence 46, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-46

Alignment Scores:
Pred. No.:              9.58e-45       Length:         666
Score:                  52.00          Matches:        52
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            27.8%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-46 (1-666)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
                |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 23
US-09-917-265A-48/c
; Sequence 48, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-48

Alignment Scores:
Pred. No.:                9.58e-45        Length:         666
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-48 (1-666)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
                |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 24
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

Alignment Scores:
Pred. No.:                9.62e-45        Length:         669
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-079-984A-2 (1-669)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
                |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 25
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
```

```
      MEDIUM TYPE:  Floppy Disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  WordPerfect 5.1
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/079,984A
      FILING DATE:  15-MAY-1998
    ATTORNEY/AGENT INFORMATION:
      NAME:  Austin R. Miller
      REGISTRATION NUMBER:  16,602
      REFERENCE/DOCKET NUMBER:  1051-98
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (215) 563-1810
      TELEFAX:  (215) 568-6946
  INFORMATION FOR SEQ ID NO:  12:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  669 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA to mRNA
    ORIGINAL SOURCE:
      ORGANISM:  Canis familiaris
    FEATURE:
      NAME/KEY:  Canine IL12
      LOCATION:  1 to 666
      IDENTIFICATION METHOD:  Similarity
S-09-079-984A-12

lignment Scores:
red. No.:              9.62e-45      Length:        669
core:                  52.00         Matches:       52
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            27.8%         Indels:        0
B:                     3             Gaps:          0

S-10-821-670A-102 (1-187) x US-09-079-984A-12 (1-669)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
b        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

ESULT 26
S-09-390-729-2
  Sequence 2, Application US/09390729
  Patent No. 6562334
  GENERAL INFORMATION:
    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
    APPLICANT:  Yamada, Katsushige
    TITLE OF INVENTION:  Canine interleukin 12, a production method
    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
    TITLE OF INVENTION:  method using it
    NUMBER OF SEQUENCES:  16
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Miller & Christenbury Intellectual Property
      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
      STREET:  1600 Market Street, 39th Floor
      CITY:  Philadelphia
      STATE:  PA
      COUNTRY:  USA
      ZIP:  19103
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy Disk
      COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/390,729
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  09/079,984
;     FILING DATE:  15-MAY-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Austin R. Miller
;     REGISTRATION NUMBER:  16,602
;     REFERENCE/DOCKET NUMBER:  1051-98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-1810
;     TELEFAX:  (215) 568-6946
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  669 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM:  Canis familiaris
;   FEATURE:
;     NAME/KEY:  Canine IL12
;     LOCATION:  1 to 666
;     IDENTIFICATION METHOD:  Similarity
US-09-390-729-2

Alignment Scores:
Pred. No.:              9.62e-45      Length:        669
Score:                  52.00         Matches:       52
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            27.8%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-102 (1-187) x US-09-390-729-2 (1-669)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 27
US-09-390-729-12
; Sequence 12, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
```

```
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
JS-09-390-729-12

Alignment Scores:
Pred. No.:                9.62e-45        Length:         669
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       3               Gaps:           0

JS-10-821-670A-102 (1-187) x US-09-390-729-12 (1-669)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 28
JS-09-917-265A-104
; Sequence 104, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-09-917-265A-104

Alignment Scores:
Pred. No.:                2e-44           Length:         1455
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-104 (1-1455)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

RESULT 29
US-09-917-265A-106/c
; Sequence 106, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-106

Alignment Scores:
Pred. No.:                2e-44           Length:         1455
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-106 (1-1455)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

RESULT 30
US-09-917-265A-66
```

```
  Sequence 66, Application US/09917265A
  Patent No. 6818444
  GENERAL INFORMATION:
   APPLICANT: Wonderling, Ramani S.
   APPLICANT:  Boroughs, Karen L.
   TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
   TITLE OF INVENTION:  THEREOF
   FILE REFERENCE: IM-5
   CURRENT APPLICATION NUMBER: US/09/917,265A
   CURRENT FILING DATE:  2001-07-27
   PRIOR APPLICATION NUMBER: 60/223,016
   PRIOR FILING DATE: 2000-08-04
   NUMBER OF SEQ ID NOS: 111
   SOFTWARE: PatentIn version 3.2
  SEQ ID NO 66
    LENGTH: 1533
    TYPE: DNA
    ORGANISM: Canis familiaris
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)..(1533)
S-09-917-265A-66

lignment Scores:
red. No.:              2.1e-44        Length:        1533
core:                  52.00          Matches:       52
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            27.8%          Indels:        0
B:                     3              Gaps:          0

S-10-821-670A-102 (1-187) x US-09-917-265A-66 (1-1533)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
b       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

ESULT 31
S-09-917-265A-68/c
 Sequence 68, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 68
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Canis familiaris
S-09-917-265A-68

lignment Scores:
red. No.:              2.1e-44        Length:        1533
core:                  52.00          Matches:       52
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            27.8%          Indels:        0
B:                     3              Gaps:          0

S-10-821-670A-102 (1-187) x US-09-917-265A-68 (1-1533)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 32
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

Alignment Scores:
Pred. No.:             2.19e-44       Length:        1599
Score:                 52.00          Matches:       52
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           27.8%          Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265A-61 (1-1599)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db      1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 33
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
```

```
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
JS-09-917-265A-63

Alignment Scores:
Pred. No.:                2.19e-44      Length:          1599
Score:                    52.00         Matches:         52
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              27.8%         Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-102 (1-187) x US-09-917-265A-63 (1-1599)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 34
US-09-949-016-20385
; Sequence 20385, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20385
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
JS-09-949-016-20385

Alignment Scores:
Pred. No.:                6.94e-21      Length:          601
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-102 (1-187) x US-09-949-016-20385 (1-601)

Qy         149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          91 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 150

Qy         169 AlaPheArgIleArgAlaValThrIle 177
               |||||||||||||||||||||||||
Db         151 GCTTTCAGAATTCGGGCAGTGACTATT 177

RESULT 35
US-09-949-016-87352
; Sequence 87352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87352
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87352

Alignment Scores:
Pred. No.:                6.94e-21      Length:          601
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-102 (1-187) x US-09-949-016-87352 (1-601)

Qy         149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          91 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 150

Qy         169 AlaPheArgIleArgAlaValThrIle 177
               |||||||||||||||||||||||||
Db         151 GCTTTCAGAATTCGGGCAGTGACTATT 177

RESULT 36
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
'S-08-186-529-3

lignment Scores:
red. No.:              7.58e-21       Length:        660
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-102 (1-187) x US-08-186-529-3 (1-660)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b       601 GCTTTCAGAATTCGGGCAGTGACTATT 627

ESULT 37
S-08-640-386A-3
 Sequence 3, Application US/08640386A
 Patent No. 5756085
  GENERAL INFORMATION:
    APPLICANT:  Sykes, Megan
    APPLICANT:  Wolf, Stanley F.
    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
    NUMBER OF SEQUENCES:  4
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
      STREET:  87 CambridgePark Drive
      CITY:  Cambridge
      STATE:  MA
      COUNTRY:  USA
      ZIP:  02140
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/640,386A
      FILING DATE:
      CLASSIFICATION:  424
    ATTORNEY/AGENT INFORMATION:
      NAME:  Brown, Scott A.
      REGISTRATION NUMBER:  32,724
      REFERENCE/DOCKET NUMBER:  GI 5225A
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

Alignment Scores:
Pred. No.:              7.58e-21       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-102 (1-187) x US-08-640-386A-3 (1-660)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||
Db       601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 38
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
```

```
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
JS-08-184-009-199

Alignment Scores:
Pred. No.:                8.24e-21        Length:         721
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       2               Gaps:           0

JS-10-821-670A-102 (1-187) x US-08-184-009-199 (1-721)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 39
JS-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
JS-08-458-356-199

Alignment Scores:
Pred. No.:                8.24e-21        Length:         721
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x US-08-458-356-199 (1-721)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 40
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

Alignment Scores:
Pred. No.:                8.24e-21        Length:         721
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-08-460-736-199 (1-721)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661
```

```
y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
b        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

ESULT 41
S-09-535-370-199
 Sequence 199, Application US/09535370
 Patent No. 6537594
   GENERAL INFORMATION:
        APPLICANT: Paoletti, Enzo
                   Tartaglia, James
                   Cox, William I.
        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
        NUMBER OF SEQUENCES: 217
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: Curtis, Morris & Safford
             STREET: 530 Fifth Avenue
             CITY: New York
             STATE: NY
             COUNTRY: USA
             ZIP: 10036
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.25
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/535,370
             FILING DATE: 24-Mar-2000
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 08/460,736
             FILING DATE: <Unknown>
        ATTORNEY/AGENT INFORMATION:
             NAME: Frommer, William S.
             REGISTRATION NUMBER: 25,506
             REFERENCE/DOCKET NUMBER: 454310-2530
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (212) 840-3333
             TELEFAX: (212) 840-0712
             TELEX: 425066CURTMS
    INFORMATION FOR SEQ ID NO: 199:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 721 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
S-09-535-370-199

lignment Scores:
red. No.:                8.24e-21        Length:         721
core:                    29.00           Matches:        29
ercent Similarity:       100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              15.5%           Indels:         0
B:                       3               Gaps:           0

S-10-821-670A-102 (1-187) x US-09-535-370-199 (1-721)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
b        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

ESULT 42
S-09-663-667-199
; Sequence 199, Application US/09663667
; Patent No. 6780407
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,667
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/184,009
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;    INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-663-667-199

Alignment Scores:
Pred. No.:                8.24e-21        Length:         721
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-663-667-199 (1-721)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
Db       662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 43
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
```

```
;            CITY: Gainesville
;            STATE: Florida
;            COUNTRY: United States of America
;            ZIP: 32606
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/848,760B
;            FILING DATE: 25-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: 09-APR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: PACE, DORAN R.
;            REGISTRATION NUMBER: 38,261
;            REFERENCE/DOCKET NUMBER: CNG-100C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (352) 375-8100
;            TELEFAX: (352) 372-5800
;  INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
JS-08-848-760B-21

Alignment Scores:
Pred. No.:              8.68e-21      Length:        762
Score:                  29.00         Matches:       29
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            15.5%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-102 (1-187) x US-08-848-760B-21 (1-762)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||
Db       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 44
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. 6730512
;  GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/826,025
;            FILING DATE: 04-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;  INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

Alignment Scores:
Pred. No.:              8.68e-21      Length:        762
Score:                  29.00         Matches:       29
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            15.5%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-102 (1-187) x US-09-826-025-21 (1-762)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||
Db       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 45
US-09-543-679A-2890
; Sequence 2890, Application US/09543679A
; Patent No. 7034007
;  GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
```

```
            NAME: Amzel, Viviana
            REGISTRATION NUMBER: 30,930
            REFERENCE/DOCKET NUMBER: EPI-0067191b
         TELECOMMUNICATION INFORMATION:
            TELEPHONE: 609-409-3035
            TELEFAX: 413-254-9245
            TELEX: <Unknown>
   INFORMATION FOR SEQ ID NO: 2890:
         SEQUENCE CHARACTERISTICS:
            LENGTH: 762 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
         SEQUENCE DESCRIPTION: SEQ ID NO: 2890:
S-09-543-679A-2890

lignment Scores:
red. No.:               8.68e-21        Length:         762
core:                   29.00           Matches:        29
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             15.5%           Indels:         0
B:                      5               Gaps:           0

S-10-821-670A-102 (1-187) x US-09-543-679A-2890 (1-762)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||||
b       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

ESULT 46
S-09-949-016-2462
 Sequence 2462, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
  APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
  CURRENT APPLICATION NUMBER: US/09/949,016
  CURRENT FILING DATE:  2000-04-14
  PRIOR APPLICATION NUMBER: 60/241,755
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/237,768
  PRIOR FILING DATE: 2000-10-03
  PRIOR APPLICATION NUMBER: 60/231,498
  PRIOR FILING DATE: 2000-09-08
  NUMBER OF SEQ ID NOS: 207012
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2462
    LENGTH: 1019
    TYPE: DNA
    ORGANISM: Human
S-09-949-016-2462

lignment Scores:
red. No.:               1.14e-20        Length:         1019
core:                   29.00           Matches:        29
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             15.5%           Indels:         0
B:                      3               Gaps:           0

S-10-821-670A-102 (1-187) x US-09-949-016-2462 (1-1019)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       703 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 762

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||||
Db      763 GCTTTCAGAATTCGGGCAGTGACTATT 789

RESULT 47
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  170..826
US-08-751-767A-1

Alignment Scores:
Pred. No.:              1.15e-20        Length:         1026
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x US-08-751-767A-1 (1-1026)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||||
Db      770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 48
US-09-023-655-1041
; Sequence 1041, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
```

```
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1041:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g180623
JS-09-023-655-1041

Alignment Scores:
Pred. No.:                1.15e-20        Length:         1026
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       3               Gaps:           0

JS-10-821-670A-102 (1-187) x US-09-023-655-1041 (1-1026)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 49
JS-09-949-016-130
; Sequence 130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-130

Alignment Scores:
Pred. No.:                1.15e-20        Length:         1026
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-949-016-130 (1-1026)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 50
US-09-634-368-6
; Sequence 6, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-09-634-368-6

Alignment Scores:
Pred. No.:                1.42e-20        Length:         1287
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-634-368-6 (1-1287)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254
```

```
ESULT 51
S-08-684-687-3
 Sequence 3, Application US/08684687
 Patent No. 5830451
  GENERAL INFORMATION:
    APPLICANT:  KIEFF, ELLIOTT D.
    APPLICANT:  DEVERGNE, ODILE
    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
    TITLE OF INVENTION:  THEREFOR
    NUMBER OF SEQUENCES:  8
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
      STREET:  600 ATLANTIC AVENUE
      CITY:  BOSTON
      STATE:  MA
      COUNTRY:  USA
      ZIP:  02210
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/684,687
      FILING DATE:
      CLASSIFICATION:  514
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  60/005,092
      FILING DATE:  11-OCT-1995
    ATTORNEY/AGENT INFORMATION:
      NAME:  GATES, EDWARD R.
      REGISTRATION NUMBER:  31,616
      REFERENCE/DOCKET NUMBER:  B0801/7051
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  617-720-3500
      TELEFAX:  617-720-2441
  INFORMATION FOR SEQ ID NO:  3:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  1316 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA to mRNA
    HYPOTHETICAL:  NO
    ANTI-SENSE:  NO
    ORIGINAL SOURCE:
      ORGANISM:  HOMO SAPIENS
    FEATURE:
      NAME/KEY:  CDS
      LOCATION:  102..863
S-08-684-687-3

lignment Scores:
red. No.:              1.45e-20       Length:        1316
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-102 (1-187) x US-08-684-687-3 (1-1316)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b       804 GCTTTCAGAATTCGGGCAGTGACTATT 830

ESULT 52
S-09-851-520-3
 Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

Alignment Scores:
Pred. No.:              1.45e-20       Length:        1316
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-102 (1-187) x US-09-851-520-3 (1-1316)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
Db      804 GCTTTCAGAATTCGGGCAGTGACTATT 830

RESULT 53
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
JS-08-265-087-3

Alignment Scores:
Pred. No.:                1.5e-20        Length:          1364
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       2              Gaps:            0

JS-10-821-670A-102 (1-187) x US-08-265-087-3 (1-1364)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        803 GCTTTCAGAATTCGGGCAGTGACTATT 829

RESULT 54
JS-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
; GENERAL INFORMATION:
;   APPLICANT:  Scott, Phillip
;   APPLICANT:  Trinchieri, Giorgio
;   TITLE OF INVENTION:  Compositions and Methods for Use of
;   TITLE OF INVENTION:  IL-12 as an Adjuvant
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Howson and Howson
;     STREET:  Spring House Corporate Center, PO Box 457
;     CITY:  Spring House
;     STATE:  Pennsylvania
;     COUNTRY:  USA
;     ZIP:  19477
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/621,493
;     FILING DATE:  25-MAR-1996
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/265,087
;     FILING DATE:  17-JUN-1994
;     APPLICATION NUMBER:  US 08/229,282
;     FILING DATE:  18-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bak, Mary E.
;     REGISTRATION NUMBER:  31,215
;     REFERENCE/DOCKET NUMBER:  WST51AUSA
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  215-540-9206
;     TELEFAX:  215-540-5818
; INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1364 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  101..859
US-08-621-493-3

Alignment Scores:
Pred. No.:                1.5e-20        Length:          1364
Score:                    29.00          Matches:         29
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              15.5%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x US-08-621-493-3 (1-1364)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        803 GCTTTCAGAATTCGGGCAGTGACTATT 829

RESULT 55
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
; GENERAL INFORMATION:
;   APPLICANT:  Scott, Phillip
;   APPLICANT:  Trinchieri, Giorgio
;   TITLE OF INVENTION:  Compositions and Methods for Use of
;   TITLE OF INVENTION:  IL-12 as an Adjuvant
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Howson and Howson
;     STREET:  Spring House Corporate Center, PO Box 457
;     CITY:  Spring House
;     STATE:  Pennsylvania
;     COUNTRY:  USA
;     ZIP:  19477
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/965,688
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/621,493
;     FILING DATE:  25-MAR-1996
;     APPLICATION NUMBER:  08/265,087
;     FILING DATE:  17-JUN-1994
;     APPLICATION NUMBER:  US 08/229,282
;     FILING DATE:  18-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bak, Mary E.
;     REGISTRATION NUMBER:  31,215
;     REFERENCE/DOCKET NUMBER:  WST51AUSA
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  215-540-9206
;     TELEFAX:  215-540-5818
; INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1364 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
```

LOCATION: 101..859
S-08-965-688-3

lignment Scores:
red. No.: 1.5e-20 Length: 1364
core: 29.00 Matches: 29
ercent Similarity: 100.0% Conservative: 0
est Local Similarity: 100.0% Mismatches: 0
uery Match: 15.5% Indels: 0
B: 2 Gaps: 0

S-10-821-670A-102 (1-187) x US-08-965-688-3 (1-1364)

y 149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
b 743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

y 169 AlaPheArgIleArgAlaValThrIle 177
b 803 GCTTTCAGAATTCGGGCAGTGACTATT 829

ESULT 56
S-09-260-173-3
Sequence 3, Application US/09260173
Patent No. 6168923
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/260,173
FILING DATE: 01-Mar-1999
CLASSIFICATION: <Unknown>
17-JUN-1994
18-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,688
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 101..859

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

Alignment Scores:
Pred. No.: 1.5e-20 Length: 1364
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 15.5% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-102 (1-187) x US-09-260-173-3 (1-1364)

Qy 149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
Db 743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

Qy 169 AlaPheArgIleArgAlaValThrIle 177
Db 803 GCTTTCAGAATTCGGGCAGTGACTATT 829

RESULT 57
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
; APPLICANT: TRINCHIERI, GIORGIO
; APPLICANT: PERUSSIA, BICE
; APPLICANT: CLARK, STEVEN C.
; APPLICANT: WONG, GORDON G.
; APPLICANT: HEWICK, RODNEY
; APPLICANT: KOBAYASHI, MICHIKO
; TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
; FILE REFERENCE: 01142.0142.0100
; CURRENT APPLICATION NUMBER: US/09/924,703
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/325,958
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/858,000
; PRIOR FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: 08/403,013
; PRIOR FILING DATE: 1995-03-13
; PRIOR APPLICATION NUMBER: 07/584,941
; PRIOR FILING DATE: 1990-09-18
; PRIOR APPLICATION NUMBER: 07/307,817
; PRIOR FILING DATE: 1989-02-07
; PRIOR APPLICATION NUMBER: 07/269,945
; PRIOR FILING DATE: 1988-11-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
; NAME/KEY: CDS
; LOCATION: (114)..(872)
US-09-924-703-5

Alignment Scores:
Pred. No.: 1.53e-20 Length: 1395
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 15.5% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-102 (1-187) x US-09-924-703-5 (1-1395)

Qy 149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168

```
Db        756 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 815

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        816 GCTTTCAGAATTCGGGCAGTGACTATT 842

RESULT 58
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
;   APPLICANT:  ANDERSON, ROBERT J.
;   APPLICANT:  GRANT, HUGH
;   APPLICANT:  MACDONALD, IAN D.
;   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;   NUMBER OF SEQUENCES:  80
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  NIXON & VANDERHYE P.C.
;     STREET:  1100 NORTH GLEBE ROAD
;     CITY:  ARLINGTON
;     STATE:  VA
;     COUNTRY:  USA
;     ZIP:  22201
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/751,767A
;     FILING DATE:  08-NOV-1996
;     CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  SADOFF, B.J.
;     REGISTRATION NUMBER:  36,663
;     REFERENCE/DOCKET NUMBER:  117-221
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  7038164091
;     TELEFAX:  7038164100
; INFORMATION FOR SEQ ID NO:  11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1560 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  1..1557
US-08-751-767A-11

Alignment Scores:
Pred. No.:                1.71e-20        Length:         1560
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x US-08-751-767A-11 (1-1560)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1500

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       1501 GCTTTCAGAATTCGGGCAGTGACTATT 1527

RESULT 59
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
;   APPLICANT:  ANDERSON, ROBERT J.
;   APPLICANT:  GRANT, HUGH
;   APPLICANT:  MACDONALD, IAN D.
;   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;   NUMBER OF SEQUENCES:  80
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  NIXON & VANDERHYE P.C.
;     STREET:  1100 NORTH GLEBE ROAD
;     CITY:  ARLINGTON
;     STATE:  VA
;     COUNTRY:  USA
;     ZIP:  22201
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/751,767A
;     FILING DATE:  08-NOV-1996
;     CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  SADOFF, B.J.
;     REGISTRATION NUMBER:  36,663
;     REFERENCE/DOCKET NUMBER:  117-221
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  7038164091
;     TELEFAX:  7038164100
; INFORMATION FOR SEQ ID NO:  9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1623 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  1..1620
US-08-751-767A-9

Alignment Scores:
Pred. No.:                1.77e-20        Length:         1623
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x US-08-751-767A-9 (1-1623)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1504 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1563

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       1564 GCTTTCAGAATTCGGGCAGTGACTATT 1590

RESULT 60
US-09-310-842-2
; Sequence 2, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
```

```
  NUMBER OF SEQ ID NOS: 13
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
    LENGTH: 1645
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    NAME/KEY: gene
    LOCATION: (1)..(1645)
    OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
    OTHER INFORMATION: Dumbbell
    FEATURE:
    NAME/KEY: misc_binding
    LOCATION: (1)..(2)
    OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
    OTHER INFORMATION: position 1 to 2  can be modified with amino or caroxy
    OTHER INFORMATION: features
    FEATURE:
    NAME/KEY: misc_binding
    LOCATION: (1644)..(1645)
    OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1644
    OTHER INFORMATION: to 1645  can be modified with amino or caroxy features
    FEATURE:
    OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
    OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
S-09-310-842-2

lignment Scores:
red. No.:               1.79e-20        Length:         1645
core:                   29.00           Matches:        29
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             15.5%           Indels:         0
B:                      3               Gaps:           0

S-10-821-670A-102 (1-187) x US-09-310-842-2 (1-1645)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1275 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1334

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||
b       1335 GCTTTCAGAATTCGGGCAGTGACTATT 1361

ESULT 61
S-09-543-679A-2893
 Sequence 2893, Application US/09543679A
 Patent No. 7034007
   GENERAL INFORMATION:
        APPLICANT: NYCE, Jonathan W.
        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
                            OF AIRWAY DISORDERS ASSOCIATED WITH
                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
        NUMBER OF SEQUENCES: 3111
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
             STREET: 7 Clarke Drive
             CITY: Cranbury
             STATE: NJ
             COUNTRY: USA
             ZIP: 08512
        COMPUTER READABLE FORM:
             MEDIUM TYPE: CD-R
             COMPUTER: IBM Compatible
             OPERATING SYSTEM: DOS
             SOFTWARE: N/A
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/543,679A
             FILING DATE: 13-Apr-2000
             CLASSIFICATION: UNKNOWN
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 60/127,958
             FILING DATE: 1998-08-03
        ATTORNEY/AGENT INFORMATION:
             NAME: Amzel, Viviana
             REGISTRATION NUMBER: 30,930
             REFERENCE/DOCKET NUMBER: EPI-0067191b
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: 609-409-3035
             TELEFAX: 413-254-9245
             TELEX: <Unknown>
   INFORMATION FOR SEQ ID NO: 2893:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 4521 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        SEQUENCE DESCRIPTION: SEQ ID NO: 2893:
US-09-543-679A-2893

Alignment Scores:
Pred. No.:              4.65e-20        Length:         4521
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-543-679A-2893 (1-4521)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 62
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
```

; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3222..4841
US-08-751-767A-7

Alignment Scores:

Pred. No.:	6.21e-20	Length:	6139
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-102 (1-187) x US-08-751-767A-7 (1-6139)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4725 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 4784

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       4785 GCTTTCAGAATTCGGGCAGTGACTATT 4811
```

RESULT 63
US-09-949-016-11872
; Sequence 11872, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11872
; LENGTH: 10764
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11872

Alignment Scores:

Pred. No.:	1.05e-19	Length:	10764
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-949-016-11872 (1-10764)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8448 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 8507

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       8508 GCTTTCAGAATTCGGGCAGTGACTATT 8534
```

RESULT 64
US-09-949-016-14204
; Sequence 14204, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14204
; LENGTH: 10765
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14204

Alignment Scores:

Pred. No.:	1.05e-19	Length:	10765
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-949-016-14204 (1-10765)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8448 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 8507

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       8508 GCTTTCAGAATTCGGGCAGTGACTATT 8534
```

RESULT 65
US-09-949-016-20381
; Sequence 20381, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20381
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-20381

Alignment Scores:

Pred. No.:	7.59e-20	Length:	601
Score:	28.00	Matches:	28
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.0%	Indels:	0
DB:	3	Gaps:	0

```
S-10-821-670A-102 (1-187) x US-09-949-016-20381 (1-601)

Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 194

Qy         52 AlaCysLeuProLeuGluLeuThr 59
              |||||||||||||||||||||||
Db        195 GCCTGTTTACCATTGGAATTAACC 218

RESULT 66
US-09-949-016-87348
; Sequence 87348, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87348
;  LENGTH: 601
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-87348

Alignment Scores:
Pred. No.:                7.59e-20        Length:          601
Score:                    28.00           Matches:         28
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              15.0%           Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-102 (1-187) x US-09-949-016-87348 (1-601)

Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 194

Qy         52 AlaCysLeuProLeuGluLeuThr 59
              |||||||||||||||||||||||
Db        195 GCCTGTTTACCATTGGAATTAACC 218

RESULT 67
US-09-011-143-24
; Sequence 24, Application US/09011143
; Patent No. 6472509
; GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-24

Alignment Scores:
Pred. No.:                1.34e-18        Length:          79
Score:                    26.00           Matches:         26
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              13.9%           Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-102 (1-187) x US-09-011-143-24 (1-79)

Qy         40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

Qy         60 MetAsnGluSerCysLeu 65
              |||||||||||||||||
Db         62 ATGAATGAGAGTTGCCTG 79

RESULT 68
US-09-302-495-24
; Sequence 24, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
```

```
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 79 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
JS-09-302-495-24

Alignment Scores:
Pred. No.:                1.34e-18        Length:         79
Score:                    26.00           Matches:        26
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              13.9%           Indels:         0
DB:                       3               Gaps:           0

JS-10-821-670A-102 (1-187) x US-09-302-495-24 (1-79)

Qy          40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

Qy          60 MetAsnGluSerCysLeu 65
               |||||||||||||||||
Db          62 ATGAATGAGAGTTGCCTG 79

RESULT 69
US-10-079-616-24
; Sequence 24, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 79 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-079-616-24

Alignment Scores:
Pred. No.:                1.34e-18        Length:         79
Score:                    26.00           Matches:        26
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              13.9%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-079-616-24 (1-79)

Qy          40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

Qy          60 MetAsnGluSerCysLeu 65
               |||||||||||||||||
Db          62 ATGAATGAGAGTTGCCTG 79

RESULT 70
US-09-011-143-25/c
; Sequence 25, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-25

Alignment Scores:
Pred. No.:              0.000226        Length:         36
Score:                  12.00           Matches:        12
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.4%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-011-143-25 (1-36)

Qy        106 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 117
              |||||||||||||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

RESULT 71
US-09-302-495-25/c
; Sequence 25, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 36 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-302-495-25

Alignment Scores:
Pred. No.:              0.000226        Length:         36
Score:                  12.00           Matches:        12
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.4%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-302-495-25 (1-36)

Qy        106 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 117
              |||||||||||||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

RESULT 72
US-10-079-616-25/c
; Sequence 25, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 36 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
```

```
:             TOPOLOGY: linear
:        MOLECULE TYPE: cDNA
:        SEQUENCE DESCRIPTION: SEQ ID NO: 25:
JS-10-079-616-25

Alignment Scores:
Pred. No.:              0.000226        Length:         36
Score:                  12.00           Matches:        12
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.4%            Indels:         0
DB:                     3               Gaps:           0

JS-10-821-670A-102 (1-187) x US-10-079-616-25 (1-36)

Qy       106 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 117
             ||||||||||||||||||||||||||||||||||||
Db        36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

RESULT 73
JS-09-917-265A-91
; Sequence 91, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
JS-09-917-265A-91

Alignment Scores:
Pred. No.:              0.0292          Length:         39
Score:                  10.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.3%            Indels:         0
DB:                     3               Gaps:           0

JS-10-821-670A-102 (1-187) x US-09-917-265A-91 (1-39)

Qy         1 GlyMetPheGlnCysLeuAsnHisSerGln 10
             ||||||||||||||||||||||||||||||
Db        10 GGGATGTTCCAGTGCCTCAACCACTCCCAA 39

RESULT 74
JS-09-634-368-1
; Sequence 1, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine p35
;   OTHER INFORMATION: coding sequence for mature protein
US-09-634-368-1

Alignment Scores:
Pred. No.:              0.374           Length:         582
Score:                  10.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.3%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-634-368-1 (1-582)

Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        298 AGCATCTATGAGGACTTGAAGATGTACCAG 327

RESULT 75
US-08-385-335A-10
; Sequence 10, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  713 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-385-335A-10

Alignment Scores:
Pred. No.:              0.453           Length:         713
Score:                  10.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.3%            Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x US-08-385-335A-10 (1-713)
```

```
Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        410 AGCATCTATGAGGACTTGAAGATGTACCAG 439

RESULT 76
US-09-634-368-5
; Sequence 5, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35 fusion protein coding sequence
US-09-634-368-5

Alignment Scores:
Pred. No.:                0.785          Length:          1278
Score:                    10.00          Matches:         10
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              5.3%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-634-368-5 (1-1278)

Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        994 AGCATCTATGAGGACTTGAAGATGTACCAG 1023

RESULT 77
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

Alignment Scores:
Pred. No.:                0.953          Length:          1569
Score:                    10.00          Matches:         10
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              5.3%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-634-368-12 (1-1569)

Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        298 AGCATCTATGAGGACTTGAAGATGTACCAG 327

RESULT 78
US-09-634-368-11
; Sequence 11, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-09-634-368-11

Alignment Scores:
Pred. No.:                1.21           Length:          2013
Score:                    10.00          Matches:         10
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              5.3%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-634-368-11 (1-2013)

Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        298 AGCATCTATGAGGACTTGAAGATGTACCAG 327

RESULT 79
US-09-634-368-13
; Sequence 13, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

Alignment Scores:
Pred. No.:                1.6            Length:          2709
Score:                    10.00          Matches:         10
```

```
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            5.3%            Indels:        0
DB:                     3               Gaps:          0

US-10-821-670A-102 (1-187) x US-09-634-368-13 (1-2709)

Qy          94 SerIleTyrGluAspLeuLysMetTyrGln 103
               |||||||||||||||||||||||||||||||
Db         994 AGCATCTATGAGGACTTGAAGATGTACCAG 1023

RESULT 80
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2377..3384
;      OTHER INFORMATION:  /product= "p40 gene product"
US-08-659-206A-4

Alignment Scores:
Pred. No.:              3.53            Length:        6295
Score:                  10.00           Matches:       10
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            5.3%            Indels:        0
DB:                     2               Gaps:          0

US-10-821-670A-102 (1-187) x US-08-659-206A-4 (1-6295)

Qy          94 SerIleTyrGluAspLeuLysMetTyrGln 103
               |||||||||||||||||||||||||||||||
Db        1391 AGCATCTATGAGGACTTGAAGATGTACCAG 1420

RESULT 81
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Plasmid DNA"
;    IMMEDIATE SOURCE:
;      CLONE:  pWRG3169
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..628
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  629..810
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(953..1258, 1332..1673)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1797..2024
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1

Alignment Scores:
Pred. No.:              4.06            Length:        7287
Score:                  10.00           Matches:       10
```

```
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            5.3%            Indels:        0
B:                     2               Gaps:          0

S-10-821-670A-102 (1-187) x US-08-659-206A-1 (1-7287)

y         94 SerIleTyrGluAspLeuLysMetTyrGln 103
             |||||||||||||||||||||||||||||||
b       1389 AGCATCTATGAGGACTTGAAGATGTACCAG 1418

ESULT 82
S-09-917-265A-96/c
; Sequence 96, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
S-09-917-265A-96

lignment Scores:
red. No.:              0.412           Length:        51
core:                  9.00            Matches:       9
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            4.8%            Indels:        0
B:                     3               Gaps:          0

S-10-821-670A-102 (1-187) x US-09-917-265A-96 (1-51)

y         177 IleAsnArgMetMetSerTyrLeuAsn 185
              |||||||||||||||||||||||||||
b          49 ATCAATAGAATGATGTCCTACTTGAAC 23

ESULT 83
S-09-396-196G-121547
; Sequence 121547, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 121547
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
S-09-396-196G-121547

lignment Scores:
Pred. No.:             2.3             Length:        25
Score:                 8.00            Matches:       8
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           4.3%            Indels:        0
DB:                    3               Gaps:          0

US-10-821-670A-102 (1-187) x US-09-396-196G-121547 (1-25)

Qy        162 LysLeuCysIleLeuLeuHisAla 169
              |||||||||||||||||||||||||
Db          1 AAGCTCTGCATCCTGCTTCACGCC 24

RESULT 84
US-09-917-265A-90/c
; Sequence 90, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-90

Alignment Scores:
Pred. No.:             2.47            Length:        27
Score:                 8.00            Matches:       8
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           4.3%            Indels:        0
DB:                    3               Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265A-90 (1-27)

Qy        180 MetMetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||||||
Db         27 ATGATGAGCTATCTGAATGCTTCC 4

RESULT 85
US-09-917-265A-92/c
; Sequence 92, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
```

US-09-917-265A-92

Alignment Scores:

Pred. No.:	3.67	Length:	41
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265A-92 (1-41)

```
Qy        180 MetMetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||||||
Db         41 ATGATGAGCTATCTGAATGCTTCC 18
```

RESULT 86
US-09-949-016-60737/c
; Sequence 60737, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60737
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60737

Alignment Scores:

Pred. No.:	46.2	Length:	601
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-949-016-60737 (1-601)

```
Qy         72 LeuIleThrAsnGlySerCysLeu 79
              |||||||||||||||||||||||||
Db        408 TTAATAACAAATGGTTCATGTTTG 385
```

RESULT 87
US-09-949-016-60738/c
; Sequence 60738, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60738
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60738

Alignment Scores:

Pred. No.:	46.2	Length:	601
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-949-016-60738 (1-601)

```
Qy         72 LeuIleThrAsnGlySerCysLeu 79
              |||||||||||||||||||||||||
Db         49 TTAATAACAAATGGTTCATGTTTG 26
```

RESULT 88
US-09-949-016-60739/c
; Sequence 60739, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60739
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60739

Alignment Scores:

Pred. No.:	46.2	Length:	601
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-949-016-60739 (1-601)

```
Qy         72 LeuIleThrAsnGlySerCysLeu 79
              |||||||||||||||||||||||||
Db         48 TTAATAACAAATGGTTCATGTTTG 25
```

RESULT 89
US-09-949-016-111391
; Sequence 111391, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

```
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111391
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
.S-09-949-016-111391

:lignment Scores:
:red. No.:                46.2          Length:         601
:core:                    8.00          Matches:        8
:ercent Similarity:       100.0%        Conservative:   0
:est Local Similarity:    100.0%        Mismatches:     0
:uery Match:              4.3%          Indels:         0
:B:                       3             Gaps:           0

.S-10-821-670A-102 (1-187) x US-09-949-016-111391 (1-601)

:y        158 LysThrLysIleLysLeuCysIle 165
              |||||||||||||||||||||||
:b        505 AAAACCAAGATCAAACTTTGTATA 528

:ESULT 90
.S-09-949-016-111392
; Sequence 111392, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111392
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
.S-09-949-016-111392

:lignment Scores:
:red. No.:                46.2          Length:         601
:core:                    8.00          Matches:        8
:ercent Similarity:       100.0%        Conservative:   0
:est Local Similarity:    100.0%        Mismatches:     0
:uery Match:              4.3%          Indels:         0
:B:                       3             Gaps:           0

.S-10-821-670A-102 (1-187) x US-09-949-016-111392 (1-601)

:y        158 LysThrLysIleLysLeuCysIle 165
              |||||||||||||||||||||||
:b        506 AAAACCAAGATCAAACTTTGTATA 529

:ESULT 91
.S-09-949-016-154644/c
; Sequence 154644, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 154644
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-154644

Alignment Scores:
Pred. No.:                46.2          Length:         601
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              4.3%          Indels:         0
DB:                       3             Gaps:           0

US-10-821-670A-102 (1-187) x US-09-949-016-154644 (1-601)

Qy        162 LysLeuCysIleLeuLeuHisAla 169
              |||||||||||||||||||||||
Db        354 AAGCTGTGTATTTTATTGCATGCA 331

RESULT 92
US-09-949-016-154645/c
; Sequence 154645, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 154645
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-154645

Alignment Scores:
Pred. No.:                46.2          Length:         601
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              4.3%          Indels:         0
DB:                       3             Gaps:           0

US-10-821-670A-102 (1-187) x US-09-949-016-154645 (1-601)

Qy        162 LysLeuCysIleLeuLeuHisAla 169
              |||||||||||||||||||||||
Db        596 AAGCTGTGTATTTTATTGCATGCA 573

RESULT 93
US-09-134-000C-3234
; Sequence 3234, Application US/09134000C
```

; Patent No. 6617156
: GENERAL INFORMATION:
: APPLICANT: Lynn Doucette-Stamm et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
: TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
: CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/055,778
: PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
: SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3234
; LENGTH: 1380
: TYPE: DNA
: ORGANISM: Enterococcus faecalis
US-09-134-000C-3234

Alignment Scores:

Pred. No.:	101	Length:	1380
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-134-000C-3234 (1-1380)

Qy 128 LeuThrAlaIleAspGluLeuLeu 135
||||||||||||||||||||||
Db 115 TTGACAGCTATTGACGAGTTGTTA 138

RESULT 94
US-09-605-703B-525/c
; Sequence 525, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 525
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1465)
; OTHER INFORMATION: FRXA01155
US-09-605-703B-525

Alignment Scores:

Pred. No.:	107	Length:	1465
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-605-703B-525 (1-1465)

Qy 66 AlaSerArgGluIleSerLeuIle 73
||||||||||||||||||||||
Db 909 GCATCGCGGGAGATTTCCCTAATT 886

RESULT 95
US-09-605-703B-523/c
; Sequence 523, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 523
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1570)
; OTHER INFORMATION: RXN01155
US-09-605-703B-523

Alignment Scores:

Pred. No.:	114	Length:	1570
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-605-703B-523 (1-1570)

Qy 66 AlaSerArgGluIleSerLeuIle 73
||||||||||||||||||||||
Db 909 GCATCGCGGGAGATTTCCCTAATT 886

RESULT 96
US-09-902-540-8882/c
; Sequence 8882, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8882
; LENGTH: 1697
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8882

Alignment Scores:

Pred. No.:	123	Length:	1697
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0

```
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            4.3%            Indels:        0
B:                     3               Gaps:          0

S-10-821-670A-102 (1-187) x US-09-902-540-8882 (1-1697)

y        143 ValThrValProGlnAsnSerSer 150
             ||||||||||||||||||||||||
b        155 GTCACGGTGCCCCAGAACTCCTCC 132

ESULT 97
S-10-104-047-458
; Sequence 458, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 6943241el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 458
;   LENGTH: 2792
;   TYPE: DNA
;   ORGANISM: Homo sapiens
S-10-104-047-458

lignment Scores:
red. No.:              197             Length:        2792
core:                  8.00            Matches:       8
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            4.3%            Indels:        0
B:                     3               Gaps:          0

S-10-821-670A-102 (1-187) x US-10-104-047-458 (1-2792)

y        133 GluLeuLeuGlnAlaLeuAsnVal 140
             |||||||||||||||||||||||||
b        114 GAATTGCTGCAGGCATTAAATGTA 137

ESULT 98
S-09-221-017B-775
; Sequence 775, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
;   APPLICANT:  Ross, Bruce C.
;   TITLE OF INVENTION:  P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;   NUMBER OF SEQUENCES:  1120
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  MORRISON & FOERSTER
;     STREET:  755 PAGE MILL ROAD
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94304-1018
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  Windows
;     SOFTWARE:  FastSEQ for Windows Version 2.0b
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/221,017B
;     FILING DATE:  23-DEC-1998
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PP1182
;     FILING DATE:  31-DEC-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PP1546
;     FILING DATE:  30-JAN-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PP2911
;     FILING DATE:  09-APR-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/AU98/01023
;     FILING DATE:  10-DEC-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Monroy, Gladys H
;     REGISTRATION NUMBER:  32,430
;     REFERENCE/DOCKET NUMBER:  27340-20021.00
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  650-813-5600
;     TELEFAX:  650-494-0792
;     TELEX:  706141
; INFORMATION FOR SEQ ID NO:  775:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  2957 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  circular
;   MOLECULE TYPE:  DNA (genomic)
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  UNKNOWN
;   ORIGINAL SOURCE:
;     ORGANISM:  PORYPHYROMONAS GINGIVALIS
;   FEATURE:
;     NAME/KEY:  misc_feature
;     LOCATION:  1...2957
US-09-221-017B-775

Alignment Scores:
Pred. No.:             208             Length:        2957
Score:                 8.00            Matches:       8
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           4.3%            Indels:        0
DB:                    3               Gaps:          0

US-10-821-670A-102 (1-187) x US-09-221-017B-775 (1-2957)

Qy         47 ThrSerThrValGluAlaCysLeu 54
              |||||||||||||||||||||||||
Db       1549 ACATCGACCGTGGAGGCGTGTTTG 1572

RESULT 99
US-10-104-047-401
; Sequence 401, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 6943241el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 401
;   LENGTH: 3098
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-104-047-401

Alignment Scores:
Pred. No.:             217             Length:        3098
Score:                 8.00            Matches:       8
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           4.3%            Indels:        0
DB:                    3               Gaps:          0
```

US-10-821-670A-102 (1-187) x US-10-104-047-401 (1-3098)

Qy 76 GlySerCysLeuAlaSerArgLys 83
||||||||||||||||||||||
Db 42 GGGTCATGCCTGGCCAGCAGAAAG 65

RESULT 100
US-09-949-016-15763
; Sequence 15763, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15763
; LENGTH: 4447
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15763

Alignment Scores:

Pred. No.:	305	Length:	4447
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-949-016-15763 (1-4447)

Qy 76 GlySerCysLeuAlaSerArgLys 83
||||||||||||||||||||||
Db 3753 GGTTCTTGTCTGGCGTCCAGGAAG 3776

Search completed: June 10, 2006, 04:51:43
Job time : 130.602 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

)M protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:35:52 ; Search time 2591.08 Seconds
(without alignments)
6053.601 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 187
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size: 1

Total number of hits satisfying chosen parameters: 96471816

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110453_27580/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rst -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10821670_@CGN_1_1_22222_@runat_07062006_110453_27580 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	15.5	762	14	DQ033872	DQ033872 Homo sapi
2	29	15.5	863	4	CD013916	CD013916 90138296
3	29	15.5	935	4	CD013914	CD013914 90138124
4	29	15.5	1136	4	CD013915	CD013915 90138132
5	29	15.5	1938	6	BC035571	BC035571 Homo sapi
6	28	15.0	762	14	DQ033873	DQ033873 Pan trogl
7	28	15.0	812	2	BG702253	BG702253 602683459
8	28	15.0	832	2	BI523569	BI523569 603175938
9	24	12.8	581	3	BP260963	BP260963 BP260963
10	24	12.8	777	14	CT080894	CT080894 Sus scrof
11	21	11.2	592	12	CE159257	CE159257 tigr-gss-
c 12	21	11.2	778	1	AJ820622	AJ820622 AJ820622
13	20	10.7	342	2	BM257856	BM257856 521721 MA
14	20	10.7	344	14	BX537236	BX537236 INRA porc
15	18	9.6	447	2	BI824638	BI824638 603033580
c 16	17	9.1	1099	2	BI523344	BI523344 603175938
c 17	16	8.6	777	4	CB168830	CB168830 CWI602769
c 18	13	7.0	528	1	AI332701	AI332701 qq19a07.x
19	10	5.3	373	7	BF552757	BF552757 UI-R-C0-i
20	10	5.3	427	10	DT930939	DT930939 S13.1784
21	10	5.3	456	10	DT913216	DT913216 S13.1426
22	10	5.3	561	3	BU699383	BU699383 LL2in1157
23	10	5.3	563	3	BU698113	BU698113 LL2in1206
24	10	5.3	589	1	AI050362	AI050362 ub30a07.r
c 25	10	5.3	614	11	AZ729972	AZ729972 RPCI-24-1
26	10	5.3	692	5	CJ137697	CJ137697 CJ137697
c 27	10	5.3	941	13	CZ271875	CZ271875 ZMMBF0051
28	10	5.3	1299	6	AK153729	AK153729 Mus muscu
29	9	4.8	192	4	BY368866	BY368866 BY368866
c 30	9	4.8	234	10	DV345207	DV345207 NABWE87TR
31	9	4.8	304	5	CF799003	CF799003 Lr_PAHCF_
32	9	4.8	412	4	CB801533	CB801533 AMGNNUC:S
33	9	4.8	425	5	CF798662	CF798662 Lr_PAHCF_
c 34	9	4.8	453	11	AZ215995	AZ215995 Sheared_D
35	9	4.8	495	8	CO869708	CO869708 Lr_JV2CF_
36	9	4.8	512	9	DR008986	DR008986 Lr_Cu2CF_
37	9	4.8	539	14	CR813130	CR813130 GR0AAA37C
38	9	4.8	551	10	DT919655	DT919655 PCRS30821
39	9	4.8	558	9	CX570753	CX570753 RVL1941 W
40	9	4.8	568	14	CR795312	CR795312 GR0AAA12D
c 41	9	4.8	577	4	CA153972	CA153972 SCVPRZ203
42	9	4.8	610	11	BH488094	BH488094 BOGBX77TR
43	9	4.8	617	13	CZ102767	CZ102767 OM__Ba011
44	9	4.8	663	5	CF809729	CF809729 Lr_LC1ED_
45	9	4.8	671	9	DR008485	DR008485 Lr_Cu2CF_
46	9	4.8	679	8	CO408614	CO408614 Lr_CHECF_
47	9	4.8	680	5	CF810266	CF810266 Lr_LC1ED_
48	9	4.8	705	11	AZ306792	AZ306792 1M0008F02
49	9	4.8	710	13	CW744074	CW744074 MARC_9128
50	9	4.8	731	9	DR009499	DR009499 Lr_Cu2CF_
c 51	9	4.8	773	13	CZ119478	CZ119478 OA_BBa000
52	9	4.8	788	9	DR008334	DR008334 Lr_Cu2CF_
53	9	4.8	796	2	BM397339	BM397339 5009-0-31
54	9	4.8	822	4	BX835464	BX835464 BX835464
55	9	4.8	825	12	CG385421	CG385421 OGYBY32TV
c 56	9	4.8	831	14	CT469425	CT469425 Sus scrof
57	9	4.8	918	14	CNS01EWE	AL141087 Anopheles
c 58	9	4.8	1083	12	CL092806	CL092806 ISB1-22J9
c 59	9	4.8	1215	8	CV123647	CV123647 OSTF30015
c 60	8	4.3	108	5	CK549365	CK549365 swkz0_005
c 61	8	4.3	131	11	AZ818875	AZ818875 2M0089I12
c 62	8	4.3	136	1	AV088513	AV088513 AV088513
63	8	4.3	144	2	BF751315	BF751315 RC3-BN042
c 64	8	4.3	181	1	AV093643	AV093643 AV093643
c 65	8	4.3	191	1	AI996576	AI996576 701667517
66	8	4.3	204	5	CF773702	CF773702 AG_FSL_21
67	8	4.3	216	5	CD957154	CD957154 SCH_190 G
c 68	8	4.3	218	1	AI523278	AI523278 ar71b08.x
c 69	8	4.3	226	3	BQ359215	BQ359215 RC3-HN002
70	8	4.3	238	1	AI488162	AI488162 EST246484
71	8	4.3	270	4	BX106716	BX106716 BX106716
72	8	4.3	270	11	AQ313634	AQ313634 RPCI11-96
73	8	4.3	272	13	CL398698	CL398698 ZMMBBb040
74	8	4.3	276	10	DR380792	DR380792 987564 CE
75	8	4.3	280	10	DY123482	DY123482 001212BAM
c 76	8	4.3	284	13	CW284805	CW284805 104_761_1
c 77	8	4.3	291	9	DR111969	DR111969 RTS1_25_A

c	78	8	4.3	298	2	BG883630 BG883630 fp27g12.y
	79	8	4.3	305	2	BF947586 BF947586 QV2-NN004
c	80	8	4.3	309	10	DY190750 DY190750 000929BEM
	81	8	4.3	310	10	Z43509 Z43509 HSC1EA031 n
c	82	8	4.3	320	4	BX722217 BX722217 BX722217
c	83	8	4.3	320	7	AW828155 AW828155 ra67c01.y
c	84	8	4.3	323	2	BM133293 BM133293 NXLV_002_
c	85	8	4.3	323	14	DX058631 DX058631 KBrB064E1
	86	8	4.3	326	2	BM148903 BM148903 TCAAP2E52
c	87	8	4.3	333	9	DN091358 DN091358 JGI_CABE4
c	88	8	4.3	334	10	DV663472 DV663472 CGN-151 P
c	89	8	4.3	334	10	DV663813 DV663813 CGN-632 P
c	90	8	4.3	334	10	DV672452 DV672452 CGN-8068
c	91	8	4.3	334	10	DV673948 DV673948 CGN-10251
c	92	8	4.3	334	10	DV674662 DV674662 CGN-11317
c	93	8	4.3	334	10	DV678489 DV678489 CGN-16277
c	94	8	4.3	334	10	DV678500 DV678500 CGN-16295
	95	8	4.3	337	8	CN153290 CN153290 940391 MA
c	96	8	4.3	337	8	CN155402 CN155402 942695 MA
	97	8	4.3	344	11	AZ772692 AZ772692 1M0583I18
c	98	8	4.3	345	7	BE710882 BE710882 QV1-HT063
	99	8	4.3	351	5	CK690084 CK690084 ZF101-P00
c	100	8	4.3	352	4	BY098863 BY098863 BY098863
	101	8	4.3	354	4	BY230958 BY230958 BY230958
	102	8	4.3	360	4	C46546 C46546 C46546 Yuji
	103	8	4.3	360	4	CB201202 CB201202 AGENCOURT
c	104	8	4.3	361	4	BY164439 BY164439 BY164439
	105	8	4.3	361	14	CR260601 CR260601 Reverse s
	106	8	4.3	365	1	AA375202 AA375202 EST87514
c	107	8	4.3	370	10	DV698507 DV698507 CGN-44173
	108	8	4.3	371	4	C09043 C09043 C09043 Yuji
	109	8	4.3	373	3	BU695376 BU695376 B1-30 Hem
c	110	8	4.3	376	8	CO000091 CO000091 UMC-bend_
	111	8	4.3	378	1	AI841318 AI841318 UI-M-AM0-
	112	8	4.3	379	14	ATH552010 AJ552010 Arabidops
	113	8	4.3	383	12	CL009900 CL009900 ZMMBBb055
c	114	8	4.3	385	11	BH585965 BH585965 BOHMK88TF
	115	8	4.3	385	12	CC601798 CC601798 ZMMBBc041
	116	8	4.3	391	2	BM287504 BM287504 528243 MA
c	117	8	4.3	391	4	BY097373 BY097373 BY097373
c	118	8	4.3	394	8	CN497033 CN497033 Mdfw20231
c	119	8	4.3	398	8	CN726153 CN726153 17ACDHMS_
	120	8	4.3	400	10	DR396789 DR396789 USDA-FP_1
	121	8	4.3	401	2	BI071670 BI071670 C061P76U_
c	122	8	4.3	401	3	BP823896 BP823896 BP823896
	123	8	4.3	402	5	CD725739 CD725739 216 Penni
c	124	8	4.3	402	11	BH368219 BH368219 AG-ND-105
	125	8	4.3	406	9	DN276723 DN276723 1155910 M
c	126	8	4.3	408	10	DV897556 DV897556 POSM06050
c	127	8	4.3	415	11	AZ705413 AZ705413 RPCI-23-2
	128	8	4.3	417	10	DR362368 DR362368 163298 CE
c	129	8	4.3	421	1	AA083930 AA083930 zm63g09.r
	130	8	4.3	422	10	DR362367 DR362367 4494932 C
	131	8	4.3	423	12	CC178915 CC178915 SALK_0552
c	132	8	4.3	425	7	AW482931 AW482931 48847 MAR
	133	8	4.3	426	5	CK693569 CK693569 ZF101-P00
	134	8	4.3	429	11	BH204368 BH204368 Sm1-46F18
	135	8	4.3	432	5	CK713311 CK713311 ZF201-P00
c	136	8	4.3	434	11	AQ512084 AQ512084 HS_5065_B
	137	8	4.3	437	9	DN105428 DN105428 1101391 M
c	138	8	4.3	438	10	DV700767 DV700767 CGN-46830
	139	8	4.3	439	11	BH812535 BH812535 SALK_0619
	140	8	4.3	441	10	H09001 H09001 yl96f05.r1
	141	8	4.3	444	11	AQ501672 AQ501672 V17D1 mTn
c	142	8	4.3	445	10	DV666678 DV666678 CGN-4638
c	143	8	4.3	445	10	DV674627 DV674627 CGN-11254
c	144	8	4.3	447	9	DN105122 DN105122 1101007 M
	145	8	4.3	448	1	AL912520 AL912520 AL912520
	146	8	4.3	448	11	AQ132489 AQ132489 HS_3002_B
c	147	8	4.3	450	1	AV562903 AV562903 AV562903
c	148	8	4.3	450	2	BG946659 BG946659 949012G07
c	149	8	4.3	450	5	CI105760 CI105760 CI105760
	150	8	4.3	452	3	BQ661424 BQ661424 HM03H02u
c	151	8	4.3	452	11	AQ985208 AQ985208 RPCI-23-3
	152	8	4.3	453	11	AQ813853 AQ813853 HS_5499_B
c	153	8	4.3	454	11	AQ877381 AQ877381 HS_2145_B
c	154	8	4.3	457	11	AQ297447 AQ297447 HS_3040_B
c	155	8	4.3	458	10	DV487479 DV487479 5532_F12_
	156	8	4.3	459	10	DV867223 DV867223 CRP6955 C
	157	8	4.3	459	11	AQ583994 AQ583994 RPCI-11-4
c	158	8	4.3	464	9	DN088643 DN088643 JGI_CABE2
	159	8	4.3	465	5	CK687239 CK687239 ZF101-P00
	160	8	4.3	465	11	AQ170688 AQ170688 HS_2270_B
c	161	8	4.3	469	10	DV666701 DV666701 CGN-4668
c	162	8	4.3	472	12	CG008355 CG008355 ZUADQ64TV
	163	8	4.3	473	11	AZ658415 AZ658415 1M0535P15
c	164	8	4.3	474	10	DV677446 DV677446 CGN-14834
	165	8	4.3	476	11	BH385957 BH385957 AG-ND-137
c	166	8	4.3	476	14	BX212489 BX212489 Danio rer
c	167	8	4.3	478	5	CI330323 CI330323 CI330323
	168	8	4.3	480	5	CK695642 CK695642 ZF101-P00
	169	8	4.3	481	9	DN088644 DN088644 JGI_CABE2
	170	8	4.3	482	1	AJ676277 AJ676277 AJ676277
c	171	8	4.3	483	5	CI340728 CI340728 CI340728
	172	8	4.3	484	11	BH399641 BH399641 AG-ND-137
	173	8	4.3	486	13	CL900245 CL900245 abg60a01.
c	174	8	4.3	487	8	CV453355 CV453355 EST907264
c	175	8	4.3	488	5	CI343362 CI343362 CI343362
	176	8	4.3	489	8	CV036688 CV036688 endo-169
	177	8	4.3	489	8	CV036695 CV036695 endo-220
	178	8	4.3	489	11	AZ932002 AZ932002 474.dhz93
	179	8	4.3	490	1	AJ667392 AJ667392 AJ667392
c	180	8	4.3	490	10	DV668148 DV668148 CGN-6682
	181	8	4.3	491	1	AI993092 AI993092 701495318
c	182	8	4.3	491	5	CI325551 CI325551 CI325551
c	183	8	4.3	494	4	CB592289 CB592289 AGENCOURT
c	184	8	4.3	496	5	CF046910 CF046910 QCK30h11.
c	185	8	4.3	497	11	AZ018620 AZ018620 RPCI-23-3
	186	8	4.3	498	2	BG889246 BG889246 EST515097
c	187	8	4.3	500	5	CI163968 CI163968 CI163968
	188	8	4.3	500	10	DV126465 DV126465 CV03045A2
	189	8	4.3	501	10	DV124785 DV124785 CV03040A2
c	190	8	4.3	501	14	DX209616 DX209616 OR_ABa008
c	191	8	4.3	503	5	CI327520 CI327520 CI327520
	192	8	4.3	504	7	BE482855 BE482855 168789 BA
	193	8	4.3	504	8	CO512983 CO512983 s13dSG09B
c	194	8	4.3	504	10	DR453336 DR453336 CM012B05
	195	8	4.3	505	2	BM146309 BM146309 TCAAP1E43
c	196	8	4.3	508	5	CI053797 CI053797 CI053797
	197	8	4.3	510	10	DR389262 DR389262 USDA-FP_1
c	198	8	4.3	511	2	BM338734 BM338734 MEST231-E
	199	8	4.3	511	3	BQ465263 BQ465263 HU03B20r
	200	8	4.3	511	4	CB355634 CB355634 ZF001-P00

ALIGNMENTS

RESULT 1
DQ033872
LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

```
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
     gene            <1. .>762
                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN

Alignment Scores:
Pred. No.:                 9.59e-19        Length:         762
Score:                     29.00           Matches:        29
Percent Similarity:        100.0%          Conservative:   0
Best Local Similarity:     100.0%          Mismatches:     0
Query Match:               15.5%           Indels:         0
DB:                        14              Gaps:           0

US-10-821-670A-102 (1-187) x DQ033872 (1-762)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 2
CD013916
LOCUS       CD013916                  863 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:                 1.07e-18        Length:         863
Score:                     29.00           Matches:        29
Percent Similarity:        100.0%          Conservative:   0
Best Local Similarity:     100.0%          Mismatches:     0
Query Match:               15.5%           Indels:         0
DB:                        4               Gaps:           0

US-10-821-670A-102 (1-187) x CD013916 (1-863)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 691

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        692 GCTTTCAGAATTCGGGCAGTGACTATT 718

RESULT 3
CD013914
LOCUS       CD013914                  935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:                 1.15e-18        Length:         935
Score:                     29.00           Matches:        29
Percent Similarity:        100.0%          Conservative:   0
Best Local Similarity:     100.0%          Mismatches:     0
Query Match:               15.5%           Indels:         0
DB:                        4               Gaps:           0

US-10-821-670A-102 (1-187) x CD013914 (1-935)
```

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 763

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        764 GCTTTCAGAATTCGGGCAGTGACTATT 790

RESULT 4
CD013915
LOCUS       CD013915               1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
    PUBMED  15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .1136
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              1.36e-18       Length:         1136
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            15.5%          Indels:         0
DB:                     4              Gaps:           0

US-10-821-670A-102 (1-187) x CD013915 (1-1136)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 964

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        965 GCTTTCAGAATTCGGGCAGTGACTATT 991

RESULT 5
AC035571
LOCUS       BC035571               1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:              2.19e-18       Length:         1938
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            15.5%          Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-102 (1-187) x BC035571 (1-1938)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1385

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       1386 GCTTTCAGAATTCGGGCAGTGACTATT 1412

RESULT 6
DQ033873
LOCUS       DQ033873               762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
```

```
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN

Alignment Scores:
Pred. No.:                1e-17          Length:         762
Score:                    28.00          Matches:        28
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              15.0%          Indels:         0
DB:                       14             Gaps:           0

US-10-821-670A-102 (1-187) x DQ033873 (1-762)

Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 351

Qy         52 AlaCysLeuProLeuGluLeuThr 59
              |||||||||||||||||||||||
Db        352 GCCTGTTTACCATTGGAATTAACC 375

RESULT 7
BG702253
LOCUS       BG702253                812 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
            mRNA sequence.
ACCESSION   BG702253
VERSION     BG702253.1  GI:13973409
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10714  row: e  column: 15
            High quality sequence stop: 804.
FEATURES             Location/Qualifiers
     source          1. .812
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4816118"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for  full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health).  Note: this
                     is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                1.06e-17       Length:         812
Score:                    28.00          Matches:        28
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              15.0%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-102 (1-187) x BG702253 (1-812)

Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 665

Qy         52 AlaCysLeuProLeuGluLeuThr 59
              |||||||||||||||||||||||
Db        666 GCCTGTTTACCATTGGAATTAACC 689

RESULT 8
BI523569
LOCUS       BI523569                832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11605 row: 1 column: 09
High quality sequence start: 23
High quality sequence stop: 821.

EATURES Location/Qualifiers
source 1. .832
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5240216"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

RIGIN

lignment Scores:

red. No.:	1.08e-17	Length:	832
core:	28.00	Matches:	28
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	15.0%	Indels:	0
B:	2	Gaps:	0

S-10-821-670A-102 (1-187) x BI523569 (1-832)

```
y         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        511 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 570

y         52 AlaCysLeuProLeuGluLeuThr 59
             |||||||||||||||||||||||
b        571 GCCTGTTTACCATTGGAATTAACC 594
```

ESULT 9
P260963
OCUS BP260963 581 bp mRNA linear EST 16-SEP-2004
EFINITION BP260963 Sugano cDNA library, small intestine Homo sapiens cDNA clone HSI02082, mRNA sequence.
CCESSION BP260963
ERSION BP260963.1 GI:52176194
EYWORDS EST.
OURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
EFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
OMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5343
Fax: 81-3-5449-5416
Email: ysuzuki@hgc.jp.
EATURES Location/Qualifiers
source 1. .581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSI02082"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:

Pred. No.:	9.39e-14	Length:	581
Score:	24.00	Matches:	24
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	12.8%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x BP260963 (1-581)

```
Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 567

Qy         52 AlaCysLeuPro 55
              ||||||||||||
Db        568 GCCTGTTTACCA 579
```

RESULT 10
CT080894
LOCUS CT080894 777 bp DNA linear GSS 01-NOV-2005
DEFINITION Sus scrofa genomic clone PigE-253A7, genomic survey sequence.
ACCESSION CT080894
VERSION CT080894.1 GI:78647963
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 777)
AUTHORS Humphray,S.J., Plumb,R.W. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the SP6 end of BAC 253A7. 253A7 is part of the PigEBAC BAC Library created by Roslin Institute/RFCGR.
Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES Location/Qualifiers
source 1. .777
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="PigE-253A7"
/tissue_type="Blood cells"
/note="vector pBeloBAC11
sex male"

ORIGIN

Alignment Scores:

Pred. No.:	1.21e-13	Length:	777
Score:	24.00	Matches:	24
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	12.8%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-102 (1-187) x CT080894 (1-777)

```
Qy        108 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTGGATCAGAACATG 668

Qy        128 LeuThrAlaIle 131
              ||||||||||||
```

```
Db        669 CTGACAGCTATT 680

RESULT 11
CE159257
LOCUS       CE159257                592 bp    DNA     linear   GSS 25-SEP-2003
DEFINITION  tigr-gss-dog-17000371408491 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE159257
VERSION     CE159257.1  GI:35287296
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 592)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .592
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-10        Length:         592
Score:                  21.00           Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     12              Gaps:           0

US-10-821-670A-102 (1-187) x CE159257 (1-592)

Qy         40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 GAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACC 110

Qy         60 Met 60
              |||
Db        111 ATG 113

RESULT 12
AJ820622/c
LOCUS       AJ820622                778 bp    mRNA    linear   EST 12-MAY-2005
DEFINITION  AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
ACCESSION   AJ820622
VERSION     AJ820622.1  GI:51888098
KEYWORDS    EST.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   McGuire,K. and Glass,E.J.
  TITLE     The expanding role of microarrays in the investigation of
            macrophage responses to pathogens
  JOURNAL   Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT     Contact: McGuire K
            Genomics and Genetics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
            1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
            constructed from pooled monocytes from Bos taurus (Holstein) and
            Bos indicus (Sahiwals) cattle subjected to various stimuli,
            including infection with the protozoan parasite Theileria annulata.
FEATURES             Location/Qualifiers
     source          1. .778
                     /organism="Bos sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:29061"
                     /clone="C0006020h12"
                     /tissue_type="blood"
                     /cell_type="bovine monocyte"
                     /clone_lib="KN206"
                     /note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
                     Site_2: NotI; Normalised library constructed from pooled
                     monocytes from Bos taurus (Holstein) and Bos indicus
                     (Sahiwals) cattle subjected to various stimuli, including
                     infection with the protozoan parasite Theileria annulata"
ORIGIN

Alignment Scores:
Pred. No.:              1.39e-10        Length:         778
Score:                  21.00           Matches:        21
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     1               Gaps:           0

US-10-821-670A-102 (1-187) x AJ820622 (1-778)

Qy         108 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 127
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         756 GCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAAATCTTTCTAGACCAGAACATG 697

Qy         128 Leu 128
               |||
Db         696 CTG 694

RESULT 13
BM257856
LOCUS       BM257856                342 bp    mRNA    linear   EST 17-DEC-2001
DEFINITION  521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BM257856
VERSION     BM257856.1  GI:17893455
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
```

Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 125 row: E column: 18
Seq primer: ATTTAGGTGACACTATAG.

EATURES Location/Qualifiers
source 1. .342
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."

RIGIN

lignment Scores:

red. No.:	7.01e-10	Length:	342
core:	20.00	Matches:	20
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	10.7%	Indels:	0
B:	2	Gaps:	0

S-10-821-670A-102 (1-187) x BM257856 (1-342)

y 17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b 282 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 341

ESULT 14
X537236
OCUS BX537236 344 bp DNA linear GSS 05-JUN-2003
EFINITION INRA porcine BAC library, clone 0849A01 BAC end sequence (Uni M13), genomic survey sequence.
CCESSION BX537236
ERSION BX537236.1 GI:31455351
EYWORDS GSS; genome survey sequence.
OURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
EFERENCE 1
AUTHORS Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and Chardon,P.
TITLE Construction of a swine BAC library: application to the characterization and mapping of porcine type C endoviral elements
JOURNAL Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
PUBMED 10449899
EFERENCE 2 (bases 1 to 344)
AUTHORS Robic,A.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2003) Robic A., INRA, Laboratoire de Genetique Cellulaire, chemin de Borde rouge, BP27, Auzeville, 31626, FRANCE Phone : 05 61 28 51 15 Fax : 05 61 28 53 08 Email : arobic@toulouse.inra.fr
EATURES Location/Qualifiers
source 1. .344
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="0849A01"
/note="library Rogel gaillard et al 1999, clone 0849A01 Clone distribution : AGENAE Resource center. Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN

Alignment Scores:

Pred. No.:	7.04e-10	Length:	344
Score:	20.00	Matches:	20
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-102 (1-187) x BX537236 (1-344)

Qy 112 LysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle 131
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 AAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTGGATCAGAACATGCTGACAGCTATT 60

RESULT 15
BI824638
LOCUS BI824638 447 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5', mRNA sequence.
ACCESSION BI824638
VERSION BI824638.1 GI:15936188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11435 row: o column: 19
High quality sequence start: 3
High quality sequence stop: 445.
FEATURES Location/Qualifiers
source 1. .447
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5175018"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	9.69e-08	Length:	447
Score:	18.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0

```
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            9.6%            Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x BI824638 (1-447)

Qy        160 LysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATT 54

RESULT 16
BI523344/c
LOCUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: 1  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              2.24e-06        Length:         1099
Score:                  17.00           Matches:        17
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            9.1%            Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x BI523344 (1-1099)

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATT 472

RESULT 17
CB168830/c
LOCUS       CB168830                777 bp    mRNA    linear   EST 30-JAN-2003
DEFINITION  CWI602769160.R1 CSEQFXL41 testes Bos taurus cDNA, mRNA sequence.
ACCESSION   CB168830
VERSION     CB168830.1  GI:28154956
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Bovine ESTs (Adelson and Gill)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="testes"
                     /clone_lib="CSEQFXL41 testes"
                     /note="Organ: testes; Vector: pBluescript SK+; Site_1:
                     NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     non-normalized library, sequenced 3' with M13R primer."
ORIGIN

Alignment Scores:
Pred. No.:              1.72e-05        Length:         777
Score:                  16.00           Matches:        16
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            8.6%            Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-102 (1-187) x CB168830 (1-777)

Qy        162 LysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 AAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATC 572

RESULT 18
AI332701/c
LOCUS       AI332701                528 bp    mRNA    linear   EST 13-FEB-1999
DEFINITION  qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948
            3' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   AI332701
VERSION     AI332701.1  GI:4069260
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1469 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.

EATURES Location/Qualifiers
source 1. .528
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1932948"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

RIGIN

lignment Scores:

red. No.:	0.014	Length:	528
core:	13.00	Matches:	13
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	7.0%	Indels:	0
B:	1	Gaps:	0

'S-10-821-670A-102 (1-187) x AI332701 (1-528)

```
y        165 IleLeuLeuHisAlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||||||||||||||
b        528 ATACTTCTCCATGCTTTCAGAATTCGGGCAGTGACTATT 490
```

ESULT 19
F552757
OCUS BF552757 373 bp mRNA linear EST 12-DEC-2000
EFINITION UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
CCESSION BF552757
ERSION BF552757.1 GI:11662487
EYWORDS EST.
OURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
EFERENCE 1 (bases 1 to 373)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
OMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID= 1782759
Seq primer: M13 Forward.

FEATURES Location/Qualifiers
source 1. .373
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-iz-d-02-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-C0"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"

ORIGIN

Alignment Scores:

Pred. No.:	11.7	Length:	373
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.3%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x BF552757 (1-373)

```
Qy          94 SerIleTyrGluAspLeuLysMetTyrGln 103
               |||||||||||||||||||||||||||||
Db          98 AGCATCTATGAGGACTTGAAGATGTACCAG 127
```

RESULT 20
DT930939
LOCUS DT930939 427 bp mRNA linear EST 20-SEP-2005
DEFINITION S13.1784 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION DT930939
VERSION DT930939.1 GI:75963455
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 427)
AUTHORS Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and Lemischka,I.R.
TITLE Diversification of Stem Cell Molecular Repertoire by Alternative Splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657

```
          Fax: 609 258 1704
          Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
                     /note="cDNA library was made from FACS-purified
                     hematopoietic stem cells"
ORIGIN

Alignment Scores:
Pred. No.:                 13.2          Length:         427
Score:                     10.00         Matches:        10
Percent Similarity:        100.0%        Conservative:   0
Best Local Similarity:     100.0%        Mismatches:     0
Query Match:               5.3%          Indels:         0
DB:                        10            Gaps:           0

US-10-821-670A-102 (1-187) x DT930939 (1-427)

Qy          94 SerIleTyrGluAspLeuLysMetTyrGln 103
               |||||||||||||||||||||||||||||
Db         382 AGCATCTATGAGGACTTGAAGATGTACCAG 411

RESULT 21
DT913216
LOCUS       DT913216                 456 bp    mRNA    linear   EST 19-SEP-2005
DEFINITION  S13.1426 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION   DT913216
VERSION     DT913216.1  GI:75893697
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
                     /note="cDNA library was made from FACS-purified
                     hematopoietic stem cells"
ORIGIN

Alignment Scores:
Pred. No.:                 14            Length:         456
Score:                     10.00         Matches:        10
Percent Similarity:        100.0%        Conservative:   0
Best Local Similarity:     100.0%        Mismatches:     0
Query Match:               5.3%          Indels:         0
DB:                        10            Gaps:           0

US-10-821-670A-102 (1-187) x DT913216 (1-456)

Qy          94 SerIleTyrGluAspLeuLysMetTyrGln 103
               |||||||||||||||||||||||||||||
Db         382 AGCATCTATGAGGACTTGAAGATGTACCAG 411

RESULT 22
BU699383
LOCUS       BU699383                 561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was  performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to  biotinylated RNA transcribed from
                     the driver, AA4.1neg cDNA library in pSport2 with  inserts
                     cloned in the complementary orientation. For detailed
                     protocols and additional  information please see our
                     website at http://stemcell.princeton.edu."
ORIGIN

Alignment Scores:
Pred. No.:                 16.8          Length:         561
Score:                     10.00         Matches:        10
Percent Similarity:        100.0%        Conservative:   0
Best Local Similarity:     100.0%        Mismatches:     0
Query Match:               5.3%          Indels:         0
DB:                        3             Gaps:           0

US-10-821-670A-102 (1-187) x BU699383 (1-561)
```

```
Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        299 AGCATCTATGAGGACTTGAAGATGTACCAG 328

RESULT 23
AI050362
LOCUS       AI050362                  563 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:23610620
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was  performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to  biotinylated RNA transcribed from
                     the driver, AA4.1neg cDNA library in pSport2 with  inserts
                     cloned in the complementary orientation. For detailed
                     protocols and additional  information please see our
                     website at http://stemcell.princeton.edu."
ORIGIN

Alignment Scores:
Pred. No.:                16.9          Length:          563
Score:                    10.00         Matches:         10
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              5.3%          Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-102 (1-187) x BU698113 (1-563)
```

```
Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        315 AGCATCTATGAGGACTTGAAGATGTACCAG 344

RESULT 24
AI050362
LOCUS       AI050362                  589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:                17.6          Length:          589
Score:                    10.00         Matches:         10
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              5.3%          Indels:          0
DB:                       1             Gaps:            0

US-10-821-670A-102 (1-187) x AI050362 (1-589)
```

```
Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        324 AGCATCTATGAGGACTTGAAGATGTACCAG 353

RESULT 25
AZ729972/c
LOCUS       AZ729972                  614 bp    DNA     linear   GSS 25-JAN-2001
DEFINITION  RPCI-24-117G9.TV RPCI-24 Mus musculus genomic clone RPCI-24-117G9,
            genomic survey sequence.
ACCESSION   AZ729972
VERSION     AZ729972.1  GI:12488267
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 614)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-24-117G9.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 117  row: G  column: 9
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .614
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-117G9"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /clone_lib="RPCI-24"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
ORIGIN

Alignment Scores:
Pred. No.:                18.2          Length:        614
Score:                    10.00         Matches:       10
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              5.3%          Indels:        0
DB:                       11            Gaps:          0

US-10-821-670A-102 (1-187) x AZ729972 (1-614)

Qy         64 CysLeuAlaSerArgGluIleSerLeuIle 73
              ||||||||||||||||||||||||||||||
Db        350 TGTTTAGCTTCTAGAGAAATTAGTCTCATC 321

RESULT 26
CJ137697
LOCUS       CJ137697                  692 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ137697 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            thymus 3 days neonate Mus musculus cDNA clone A630064E02 5', mRNA
            sequence.
ACCESSION   CJ137697
VERSION     CJ137697.1  GI:76238025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
  PUBMED    16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Dr. John Todd (
            Dept. of Medical Genetics Wellcome Trust Centre for Molecular
            Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes
            Hospital Cambridge ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="A630064E02"
                     /tissue_type="thymus"
                     /dev_stage="3 days neonate"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J thymus 3 days neonate"
ORIGIN

Alignment Scores:
Pred. No.:                20.3          Length:        692
Score:                    10.00         Matches:       10
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              5.3%          Indels:        0
DB:                       5             Gaps:          0

US-10-821-670A-102 (1-187) x CJ137697 (1-692)

Qy         94 SerIleTyrGluAspLeuLysMetTyrGln 103
              |||||||||||||||||||||||||||||
Db        518 AGCATCTATGAGGACTTGAAGATGTACCAG 547

RESULT 27
CZ271875/c
LOCUS       CZ271875                  941 bp    DNA     linear   GSS 14-MAR-2005
DEFINITION  ZMMBF0051D18f ZMMBF Zea mays genomic clone ZMMBF0051D18 5', genomic
            survey sequence.
ACCESSION   CZ271875
VERSION     CZ271875.1  GI:61108687
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
EFERENCE 1 (bases 1 to 941)
AUTHORS Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,G. and Messing,J.
TITLE Construction, Sequencing and Characterization of a Fosmid Library of the B73 Maize Genome
JOURNAL Unpublished (2005)
OMMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: Fos_F
Class: fosmid ends.
EATURES Location/Qualifiers
source 1. .941
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBF0051D18"
/lab_host="EPI100-T1"
/clone_lib="ZMMBF"
/note="Vector: pEpiFOS-5; Site_1: Eco72I"
RIGIN

lignment Scores:

red. No.:	26.6	Length:	941
core:	10.00	Matches:	10
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	5.3%	Indels:	0
B:	13	Gaps:	0

S-10-821-670A-102 (1-187) x CZ271875 (1-941)

y 47 ThrSerThrValGluAlaCysLeuProLeu 56
b 935 ACATCTACTGTTGAAGCATGTTTGCCATTG 906

ESULT 28
K153729
OCUS AK153729 1299 bp mRNA linear HTC 21-SEP-2005
EFINITION Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630064E02 product:interleukin 12a, full insert sequence.
CCESSION AK153729
ERSION AK153729.1 GI:74148962
EYWORDS HTC; CAP trapper.
OURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
EFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
EFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
EFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L.,

```
                Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M.,
                Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R.,
                Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G.,
                di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G.,
                Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M.,
                Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E.,
                Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N.,
                Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T.,
                Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H.,
                Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K.,
                Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J.,
                Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L.,
                Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S.,
                Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H.,
                Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O.,
                Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G.,
                Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z.,
                Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A.,
                Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S.,
                Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D.,
                Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R.,
                Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S.,
                Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R.,
                Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A.,
                Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T.,
                Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A.,
                Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M.,
                Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M.,
                Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M.,
                Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M.,
                Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
                Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
  CONSRTM       FANTOM Consortium
  TITLE         The transcriptional landscape of the mammalian genome
  JOURNAL       Science 309 (5740), 1559-1563 (2005)
  PUBMED        16141072
REFERENCE       7
  AUTHORS       Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
                Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
                Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
                Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
                Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
                Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
                Wahlestedt,C.
  CONSRTM       RIKEN Genome Exploration Research Group
  TITLE         Antisense transcription in the mammalian transcriptome
  JOURNAL       Science 309 (5740), 1564-1566 (2005)
  PUBMED        16141073
REFERENCE       8  (bases 1 to 1299)
  AUTHORS       Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
                Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
                Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
                Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
                Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
                Muramatsu,M. and Hayashizaki,Y.
  TITLE         Direct Submission
  JOURNAL       Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
                Physical and Chemical Research (RIKEN), Laboratory for Genome
                Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
                URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                Fax:81-45-503-9216)
COMMENT         cDNA library was prepared and sequenced in Mouse Genome
                Encyclopedia Project of Genome Exploration Research Group in Riken
                Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                Division of Experimental Animal Research in Riken contributed to
                prepare mouse tissues.
                Please visit our web site for further details.
                URL:http://genome.gsc.riken.jp/
                URL:http://fantom.gsc.riken.jp/.
FEATURES                Location/Qualifiers
     source             1. .1299
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="FANTOM_DB:A630064E02"
                        /db_xref="taxon:10090"
                        /clone="A630064E02"
                        /tissue_type="thymus"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="3 days neonate"
     misc_feature       1. .1299
                        /note="interleukin 12a (MGD|MGI:96539 GB|NM_008351,
                        evidence: BLASTN, 100%, match=776)
                        putative"
ORIGIN

Alignment Scores:
Pred. No.:                35.3            Length:          1299
Score:                    10.00           Matches:         10
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              5.3%            Indels:          0
DB:                       6               Gaps:            0

US-10-821-670A-102 (1-187) x AK153729 (1-1299)

Qy          94 SerIleTyrGluAspLeuLysMetTyrGln 103
               ||||||||||||||||||||||||||||||
Db         518 AGCATCTATGAGGACTTGAAGATGTACCAG 547

RESULT 29
BY368866
LOCUS       BY368866                  192 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  BY368866 RIKEN full-length enriched, 6 days neonate spleen Mus
            musculus cDNA clone F430208H13 3', mRNA sequence.
ACCESSION   BY368866
VERSION     BY368866.1  GI:26598354
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 192)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
```

```
  PUBMED   12466851
OMMENT     Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
           Sciences Center(GSC), Yokohama Institute
           The Institute of Physical and Chemical Research (RIKEN)
           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
           Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
           Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
           Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
           Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
           Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
           Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
           Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
           prepare full-length cDNA libraries for rapid discovery of new
           genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
           sequencing pipeline with 384 multicapillary sequencer. Genome Res.
           10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
           encyclopedia: real-time sequence clustering for construction of a
           nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
           Encyclopedia Project of Genome Exploration Research Group in Riken
           Genomic Sciences Center and Genome Science Laboratory in RIKEN.
           Division of Experimental Animal Research in Riken contributed to
           prepare mouse tissues.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
           further details.
EATURES              Location/Qualifiers
     source          1. .192
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F430208H13"
                     /tissue_type="spleen"
                     /dev_stage="6 days neonate"
                     /clone_lib="RIKEN full-length enriched, 6 days neonate
                     spleen"
RIGIN

lignment Scores:
red. No.:              68.2          Length:        192
core:                  9.00          Matches:       9
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            4.8%          Indels:        0
B:                     4             Gaps:          0

S-10-821-670A-102 (1-187) x BY368866 (1-192)

y        160 LysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||
b        161 AAAATAAAGTTGTGTATTCTATTACAT 187

ESULT 30
V345207/c
OCUS       DV345207                 234 bp    mRNA    linear   EST 17-OCT-2005
EFINITION  NABWE87TR Aedes aegypti infected with Brugia Malayi Aedes aegypti
           cDNA clone NABWE87, mRNA sequence.
CCESSION   DV345207
ERSION     DV345207.1  GI:77794432
EYWORDS    EST.
OURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM Aedes aegypti
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
           Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
REFERENCE  1  (bases 1 to 234)
  AUTHORS  Loftus,B., Utterback,T., Pertea,G., Koo,H., Mori,A., Schneider,J.,
           Lovin,D., deBruyn,B., Song,Z., Raikhel,A., de Fatima,B.M.,
           Casavant,T., Soares,B. and Severson,D.
  TITLE    Aedes aegypti cDNA sequencing
  JOURNAL  Unpublished (2005)
COMMENT    Contact: David Severson
           The Institute for Genomic Research (TIGR; www.tigr.org); University
           of Notre Dame, Department of Biological Sciences
           9712 Medical Center Drive, Rockville, MD 20850, USA
           Sequencing performed at TIGR (http://www.tigr.org) Venter
           Institute/JTC (JCVIJTC; http://venterinstitute.org) NABWE87TR
           Seq primer: REVERSE-CAGGAAACAGCTATGACC.
FEATURES             Location/Qualifiers
     source          1. .234
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /db_xref="taxon:7159"
                     /clone="NABWE87"
                     /sex="Female"
                     /tissue_type="adult females at 24 h, 3 days and 12 days
                     post feeding on a Brugia malayi infected blood meal"
                     /dev_stage="Adult"
                     /clone_lib="Aedes aegypti infected with Brugia Malayi"
ORIGIN

Alignment Scores:
Pred. No.:             81.2          Length:        234
Score:                 9.00          Matches:       9
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           4.8%          Indels:        0
DB:                    10            Gaps:          0

US-10-821-670A-102 (1-187) x DV345207 (1-234)

Qy         11 ThrLeuLeuArgAlaIleSerAsnThr 19
              |||||||||||||||||||||||||||
Db         28 ACACTTTTGAGAGCCATATCGAACACA 2

RESULT 31
CF799003
LOCUS      CF799003                 304 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION Lr_PAHCF_12D05_M13R Earthworm Fluorantene Exposure Library
           Lumbricus rubellus cDNA clone Lr_PAHCF_12D05 5' similar to
           ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
           terrestris, mRNA sequence.
ACCESSION  CF799003
VERSION    CF799003.1  GI:37803573
KEYWORDS   EST.
SOURCE     Lumbricus rubellus (humus earthworm)
  ORGANISM Lumbricus rubellus
           Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
           Lumbricina; Lumbricidae; Lumbricus.
REFERENCE  1  (bases 1 to 304)
  AUTHORS  Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S., Kille,P. and
           Blaxter,M.
  TITLE    The Lumbricus rubellus EST program - Sequences from a Fluorantene
           Exposure library
  JOURNAL  Unpublished (2003)
COMMENT    Contact: Jennifer Chaseley
           BIOSI 1
           Cardiff University
           Main College, Museum Avenue, Cardiff, CF11 3TL, UK
           Tel: +44 2920876680
           Fax: +44 2920874305
           Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
           Sequencing was performed in Cardiff using the pBluescriptII XR cDNA
           library (Stratagene) protocol.
           PCR PRimers
           FORWARD: gttttcccagtcacgacg
           BACKWARD: caggaaacagctatgaccatg
           Plate: 12  row: D  column: 05
```

```
          Seq primer: caggaaacagctatgaccatg
          High quality sequence stop: 304.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
                     /db_xref="taxon:35632"
                     /clone="Lr_PAHCF_12D05"
                     /tissue_type="Whole worm"
                     /dev_stage="Adult"
                     /clone_lib="Earthworm Fluorantene Exposure Library"
                     /note="Vector: pBluescript II SK+; The library was
                     prepared using protocols given by the supplier
                     (Stratagene)."
ORIGIN

Alignment Scores:
Pred. No.:                102           Length:         304
Score:                    9.00          Matches:        9
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              4.8%          Indels:         0
DB:                       5             Gaps:           0

US-10-821-670A-102 (1-187) x CF799003 (1-304)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        107 TGCCTCAACCATTCGCAGACGCTATTA 133

RESULT 32
CB801533
LOCUS       CB801533                412 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  AMGNNUC:SRPB2-00244-H1-A srpb2 (10220) Rattus norvegicus cDNA clone
            srpb2-00244-h1 5', mRNA sequence.
ACCESSION   CB801533
VERSION     CB801533.1  GI:29914888
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   Amgen EST Program.
  TITLE     Amgen Rat EST Program
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Dan Fitzpatrick
            Amgen, Inc
            One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00244  row: h  column: 1.
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="srpb2-00244-h1"
                     /tissue_type="prostate tissue"
                     /clone_lib="srpb2 (10220)"
                     /note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; rat
                     prostate normalized double selected poly(A+) mRNA size
                     fraction > 1 kb"
ORIGIN

Alignment Scores:
Pred. No.:                134           Length:         412
Score:                    9.00          Matches:        9
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              4.8%          Indels:         0
DB:                       4             Gaps:           0

US-10-821-670A-102 (1-187) x CB801533 (1-412)

Qy          162 LysLeuCysIleLeuLeuHisAlaPhe 170
                ||||||||||||||||||||||||||||
Db          283 AAGCTCTGTATCCTGCTCCATGCCTTC 309

RESULT 33
CF798662
LOCUS       CF798662                425 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  Lr_PAHCF_05D11_M13R Earthworm Fluorantene Exposure Library
            Lumbricus rubellus cDNA clone Lr_PAHCF_05D11 5' similar to
            ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
            terrestris, mRNA sequence.
ACCESSION   CF798662
VERSION     CF798662.1  GI:37803232
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 425)
  AUTHORS   Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S., Kille,P. and
            Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Fluorantene
            Exposure library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Cardiff using the pBluescriptII XR cDNA
            library (Stratagene) protocol.
            PCR PRimers
            FORWARD: gttttcccagtcacgacg
            BACKWARD: caggaaacagctatgaccatg
            Plate: 05  row: D  column: 11
            Seq primer: caggaaacagctatgaccatg
            High quality sequence stop: 374.
FEATURES             Location/Qualifiers
     source          1. .425
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
                     /db_xref="taxon:35632"
                     /clone="Lr_PAHCF_05D11"
                     /tissue_type="Whole worm"
                     /dev_stage="Adult"
                     /clone_lib="Earthworm Fluorantene Exposure Library"
                     /note="Vector: pBluescript II SK+; The library was
                     prepared using protocols given by the supplier
                     (Stratagene)."
ORIGIN

Alignment Scores:
Pred. No.:                138           Length:         425
Score:                    9.00          Matches:        9
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              4.8%          Indels:         0
DB:                       5             Gaps:           0

US-10-821-670A-102 (1-187) x CF798662 (1-425)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        109 TGCCTCAACCATTCGCAGACGCTATTA 135

RESULT 34
AZ215995/c
LOCUS       AZ215995                453 bp    DNA     linear   GSS 09-JUN-2000
DEFINITION  Sheared DNA-84C4.TF Sheared DNA Trypanosoma brucei genomic clone
```

```
          Sheared DNA-84C4, genomic survey sequence.
CCESSION  AZ215995
ERSION    AZ215995.1  GI:8433795
EYWORDS   GSS.
OURCE     Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
EFERENCE  1  (bases 1 to 453)
  AUTHORS   El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
            Donelson,J., Fraser,C. and Adams,M.
  TITLE     Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
  JOURNAL   Unpublished (1999)
OMMENT    Other_GSSs: Sheared DNA-84C4.TR
            Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through Research Genetics, Alabama, USA. Sheared DNA
            end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
            Seq primer: M13-Forward
            Class: shotgun.
EATURES             Location/Qualifiers
     source         1. .453
                    /organism="Trypanosoma brucei"
                    /mol_type="genomic DNA"
                    /strain="TREU927/4 GUTat 10.1"
                    /db_xref="taxon:5691"
                    /clone="Sheared DNA-84C4"
                    /clone_lib="Sheared DNA"
                    /note="Vector: pUC18; Site_1: SmaI; Constructed at The
                    Institute for Genomic Research (TIGR), Rockville, MD.
                    Genomic DNA isolated from a cloned population of
                    Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                    sheared to give a tight size distribution (approx 2 kb).
                    The v + i method used for the library construction is
                    described in detail in Smith, H.O. and Venter, J.C.
                    (Making small insert libraries for whole genome shotgun
                    sequencing projects.  In Genome Sequencing: A Practical
                    Approach, eds. M. Vaudin and B. Barell, Oxford University
                    Press, 1999)."
RIGIN

lignment Scores:
red. No.:                146             Length:         453
core:                    9.00            Matches:        9
ercent Similarity:       100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              4.8%            Indels:         0
B:                       11              Gaps:           0

S-10-821-670A-102 (1-187) x AZ215995 (1-453)

y         76 GlySerCysLeuAlaSerArgLysThr 84
             |||||||||||||||||||||||||||
b        332 GGGAGCTGTCTCGCCTCGCGAAAAACG 306

ESULT 35
O869708
OCUS       CO869708                 495 bp    mRNA    linear   EST 10-AUG-2004
EFINITION  Lr_JV2CF_06B01_SKplus Juvenile Earthworm Library Lumbricus rubellus
           cDNA clone Lr_JV2CF_06B01 similar to
           gi|3122450|sp|Q37546|NU1M_LUMTE NADH-UBIQUINONE OXIDOREDUCTASE.
           Score = 263 bits (671), Expect = 2e-70, mRNA sequence.
CCESSION   CO869708
ERSION     CO869708.1  GI:51099550
```

```
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   Chaseley,J., Hedley,B.A., Morgan,A.J., Sturzenbaum,S., Kille,P. and
            Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Juvenile
            library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Edinburgh using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13F (gttttcccagtcacgacg)
            BACKWARD: M13R (caggaaacagctatgaccatg)
            Plate: 06  row: B  column: 01
            Seq primer: SKplus
            High quality sequence start: 3
            High quality sequence stop: 474.
FEATURES            Location/Qualifiers
     source         1. .495
                    /organism="Lumbricus rubellus"
                    /mol_type="mRNA"
                    /db_xref="taxon:35632"
                    /clone="Lr_JV2CF_06B01"
                    /sex="mixed"
                    /tissue_type="Whole worm"
                    /dev_stage="Juvenile"
                    /clone_lib="Juvenile Earthworm Library"
                    /note="Organ: Whole worm"
ORIGIN

Alignment Scores:
Pred. No.:                157             Length:         495
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.8%            Indels:         0
DB:                       8               Gaps:           0

US-10-821-670A-102 (1-187) x CO869708 (1-495)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        117 TGCCTCAACCATTCGCAGACGCTATTA 143

RESULT 36
DR008986
LOCUS       DR008986                 512 bp    mRNA    linear   EST 18-MAY-2005
DEFINITION  Lr_Cu2CF_12A07 Earthworm Copper Exposure Library Lumbricus rubellus
            cDNA clone Lr_Cu2CF_12A07 similar to UniRef100_Q37546
            NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
            Score = 250 bits (638), Expect = 1e-65, mRNA sequence.
ACCESSION   DR008986
VERSION     DR008986.1  GI:66273130
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 512)
  AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
            Sturzenbaum,S., Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Copper
            exposure library
```

```
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Cardiff using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13(gttttcccagtcacgacgtt)
            BACKWARD: M13R(caggaaacagctatgaccatg)
            Plate: 12  row: A  column: 07
            Seq primer: caggaaacagctatgaccatg
            High quality sequence start: 17
            High quality sequence stop: 323.
FEATURES             Location/Qualifiers
     source          1. .512
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
                     /db_xref="taxon:35632"
                     /clone="Lr_Cu2CF_12A07"
                     /sex="mixed"
                     /tissue_type="whole worm"
                     /dev_stage="Adult"
                     /clone_lib="Earthworm Copper Exposure Library"
                     /note="Vector: pbluescript II SK; The library was prepared
                     using protocols given by the supplier (Clontech)."
ORIGIN

Alignment Scores:
Pred. No.:              162           Length:         512
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.8%          Indels:         0
DB:                     9             Gaps:           0

US-10-821-670A-102 (1-187) x DR008986 (1-512)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        135 TGCCTCAACCATTCGCAGACGCTATTA 161

RESULT 37
CR813130
LOCUS       CR813130                539 bp    DNA     linear   GSS 27-SEP-2004
DEFINITION  GR0AAA37CD06RM1 INRA BAC Bos taurus genomic clone INRAb_622G01, DNA
            sequence, genomic survey sequence.
ACCESSION   CR813130
VERSION     CR813130.1  GI:52749218
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 539)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work  was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 622 row: G column: 01
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Holstein"
                     /db_xref="taxon:9913"
                     /clone="INRAb_622G01"
                     /sex="Male"
                     /cell_type="fibroblast"
                     /clone_lib="INRA bovine BAC"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                     INRA Bovine BAC library (Male) produced by Andre Eggen
                     Genoscope sequence ID : GR0AAA37CD06RM1"
ORIGIN

Alignment Scores:
Pred. No.:              170           Length:         539
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.8%          Indels:         0
DB:                     14            Gaps:           0

US-10-821-670A-102 (1-187) x CR813130 (1-539)

Qy          61 AsnGluSerCysLeuAlaSerArgGlu 69
               |||||||||||||||||||||||||||
Db         331 AATGAGAGTTGCCTGGCTTCCAGAGAG 357

RESULT 38
DT919655
LOCUS       DT919655                551 bp    mRNA    linear   EST 19-SEP-2005
DEFINITION  PCRS30821 Hematopoietic stem cells Mus musculus cDNA, mRNA
            sequence.
ACCESSION   DT919655
VERSION     DT919655.1  GI:75900136
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .551
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
```

/note="cDNA library was made from FACS-purified hematopoietic stem cells"

RIGIN

lignment Scores:

red. No.:	173	Length:	551
core:	9.00	Matches:	9
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	4.8%	Indels:	0
B:	10	Gaps:	0

S-10-821-670A-102 (1-187) x DT919655 (1-551)

```
y        162 LysLeuCysIleLeuLeuHisAlaPhe 170
             ||||||||||||||||||||||||||||
b        180 AAGCTCTGCATCCTGCTTCACGCCTTC 206
```

ESULT 39
X570753
OCUS CX570753 558 bp mRNA linear EST 12-JAN-2005
EFINITION RVL1941 Wackym-Soares normalized rat vestibular cDNA library Rattus norvegicus cDNA 5', mRNA sequence.
CCESSION CX570753
ERSION CX570753.1 GI:57597784
EYWORDS EST.
OURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
EFERENCE 1 (bases 1 to 558)
AUTHORS Wackym,P.A. and Cioffi,J.A.
TITLE In silico analysis of the rat vestibular periphery transcriptome using a normalized cDNA library
JOURNAL Unpublished (2004)
OMMENT Contact: Wackym, P.A.
Department of Otolaryngology and Communication Sciences
9200 W. Wisconsin Ave, Milwaukee, WI, 53226, USA
Tel: 414.266.3750
Fax: 414.266.2693
Email: wackym@mcw.edu
Insert Length: 559 Std Error: 0.00
Seq primer: T7.
EATURES Location/Qualifiers
source 1. .558
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/tissue_type="Vestibular end organs, primary afferent neurons"
/clone_lib="Wackym-Soares normalized rat vestibular cDNA library"
/note="Vector: pT7T3Pac; The library was constructed and normalized according Bonaldo and Soares, Genome Analysis - A Laboratory Manual, Vol. 2: 49 - 157. Inserts are directionally cloned into the EcoRI and NotI sites. The library tag located between the NotI site and the polyA tail is TAGGTTACAC."
RIGIN

lignment Scores:

red. No.:	175	Length:	558
core:	9.00	Matches:	9
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	4.8%	Indels:	0
B:	9	Gaps:	0

S-10-821-670A-102 (1-187) x CX570753 (1-558)

```
y        162 LysLeuCysIleLeuLeuHisAlaPhe 170
             ||||||||||||||||||||||||||||
```

Db 68 AAGCTCTGTATCCTGCTCCATGCCTTC 94

RESULT 40
CR795312
LOCUS CR795312 568 bp DNA linear GSS 24-SEP-2004
DEFINITION GR0AAA12DG09RM1 INRA BAC Bos taurus genomic clone INRAb_238E06, DNA sequence, genomic survey sequence.
ACCESSION CR795312
VERSION CR795312.1 GI:52676311
KEYWORDS GSS.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 568)
AUTHORS Eggen,A., Schibler,L. and Roy,A.
TITLE Bovine BAC End Sequences from the INRA bovine BAC library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 568)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Contact: Andre Eggen
Department of Animal Genetics - LGbC
INRA
78350 Jouy-en-Josas, France
Tel: 33 1 34 65 24 24
Fax: 33 1 34 65 24 78
Email: eggen@jouy.inra.fr
Clones are derived from the INRA bovine BAC library (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library availability, please contact Andre Eggen (eggen@jouy.inra.fr). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope (Evry) Plate: 238 row: È column: 06
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .568
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Holstein"
/db_xref="taxon:9913"
/clone="INRAb_238E06"
/sex="Male"
/cell_type="fibroblast"
/clone_lib="INRA bovine BAC"
/note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull; INRA Bovine BAC library (Male) produced by Andre Eggen Genoscope sequence ID : GR0AAA12DG09RM1"
ORIGIN

Alignment Scores:

Pred. No.:	178	Length:	568
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.8%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-102 (1-187) x CR795312 (1-568)

```
Qy        61 AsnGluSerCysLeuAlaSerArgGlu 69
             |||||||||||||||||||||||||||
Db       330 AATGAGAGTTGCCTGGCTTCCAGAGAG 356
```

RESULT 41
CA153972/c
LOCUS CA153972 577 bp mRNA linear EST 24-SEP-2003
DEFINITION SCVPRZ2038B02.g RZ2 Saccharum officinarum cDNA clone SCVPRZ2038B02

```
          5', mRNA sequence.
ACCESSION CA153972
VERSION   CA153972.1  GI:35060583
KEYWORDS  EST.
SOURCE    Saccharum officinarum
  ORGANISM  Saccharum officinarum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
          complex.
REFERENCE 1  (bases 1 to 577)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT   Contact: Arruda P
          Centro de Biologia Molecular e Engenharia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parruda@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian Clone Collection Center (BCCC) at
          http://www.bcccenter.fcav.unesp.br
          Plate: 038  row: B  column: 02
          Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .577
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCVPRZ2038B02"
                     /lab_host="DH10B"
                     /clone_lib="RZ2"
                     /note="Organ: Shoot-root transition zone from young plants
                     (small insert library); Vector: pSport1; Site_1: SalI;
                     Site_2: NotI; An unidirectional cDNA library generated
                     from [Shoot-root transition zone  from young plants (small
                     insert library)]. cDNA was prepared from polyA+  mRNA
                     using SuperScript Plasmid System Kit (Invitrogen). The
                     double-strand  cDNAs were fractionated in a sepharose
                     CL-2B 40cm-columns and fragments  sizing between 0.8 and
                     1.5 Kb were directionally cloned into the vector.  Details
                     of each source of RNA and library construction can be
                     obtained at  http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Alignment Scores:
Pred. No.:                180             Length:         577
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.8%            Indels:         0
DB:                       4               Gaps:           0

US-10-821-670A-102 (1-187) x CA153972 (1-577)

Qy        134 LeuLeuGlnAlaLeuAsnValAsnSer 142
              |||||||||||||||||||||||||||
Db         51 CTTCTCCAAGCTCTCAACGTCAACTCC 25

RESULT 42
BH488094
LOCUS     BH488094                 610 bp    DNA     linear   GSS 13-DEC-2001
DEFINITION  BOGBX77TR BOGB Brassica oleracea genomic clone BOGBX77, genomic
          survey sequence.
ACCESSION BH488094
VERSION   BH488094.1  GI:17696198
KEYWORDS  GSS.
SOURCE    Brassica oleracea
  ORGANISM  Brassica oleracea
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1  (bases 1 to 610)
  AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
          Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea and its
          application to gene discovery and annotation in Arabidopsis
  JOURNAL   Genome Res. 15 (4), 487-495 (2005)
  PUBMED    15805490
COMMENT   Other_GSSs: BOGBX77TF
          Contact: Chris Town
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA.
          Tel: 301-838-3523
          Fax: 301-838-0208
          Email: cdtown@tigr.org
          DNA is from a doubled haploid provided by Tom Osborn.
          Seq primer: TR
          Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOGBX77"
                     /clone_lib="BOGB"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Alignment Scores:
Pred. No.:                189             Length:         610
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.8%            Indels:         0
DB:                       11              Gaps:           0

US-10-821-670A-102 (1-187) x BH488094 (1-610)

Qy         77 SerCysLeuAlaSerArgLysThrSer 85
              |||||||||||||||||||||||||||
Db        430 TCTTGTCTCGCATCCCGAAAGACGTCA 456

RESULT 43
CZ102767
LOCUS     CZ102767                 617 bp    DNA     linear   GSS 13-JAN-2005
DEFINITION  OM__Ba0111B06.f OM__Ba Oryza minuta genomic clone OM__Ba0111B06 5',
          genomic survey sequence.
ACCESSION CZ102767
VERSION   CZ102767.1  GI:57677146
KEYWORDS  GSS.
SOURCE    Oryza minuta
  ORGANISM  Oryza minuta
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1  (bases 1 to 617)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
          Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
          Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT   Contact: Rod A. Wing
          Arizona Genomics Institute
          University of Arizona
          Forbes Building Room 303, Tucson, AZ 85721-0036, USA
          Tel: 520 626 9595
          Fax: 520 621 1259
          Email: rwing@genome.arizona.edu
          Plate: 0111  row: B  column: 06
          Class: BAC ends.
FEATURES             Location/Qualifiers
```

```
    source          1. .617
                    /organism="Oryza minuta"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:63629"
                    /clone="OM__Ba0111B06"
                    /tissue_type="leaves"
                    /lab_host="DH10B"
                    /clone_lib="OM__Ba"
                    /note="Vector: pCUGIBAC1; Site_1: HindIII; Site_2:
                    HindIII"
RIGIN

lignment Scores:
red. No.:               191             Length:         617
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             4.8%            Indels:         0
B:                      13              Gaps:           0

S-10-821-670A-102 (1-187) x CZ102767 (1-617)

y          50 ValGluAlaCysLeuProLeuGluLeu 58
              |||||||||||||||||||||||||||||
b         540 GTCGAAGCATGTTTGCCACTAGAGTTG 566

ESULT 44
F809729
OCUS        CF809729                663 bp    mRNA    linear   EST 27-OCT-2003
EFINITION   Lr_LC1ED_30H01_SAC Lumbricus rubellus Late Cocoon Library 1
            Lumbricus rubellus cDNA clone Lr_LC1ED_30H01 5' similar to
            ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
            terrestris, mRNA sequence.
CCESSION    CF809729
ERSION      CF809729.1  GI:37998060
EYWORDS     EST.
OURCE       Lumbricus rubellus (humus earthworm)
 ORGANISM   Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
EFERENCE    1  (bases 1 to 663)
 AUTHORS    Jones,M., Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S.,
            Kille,P. and Blaxter,M.
 TITLE      The Lumbricus rubellus EST program - Sequences from a cocoon
            library
 JOURNAL    Unpublished (2003)
OMMENT      Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK.
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            The library was prepared using protocols given by the supplier
            (Stratagene).
            PCR PRimers
            FORWARD: M13R(AGCGGATAACAATTTCACACAGGA)
            BACKWARD: T7PL(CTCACTATAGGGCGAATTGG)
            Plate: 30  row: H  column: 01
            Seq primer: SAC(GGGAACAAAAGCTGGAG)
            High quality sequence stop: 503.
EATURES                 Location/Qualifiers
    source              1. .663
                        /organism="Lumbricus rubellus"
                        /mol_type="mRNA"
                        /db_xref="taxon:35632"
                        /clone="Lr_LC1ED_30H01"
                        /tissue_type="Whole worm"
                        /dev_stage="Late Cocoon"
                        /clone_lib="Lumbricus rubellus Late Cocoon Library 1"
                        /note="Vector: pBluescript II SK+; The library was
                        prepared using protocols given by the supplier
                        (Stratagene)."
ORIGIN

Alignment Scores:
Pred. No.:              204             Length:         663
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.8%            Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-102 (1-187) x CF809729 (1-663)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        179 TGCCTCAACCATTCGCAGACGCTATTA 205

RESULT 45
DR008485
LOCUS       DR008485                671 bp    mRNA    linear   EST 18-MAY-2005
DEFINITION  Lr_Cu2CF_09D10 Earthworm Copper Exposure Library Lumbricus rubellus
            cDNA clone Lr_Cu2CF_09D10 similar to UniRef100_Q37546
            NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
            Score = 362 bits (928), Expect = 6e-99, mRNA sequence.
ACCESSION   DR008485
VERSION     DR008485.1  GI:66272629
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 671)
  AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
            Sturzenbaum,S., Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Copper
            exposure library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Cardiff using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13(gttttcccagtcacgacgtt)
            BACKWARD: M13R(caggaaacagctatgaccatg)
            Plate: 09  row: D  column: 10
            Seq primer: caggaaacagctatgaccatg
            High quality sequence start: 9
            High quality sequence stop: 531.
FEATURES                Location/Qualifiers
     source             1. .671
                        /organism="Lumbricus rubellus"
                        /mol_type="mRNA"
                        /db_xref="taxon:35632"
                        /clone="Lr_Cu2CF_09D10"
                        /sex="mixed"
                        /tissue_type="whole worm"
                        /dev_stage="Adult"
                        /clone_lib="Earthworm Copper Exposure Library"
                        /note="Vector: pbluescript II SK; The library was prepared
                        using protocols given by the supplier (Clontech)."
ORIGIN

Alignment Scores:
Pred. No.:              206             Length:         671
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.8%            Indels:         0
```

```
DB:                 9              Gaps:          0

US-10-821-670A-102 (1-187) x DR008485 (1-671)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        120 TGCCTCAACCATTCGCAGACGCTATTA 146

RESULT 46
CO408614
LOCUS       CO408614                679 bp    mRNA    linear   EST 02-JUL-2004
DEFINITION  Lr_CHECF_02E05_M13R Earthworm Head Enriched library Lumbricus
            rubellus cDNA clone Lr_CHECF_02E05 similar to NU1M_LUMTE (Q37546)
            NADH-ubiquinone oxidoreductase chain 1 (EC. Score = 365 bits (936),
            Expect = e-100, mRNA sequence.
ACCESSION   CO408614
VERSION     CO408614.1  GI:49624861
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Chaseley,J., Hedley,B.A., Morgan,A.J., Sturzenbaum,S., Kille,P. and
            Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Head enriched
            library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            PCR PRimers
            FORWARD: gttttcccagtcacgacg
            BACKWARD: caggaaacagctatgaccatg
            Plate: 02  row: E  column: 05
            Seq primer: M13R (caggaaacagctatgaccatg)
            High quality sequence start: 4
            High quality sequence stop: 528.
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
                     /db_xref="taxon:35632"
                     /clone="Lr_CHECF_02E05"
                     /sex="Mixed"
                     /clone_lib="Earthworm Head Enriched library"
ORIGIN

Alignment Scores:
Pred. No.:              208           Length:         679
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.8%          Indels:         0
DB:                     8             Gaps:           0

US-10-821-670A-102 (1-187) x CO408614 (1-679)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        117 TGCCTCAACCATTCGCAGACGCTATTA 143

RESULT 47
CF810266
LOCUS       CF810266                680 bp    mRNA    linear   EST 27-OCT-2003
DEFINITION  Lr_LC1ED_39A02_SAC Lumbricus rubellus Late Cocoon Library 1
            Lumbricus rubellus cDNA clone Lr_LC1ED_39A02 5' similar to
            ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
            terrestris, mRNA sequence.
ACCESSION   CF810266
VERSION     CF810266.1  GI:37998597
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Jones,M., Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S.,
            Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a cocoon
            library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK.
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            The library was prepared using protocols given by the supplier
            (Stratagene).
            PCR PRimers
            FORWARD: M13R(AGCGGATAACAATTTCACACAGGA)
            BACKWARD: T7PL(CTCACTATAGGGCGAATTGG)
            Plate: 39  row: A  column: 02
            Seq primer: SAC(GGGAACAAAAGCTGGAG)
            High quality sequence stop: 503.
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
                     /db_xref="taxon:35632"
                     /clone="Lr_LC1ED_39A02"
                     /tissue_type="Whole worm"
                     /dev_stage="Late Cocoon"
                     /clone_lib="Lumbricus rubellus Late Cocoon Library 1"
                     /note="Vector: pBluescript II SK+; The library was
                     prepared using protocols given by the supplier
                     (Stratagene)."
ORIGIN

Alignment Scores:
Pred. No.:              208           Length:         680
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.8%          Indels:         0
DB:                     5             Gaps:           0

US-10-821-670A-102 (1-187) x CF810266 (1-680)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        119 TGCCTCAACCATTCGCAGACGCTATTA 145

RESULT 48
AZ306792
LOCUS       AZ306792                705 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0008F02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0008F02 F, genomic survey sequence.
ACCESSION   AZ306792
VERSION     AZ306792.1  GI:10345148
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 705)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
```

```
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
OMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0008  row: F  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 705.
EATURES             Location/Qualifiers
     source         1. .705
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0008F02"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
RIGIN

lignment Scores:
red. No.:               215             Length:         705
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             4.8%            Indels:         0
B:                      11              Gaps:           0

'S-10-821-670A-102 (1-187) x AZ306792 (1-705)

:y        145 ValProGlnAsnSerSerLeuGluGlu 153
              |||||||||||||||||||||||||||||
b         344 GTTCCCCAAAATAGCTCTTTAGAAGAG 370

ESULT 49
W744074
OCUS        CW744074                710 bp    DNA     linear   GSS 05-NOV-2004
EFINITION   MARC_912850 CHORI-240-314A10 Bos taurus genomic clone 1H2, genomic
            survey sequence.
CCESSION    CW744074
ERSION      CW744074.1  GI:55459493
EYWORDS     GSS.
OURCE       Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   Smith,T.P.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Harhay,G.P.
  TITLE     SNP discovery in cattle based on low coverage sequencing of BAC
            clones
  JOURNAL   Unpublished (2004)
COMMENT     Other_GSSs: MARC_912466
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Seq primer: GTAATACGACTCACTATAGGG
            Class: BAC subclone.
FEATURES            Location/Qualifiers
     source         1. .710
                    /organism="Bos taurus"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9913"
                    /clone="1H2"
                    /sex="Male"
                    /tissue_type="Blood"
                    /clone_lib="CHORI-240-314A10"
                    /note="Vector: pBLUESCRIPT SK-; Site_1: BamHI; Site_2:
                    BamHI; BAC DNA was digested with Sau3A.  Fragments were
                    sized to 800-1200 bases and subcloned into pBLUESCRIPT
                    SK-."
ORIGIN

Alignment Scores:
Pred. No.:              217             Length:         710
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.8%            Indels:         0
DB:                     13              Gaps:           0

US-10-821-670A-102 (1-187) x CW744074 (1-710)

Qy         76 GlySerCysLeuAlaSerArgLysThr 84
              |||||||||||||||||||||||||
Db         80 GGCTCCTGTCTAGCTAGCAGGAAGACT 106

RESULT 50
DR009499
LOCUS       DR009499                731 bp    mRNA    linear   EST 18-MAY-2005
DEFINITION  Lr_Cu2CF_36D11 Earthworm Copper Exposure Library Lumbricus rubellus
            cDNA clone Lr_Cu2CF_36D11 similar to UniRef100_Q37546
            NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
            Score = 380 bits (975), Expect = e-104, mRNA sequence.
ACCESSION   DR009499
VERSION     DR009499.1  GI:66273643
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
            Sturzenbaum,S., Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Copper
            exposure library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
```

```
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Cardiff using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13(gtttttcccagtcacgacgtt)
            BACKWARD: M13R(caggaaacagctatgaccatg)
            Plate: 36  row: D  column: 11
            Seq primer: caggaaacagctatgaccatg
            High quality sequence start: 2
            High quality sequence stop: 525.
FEATURES              Location/Qualifiers
     source           1. .731
                      /organism="Lumbricus rubellus"
                      /mol_type="mRNA"
                      /db_xref="taxon:35632"
                      /clone="Lr_Cu2CF_36D11"
                      /sex="mixed"
                      /tissue_type="whole worm"
                      /dev_stage="Adult"
                      /clone_lib="Earthworm Copper Exposure Library"
                      /note="Vector: pbluescript II SK; The library was prepared
                      using protocols given by the supplier (Clontech)."
ORIGIN

Alignment Scores:
Pred. No.:                222             Length:         731
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.8%            Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-102 (1-187) x DR009499 (1-731)

Qy          5 CysLeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||||||
Db        111 TGCCTCAACCATTCGCAGACGCTATTA 137

RESULT 51
CZ119478/c
LOCUS       CZ119478                773 bp    DNA     linear   GSS 13-JAN-2005
DEFINITION  OA_BBa0005O19.f OA_BBa Oryza alta genomic clone OA_BBa0005O19 5',
            genomic survey sequence.
ACCESSION   CZ119478
VERSION     CZ119478.1  GI:57710300
KEYWORDS    GSS.
SOURCE      Oryza alta
  ORGANISM  Oryza alta
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            Plate: 0005  row: O  column: 19
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .773
                      /organism="Oryza alta"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:52545"
                      /clone="OA_BBa0005O19"
                      /tissue_type="young leaves"
                      /lab_host="DH10B-T1 phage resistant"
                      /clone_lib="OA_BBa"
                      /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Alignment Scores:
Pred. No.:                233             Length:         773
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.8%            Indels:         0
DB:                       13              Gaps:           0

US-10-821-670A-102 (1-187) x CZ119478 (1-773)

Qy          77 SerCysLeuAlaSerArgLysThrSer 85
               |||||||||||||||||||||||||||
Db         561 AGCTGCTTAGCAAGCAGGAAAACAAGT 535

RESULT 52
DR008334
LOCUS       DR008334                788 bp    mRNA    linear   EST 18-MAY-2005
DEFINITION  Lr_Cu2CF_02G12 Earthworm Copper Exposure Library Lumbricus rubellus
            cDNA clone Lr_Cu2CF_02G12 similar to UniRef100_Q37546
            NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
            Score = 403 bits (1035), Expect = e-111, mRNA sequence.
ACCESSION   DR008334
VERSION     DR008334.1  GI:66272478
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
            Sturzenbaum,S., Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Copper
            exposure library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Cardiff using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13(gtttttcccagtcacgacgtt)
            BACKWARD: M13R(caggaaacagctatgaccatg)
            Plate: 02  row: G  column: 12
            Seq primer: caggaaacagctatgaccatg
            High quality sequence start: 20
            High quality sequence stop: 514.
FEATURES              Location/Qualifiers
     source           1. .788
                      /organism="Lumbricus rubellus"
                      /mol_type="mRNA"
                      /db_xref="taxon:35632"
                      /clone="Lr_Cu2CF_02G12"
                      /sex="mixed"
                      /tissue_type="whole worm"
                      /dev_stage="Adult"
                      /clone_lib="Earthworm Copper Exposure Library"
                      /note="Vector: pbluescript II SK; The library was prepared
                      using protocols given by the supplier (Clontech)."
ORIGIN

Alignment Scores:
Pred. No.:                237             Length:         788
```

```
core:                 9.00          Matches:       9
ercent Similarity:    100.0%        Conservative:  0
est Local Similarity: 100.0%        Mismatches:    0
uery Match:           4.8%          Indels:        0
B:                    9             Gaps:          0

S-10-821-670A-102 (1-187) x DR008334 (1-788)

y          5 CysLeuAsnHisSerGlnThrLeuLeu 13
             |||||||||||||||||||||||||||
b        116 TGCCTCAACCATTCGCAGACGCTATTA 142

ESULT 53
M397339
OCUS       BM397339                796 bp    mRNA    linear   EST 17-JAN-2002
EFINITION  5009-0-31-C08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
           Tetrahymena thermophila cDNA, mRNA sequence.
CCESSION   BM397339
ERSION     BM397339.1  GI:18197392
EYWORDS    EST.
OURCE      Tetrahymena thermophila
 ORGANISM  Tetrahymena thermophila
           Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
           Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
EFERENCE   1  (bases 1 to 796)
 AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
           Frankel,J. and Klobutcher,L.
 TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL   Unpublished (2002)
OMMENT     Contact: Turkewitz AP
           Molecular Genetics and Cell Biology
           University of Chicago
           920 E. 58th Street, Chicago, IL 60637, USA
           Tel: 773 702 4374
           Fax: 773 702 3172
           Email: apturkew@midway.uchicago.edu
           Seq primer: T3.
EATURES             Location/Qualifiers
    source          1. .796
                    /organism="Tetrahymena thermophila"
                    /mol_type="mRNA"
                    /strain="CU428.1"
                    /db_xref="taxon:5911"
                    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                    /note="Vector: BlueScript2 SK+; Details on library
                    preparation can be found in Chilcoat and Turkewitz (2001)
                    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
RIGIN

lignment Scores:
red. No.:             240           Length:        796
core:                 9.00          Matches:       9
ercent Similarity:    100.0%        Conservative:  0
est Local Similarity: 100.0%        Mismatches:    0
uery Match:           4.8%          Indels:        0
B:                    2             Gaps:          0

S-10-821-670A-102 (1-187) x BM397339 (1-796)

y          128 LeuThrAlaIleAspGluLeuGluGln 136
               |||||||||||||||||||||||||||
b          527 TTGACAGCAATTGACGAATTATTACAG 553

ESULT 54
X835464
OCUS       BX835464                822 bp    mRNA    linear   EST 11-FEB-2004
EFINITION  BX835464 Arabidopsis thaliana Adult vegetative tissue Col-0
           Arabidopsis thaliana cDNA clone GSLTLS14ZC06 3PRIM, mRNA sequence.
CCESSION   BX835464
ERSION     BX835464.1  GI:42529547
EYWORDS    EST.
OURCE      Arabidopsis thaliana (thale cress)
 ORGANISM  Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1  (bases 1 to 822)
  AUTHORS  Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
           Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
           Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
  TITLE    Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
           A Combined Approach to Evaluate and Improve Arabidopsis Genome
           Annotation
  JOURNAL  Unpublished (2004)
COMMENT    Contact: Genoscope
           Genoscope - Centre National de Sequencage
           2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           The sequences are based on single pass reads.
           Life Technologies (a division of Invitrogen) members carried out
           full-length librairies construction : Temple G.
           Genoscope members carried out sequencing and annotation : Castelli
           V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
           Schachter V., Weissenbach J., Salanoubat M.
           URGV INRA : Clepet C., Caboche M.
           Annotation is based on the June 2003 version of the Arabidopsis
           genome released by MIPS (Munich Information center for Protein
           Sequences).
           http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
           http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES            Location/Qualifiers
     source         1. .822
                    /organism="Arabidopsis thaliana"
                    /mol_type="mRNA"
                    /ecotype="Col-0"
                    /db_xref="taxon:3702"
                    /clone="GSLTLS14ZC06"
                    /tissue_type="Adult vegetative tissue"
                    /clone_lib="Arabidopsis thaliana Adult vegetative tissue
                    Col-0"
ORIGIN

Alignment Scores:
Pred. No.:            246           Length:        822
Score:                9.00          Matches:       9
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          4.8%          Indels:        0
DB:                   4             Gaps:          0

US-10-821-670A-102 (1-187) x BX835464 (1-822)

Qy         173 ArgAlaValThrIleAsnArgMetMet 181
               |||||||||||||||||||||||||||
Db         581 AGAGCAGTGACGATCAACAGGATGATG 607

RESULT 55
CG385421
LOCUS      CG385421                825 bp    DNA     linear   GSS 26-AUG-2003
DEFINITION OGYBY32TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0644F15,
           genomic survey sequence.
ACCESSION  CG385421
VERSION    CG385421.1  GI:34302688
KEYWORDS   GSS.
SOURCE     Zea mays
  ORGANISM Zea mays
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1  (bases 1 to 825)
  AUTHORS  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
           Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
           Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE    Consortium for Maize Genomics
  JOURNAL  Unpublished (2002)
COMMENT    Other_GSSs: OGYBY32TH
```

```
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: methylation filtered.
FEATURES             Location/Qualifiers
     source          1. .825
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0644F15"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

Alignment Scores:
Pred. No.:                247             Length:         825
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.8%            Indels:         0
DB:                       12              Gaps:           0

US-10-821-670A-102 (1-187) x CG385421 (1-825)

Qy         74 ThrAsnGlySerCysLeuAlaSerArg 82
              |||||||||||||||||||||||||||
Db        268 ACAAATGGGTCGTGTCTGGCGAGCCGA 294

RESULT 56
CT469425/c
LOCUS       CT469425                831 bp    DNA     linear   GSS 03-NOV-2005
DEFINITION  Sus scrofa genomic clone CH242-415C18, genomic survey sequence.
ACCESSION   CT469425
VERSION     CT469425.1  GI:80205278
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 831)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 415C18. 415C18
            is part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .831
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-415C18"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
ORIGIN

Alignment Scores:
Pred. No.:                249             Length:         831
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.8%            Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-102 (1-187) x CT469425 (1-831)

Qy        158 LysThrLysIleLysLeuCysIleLeu 166
              ||||||||||||||||||||||||||
Db        805 AAGACGAAGATCAAGCTATGCATTCTA 779

RESULT 57
CNS01EWE
LOCUS       CNS01EWE                918 bp    DNA     linear   GSS 30-MAY-2001
DEFINITION  Anopheles gambiae GSS T7 end of clone 03C11 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL141087
VERSION     AL141087.1  GI:6999205
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 918)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 918)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .918
                     /organism="Anopheles gambiae"
                     /mol_type="genomic DNA"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="03C11"
                     /clone_lib="NotreDame1"
                     /note="end : T7"
ORIGIN

Alignment Scores:
Pred. No.:                272             Length:         918
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.8%            Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-102 (1-187) x CNS01EWE (1-918)

Qy        162 LysLeuCysIleLeuLeuHisAlaPhe 170
              |||||||||||||||||||||||||
Db        497 AAGCTTTGCATATTGCTTCATGCTTTT 523

RESULT 58
CL092806/c
LOCUS       CL092806                1083 bp    DNA     linear   GSS 05-JAN-2004
DEFINITION  ISB1-22J9_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-22J9,
            genomic survey sequence.
ACCESSION   CL092806
VERSION     CL092806.1  GI:40586441
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
```

```
          Xenopodinae; Xenopus; Silurana.
EFERENCE  1  (bases 1 to 1083)
 AUTHORS  Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
          Mardis,E. and Wilson,R.
 TITLE    A physical map of the xenopus tropicalis genome
 JOURNAL  Unpublished (2003)
OMMENT    Contact: Richard K Wilson
          Genome Sequencing Center
          Washington University School of Medicine
          Email: submissions@watson.wustl.edu
          Insert Length: 75000   Std Error: 0.00
          Seq primer: T7 TAATACGACTCACTATAGGG
          Class: BAC ends
          High quality sequence start: 33
          High quality sequence stop: 811.
EATURES             Location/Qualifiers
    source          1. .1083
                    /organism="Xenopus tropicalis"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:8364"
                    /clone="ISB1-22J9"
                    /clone_lib="ISB1"
                    /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
                    Library Segment 1"
RIGIN

lignment Scores:
red. No.:              314          Length:        1083
core:                  9.00         Matches:       9
ercent Similarity:     100.0%       Conservative:  0
est Local Similarity:  100.0%       Mismatches:    0
uery Match:            4.8%         Indels:        0
B:                     12           Gaps:          0

S-10-821-670A-102 (1-187) x CL092806 (1-1083)

y        160 LysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||
b        798 AAAATAAAGCTGTGTATATTGTTACAT 772

ESULT 59
V123647/c
OCUS        CV123647              1215 bp    mRNA    linear   EST 31-AUG-2004
EFINITION   OSTF30015B11 pDONR201 Entry vector Caenorhabditis elegans cDNA,
            mRNA sequence.
CCESSION    CV123647
ERSION      CV123647.1  GI:51714819
EYWORDS     EST.
OURCE       Caenorhabditis elegans
 ORGANISM   Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
EFERENCE    1  (bases 1 to 1215)
 AUTHORS    Lamesch,P., Milstein,S., Hao,T., Rosenberg,J., Li,N., Sequerra,R.,
            Bosak,S., Doucette-Stamm,L., Vandenhaute,J., Hill,D.E. and Vidal,M.
 TITLE      C. elegans ORFeome Version 3.1: Increasing the coverage of ORFeome
            resources with improved gene predictions
 JOURNAL    Genome Res. (ORFeome issue) (2004) In press
OMMENT      Contact: Philippe Lamesch and Tong Hao
            Marc Vidal Lab
            DFCI
            44, Binney Street, Boston, MA 02115, USA
            Tel: 6176323910
            Fax: 6176325739
            Email: philippe_lamesch@dfci.harvard.edu
            PCR PRimers
            FORWARD: TGTCGGACGAAAAGATTTCAAT
            BACKWARD: TAGTCGCTGGTATCTTGTT.
EATURES             Location/Qualifiers
    source          1. .1215
                    /organism="Caenorhabditis elegans"
                    /mol_type="mRNA"
                    /strain="N2"
                    /db_xref="taxon:6239"
                    /sex="male and hermaphrodite"
                    /tissue_type="all tissues"
                    /cell_type="all cells"
                    /dev_stage="all stages"
                    /clone_lib="pDONR201 Entry vector"
ORIGIN

Alignment Scores:
Pred. No.:             348          Length:        1215
Score:                 9.00         Matches:       9
Percent Similarity:    100.0%       Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:           4.8%         Indels:        0
DB:                    8            Gaps:          0

US-10-821-670A-102 (1-187) x CV123647 (1-1215)

Qy         9 SerGlnThrLeuLeuArgAlaIleSer 17
             |||||||||||||||||||||||||
Db       373 TCCCAAACATTGCTTCGAGCAATATCA 347

RESULT 60
CK549365/c
LOCUS       CK549365                108 bp    mRNA    linear   EST 05-OCT-2004
DEFINITION  swkz0_005913.z1 swk Bombyx mori cDNA, mRNA sequence.
ACCESSION   CK549365
VERSION     CK549365.1  GI:40933819
KEYWORDS    EST.
SOURCE      Bombyx mori (domestic silkworm)
  ORGANISM  Bombyx mori
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
            Bombycoidea; Bombycidae; Bombyx.
REFERENCE   1  (bases 1 to 108)
  AUTHORS   Xia,Q., Zhou,Z., Lu,C., Cheng,D., Dai,F., Li,B., Zhao,P., Zha,X.,
            Cheng,T., Chai,C., Pan,G., Xu,J., Liu,C., Lin,Y., Qian,J., Hou,Y.,
            Wu,Z., Li,G., Pan,M., Li,C., Shen,Y., Lan,X., Yuan,L., Li,T.,
            Xu,H., Yang,G., Wan,Y., Zhu,Y., Yu,M., Shen,W., Wu,D., Xiang,Z.,
            Yu,J., Wang,J., Li,R.Q., Shi,J.P., Li,H., Li,G.Y., Su,J.N.,
            Wang,X.L., Li,G.Q., Zhang,Z.J., Wu,Q.F., Li,J., Zhang,Q.P., Wei,N.,
            Xu,J.Z., Sun,H.B., Dong,L., Liu,D.Y., Zhao,S.L., Zhao,X.L.,
            Meng,Q.S., Lan,F.D., Huang,X.G., Li,Y.Z., Fang,F., Li,C.F.,
            Li,D.W., Sun,Y.Q., Zhang,Z.P., Yang,Z., Huang,Y.Q., Xi,Y., Qi,Q.H.,
            He,D.D., Huang,H.Y., Zhang,X.W., Wang,Z.Q., Li,W.J., Cao,Y.Z.,
            Yu,Y., Yu,H., Ji,H., Ye,J., Chen,H., Zhou,Y., Liu,B., Wang,J.,
            Ye,J., Ji,H., Li,S., Ni,P., Zhang,J., Zhang,Y., Zheng,H., Mao,B,
            Mao,B., Ye,C., Li,S., Wang,J., Wong,G.K. and Yang,H.
  TITLE     A draft sequence for the genome of the domesticated silkworm
            (Bombyx mori)
  JOURNAL   Science 306 (5703), 1937-1940 (2004)
   PUBMED   15591204
COMMENT     Contact: Zhonghuai Xiang
            Southwest Agricultural University
            Chongqing Beibei
            Tel: 86-23-68251123
            Fax: 86-23-68251128
            Email: xzh@swau.cq.cn.
FEATURES            Location/Qualifiers
    source          1. .108
                    /organism="Bombyx mori"
                    /mol_type="mRNA"
                    /strain="DaZhao(P50)"
                    /db_xref="taxon:7091"
                    /sex="mixed"
                    /dev_stage="Embryo (nondiapause)"
                    /clone_lib="swk"
                    /note="Vector: pBluescript II SK(+)"
ORIGIN

Alignment Scores:
Pred. No.:             428          Length:        108
Score:                 8.00         Matches:       8
```

```
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.3%            Indels:        0
DB:                     5               Gaps:          0

US-10-821-670A-102 (1-187) x CK549365 (1-108)

Qy        161 IleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||
Db         67 ATTAAGTTATGCATTTTACTACAC 44

RESULT 61
AZ818875/c
LOCUS       AZ818875                131 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0089I12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0089I12 F, genomic survey sequence.
ACCESSION   AZ818875
VERSION     AZ818875.1  GI:12988783
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 131)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0089  row: I  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 131.
FEATURES             Location/Qualifiers
     source          1. .131
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0089I12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Alignment Scores:
Pred. No.:              508             Length:        131
Score:                  8.00            Matches:       8
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.3%            Indels:        0
DB:                     11              Gaps:          0

US-10-821-670A-102 (1-187) x AZ818875 (1-131)

Qy        159 ThrLysIleLysLeuCysIleLeu 166
              |||||||||||||||||||||||
Db         51 ACTAAAATAAAGCTGTGCATACTG 28

RESULT 62
AV088513/c
LOCUS       AV088513                136 bp    mRNA    linear   EST 25-JUN-1999
DEFINITION  AV088513 Mus musculus tongue C57BL/6J adult Mus musculus cDNA clone
            2310038J02, mRNA sequence.
ACCESSION   AV088513
VERSION     AV088513.1  GI:5219961
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 136)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
            Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,
            Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H.,
            Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
            Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y.,
            Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,
            Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .136
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2310038J02"
                     /sex="male"
                     /tissue_type="tongue"
                     /dev_stage="adult"
                     /clone_lib="Mus musculus tongue C57BL/6J adult"
ORIGIN

Alignment Scores:
Pred. No.:              525             Length:        136
Score:                  8.00            Matches:       8
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
```

```
uery Match:            4.3%          Indels:        0
B:                     1             Gaps:          0

'S-10-821-670A-102 (1-187) x AV088513 (1-136)

y         20 LeuGlnLysAlaArgGlnThrLeu 27
             ||||||||||||||||||||||||
b        104 CTACAAAAAGCAAGACAAACACTG 81

ESULT 63
F751315
OCUS       BF751315                144 bp    mRNA    linear   EST 10-JAN-2001
EFINITION  RC3-BN0426-061100-011-d04 BN0426 Homo sapiens cDNA, mRNA sequence.
CCESSION   BF751315
ERSION     BF751315.1  GI:12077991
EYWORDS    EST.
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
EFERENCE   1  (bases 1 to 144)
 AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
           Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
           Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
           Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
           O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
           Simpson,A.J.
 TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
           sequence tags
 JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  PUBMED   10737800
OMMENT     Contact: Simpson A.J.G.
           Laboratory of Cancer Genetics
           Ludwig Institute for Cancer Research
           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           Project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC3&t2=RC3-BN0426-
           061100-011-d04&t3=2000-11-06&t4=1)
           Seq primer: puc 18 forward
           High quality sequence start: 15
           High quality sequence stop: 143.
EATURES              Location/Qualifiers
    source           1. .144
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="BN0426"
                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
RIGIN

lignment Scores:
red. No.:              552           Length:        144
core:                  8.00          Matches:       8
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            4.3%          Indels:        0
B:                     2             Gaps:          0

S-10-821-670A-102 (1-187) x BF751315 (1-144)

Qy        160 LysIleLysLeuCysIleLeuLeu 167
                 |||||||||||||||||||||||
Db         87 AAAATAAAACTTTGCATATTATTA 110

RESULT 64
AV093643/c
LOCUS       AV093643                181 bp    mRNA    linear   EST 22-NOV-1999
DEFINITION  AV093643 Mus musculus C57BL/6J ES cell Mus musculus cDNA clone
            2400003K03, mRNA sequence.
ACCESSION   AV093643
VERSION     AV093643.1  GI:5241191
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 181)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
            Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,
            Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H.,
            Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
            Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y.,
            Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,
            Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .181
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="2400003K03"
                      /cell_type="ES cell"
                      /clone_lib="Mus musculus C57BL/6J ES cell"
ORIGIN

Alignment Scores:
Pred. No.:             676           Length:        181
Score:                 8.00          Matches:       8
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           4.3%          Indels:        0
DB:                    1             Gaps:          0

US-10-821-670A-102 (1-187) x AV093643 (1-181)

Qy         20 LeuGlnLysAlaArgGlnThrLeu 27
              ||||||||||||||||||||||||
Db        149 CTACAAAAAGCAAGACAAACACTG 126

RESULT 65
AI996576/c
LOCUS       AI996576                191 bp    mRNA    linear   EST 08-SEP-1999
DEFINITION  701667517 A. thaliana, Columbia Col-0, root-1 Arabidopsis thaliana
            cDNA clone 701667517, mRNA sequence.
ACCESSION   AI996576
```

```
VERSION     AI996576.1  GI:5843481
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 191)
  AUTHORS   Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,
            Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P.,
            Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D.,
            Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,
            Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,
            Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and
            Hanson,D.
  TITLE     Arabidopsis thaliana Gene Expression MicroArray
  JOURNAL   Unpublished (1999)
COMMENT     Contact: David Smoller, Ph.D.
            Genome Systems, Inc., a wholly owned subsidiary of Incyte
            Pharmaceuticals, Inc.
            4633 World Parkway Circle, St. Louis, MO 63134, USA
            Tel: 877-577-2733
            Fax: 314-427-3324
            Email: service@genomesystems.com.
FEATURES             Location/Qualifiers
     source          1. .191
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="701667517"
                     /tissue_type="root"
                     /dev_stage="4 - 7 weeks"
                     /clone_lib="A. thaliana, Columbia Col-0, root-1"
                     /note="Vector: pSPORT; Site_1: NotI; Site_2: SalI; cDNA
                     library was derived from untreated root tissue from
                     Arabidopsis thaliana,  Columbia Col-0, at 4 - 7 weeks.
                     Plants were grown in 1:1:1 peat  moss/vermiculite/perlite
                     soil at 22 deg. C +/- 3 deg. C under constant light,  and
                     watered with fertilizer. cDNA synthesis was initiated
                     using a NotI-oligo(dT)  primer. Double-stranded cDNA was
                     blunted, ligated to SalI adaptors, digested with  NotI,
                     size-selected, and cloned into the NotI and SalI sites of
                     the pSPORT vector."
ORIGIN

Alignment Scores:
Pred. No.:                709             Length:         191
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.3%            Indels:         0
DB:                       1               Gaps:           0

US-10-821-670A-102 (1-187) x AI996576 (1-191)

Qy          6 LeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||
Db        166 TTAAATCATTCGCAAACACTATTA 143

RESULT 66
CF773702
LOCUS       CF773702                 204 bp    mRNA    linear   EST 14-APR-2004
DEFINITION  AG_FSL_21D06 Arabidopsis ag-1 35S:AG-GR forward subtraction library
            Arabidopsis thaliana cDNA clone 21D06, mRNA sequence.
ACCESSION   CF773702
VERSION     CF773702.1  GI:46368669
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 204)
  AUTHORS   Hu,W., Wang,Y., Bowers,C. and Ma,H.
  TITLE     Isolation, sequence analysis, and expression studies of florally
            expressed cDNAs in Arabidopsis
  JOURNAL   Plant Mol. Biol. 53 (4), 545-563 (2003)
COMMENT     Contact: Hong Ma
            Hong Ma lab
            The Pennsylvania State University
            315 Wartik Laboratory, University Park, PA 16802, USA
            Tel: 8148636414
            Fax: 8148631357
            Email: hxm16@psu.edu
            Seq primer: M13 Universal
            High quality sequence stop: 204
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .204
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Landsberg erecta"
                     /db_xref="taxon:3702"
                     /clone="21D06"
                     /tissue_type="Inflorescence lacking open or older flowers"
                     /dev_stage="4 week old plants"
                     /clone_lib="Arabidopsis ag-1 35S:AG-GR forward subtraction
                     library"
                     /note="Vector: The pT-Adv vector in the AdvanTAge Cloning
                     Kit(CLONETECH); Subtractive library constructed using the
                     CLONTECH PCR-select cDNA subtraction kit. Transgenic
                     plants homozygous for the ag-1 mutation and carrying a
                     35S:AG-GR construct were generated. RNA was isolated from
                     inflorescences with floral meristems and unopened floral
                     buds and without open or older flowers from transgenic
                     plants that were treated with dexamethasone for 3 days,
                     and used for synthesis of the tester cDNA. RNA from the
                     inflorescences of transgenic plants treated with a control
                     solution without dexamethasone was used to synthesize the
                     driver cDNA. It was observed that a 3-day treatment with
                     dexamethasone can induce anther and carpel characteristics
                     in the flowers of the ag-1 35S:AG-GR plants."
ORIGIN

Alignment Scores:
Pred. No.:                751             Length:         204
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.3%            Indels:         0
DB:                       5               Gaps:           0

US-10-821-670A-102 (1-187) x CF773702 (1-204)

Qy          6 LeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||
Db        179 TTAAATCATTCGCAAACACTACTA 202

RESULT 67
CD957154
LOCUS       CD957154                 216 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  SCH_190 GeneTag2 Zea mays cDNA, mRNA sequence.
ACCESSION   CD957154
VERSION     CD957154.1  GI:32804918
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 216)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
```

```
          Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.infobiogen.fr).
EATURES             Location/Qualifiers
    source          1. .216
                    /organism="Zea mays"
                    /mol_type="mRNA"
                    /cultivar="mixture"
                    /db_xref="taxon:4577"
                    /clone_lib="GeneTag2"
RIGIN

lignment Scores:
red. No.:              790           Length:        216
core:                  8.00          Matches:       8
ercent Similarity:     100.0%        Conservative:  0
'est Local Similarity: 100.0%        Mismatches:    0
uery Match:            4.3%          Indels:        0
'B:                    5             Gaps:          0

S-10-821-670A-102 (1-187) x CD957154 (1-216)

y         88 ThrThrLeuCysLeuSerSerIle 95
             |||||||||||||||||||||||||
b        105 ACTACTTTGTGCCTGTCCTCCATT 128

.ESULT 68
.I523278/c
:OCUS       AI523278               218 bp    mRNA    linear   EST 18-MAR-1999
EFINITION   ar71b08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
            IMAGE:2128023 3', mRNA sequence.
.CCESSION   AI523278
'ERSION     AI523278.1  GI:4437413
:EYWORDS    EST.
'OURCE      Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 218)
 AUTHORS    Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
 TITLE      WashU-NCI human EST Project
 JOURNAL    Unpublished (1997)
OMMENT      Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco.
'EATURES            Location/Qualifiers
    source          1. .218
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2128023"
                    /sex="male"
                    /dev_stage="adult, age 64"
                    /lab_host="DH10B (phage resistant)"
                    /clone_lib="Barstead aorta HPLRB6"
                    /note="Organ: aorta; Vector: pT7T3D-PacI; Site_1: EcoRI;
                    Site_2: NotI; 1st strand cDNA was primed with a Not I -
                    oligo(dT) primer [5'
                    TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTTTT
                    3']; double-stranded cDNA was ligated to Eco RI adaptors
                    [5' AATTCGGATCGAACC 3' and 5' GTTGGATCGG 3'], digested
                    with Not I and cloned into the Not I and Eco RI sites of
                    the modified pT7T3 vector. Library constructed by Bob
                    Barstead."
ORIGIN

Alignment Scores:
Pred. No.:              797           Length:        218
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.3%          Indels:        0
DB:                     1             Gaps:          0

US-10-821-670A-102 (1-187) x AI523278 (1-218)

Qy          76 GlySerCysLeuAlaSerArgLys 83
               |||||||||||||||||||||||
Db         212 GGGTCATGCCTGGCCAGCAGAAAG 189

RESULT 69
BQ359215/c
LOCUS       BQ359215               226 bp    mRNA    linear   EST 20-MAY-2002
DEFINITION  RC3-HN0028-161100-011-g06 HN0028 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ359215
VERSION     BQ359215.1  GI:21026766
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 226)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC3&t2=RC3-HN0028-
            161100-011-g06&t3=2000-11-16&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 7
            High quality sequence stop: 24.
FEATURES            Location/Qualifiers
     source         1. .226
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /dev_stage="Adult"
                    /clone_lib="HN0028"
                    /note="Organ: head_normal; Vector: puc18; Site_1: SmaI;
                    Site_2: SmaI; A mini-library was made by cloning products
                    derived from  ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 -  Ludwig Institute for Cancer Research)
                    profiles into  the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
```

ORIGIN

Alignment Scores:

Pred. No.:	823	Length:	226
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x BQ359215 (1-226)

```
Qy        158 LysThrLysIleLysLeuCysIle 165
              ||||||||||||||||||||||||||
Db        130 AAAACTAAAATAAAACTTTGTATT 107
```

RESULT 70
AI488162
LOCUS AI488162 238 bp mRNA linear EST 18-MAY-2001
DEFINITION EST246484 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED21O9, mRNA sequence.
ACCESSION AI488162
VERSION AI488162.1 GI:4383533
KEYWORDS EST.
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 238)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
TITLE Generation of ESTs from tomato carpel tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES Location/Qualifiers
source 1. .238
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLED21O9"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF'"
/clone_lib="tomato ovary, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."
ORIGIN

Alignment Scores:

Pred. No.:	861	Length:	238
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	1	Gaps:	0

US-10-821-670A-102 (1-187) x AI488162 (1-238)

```
Qy         93 SerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||
Db        104 TCATCTATATATGAAGATCTTAAA 127
```

RESULT 71
BX106716
LOCUS BX106716 270 bp mRNA linear EST 06-FEB-2003
DEFINITION BX106716 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGp998A165251 ; IMAGE:2128023, mRNA sequence.
ACCESSION BX106716
VERSION BX106716.1 GI:27847098
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 270)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE Human UnigeneSet - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998A165251.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
source 1. .270
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998A165251 ; IMAGE:2128023"
/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/clone_lib="Barstead aorta HPLRB6"
/note="Organ: aorta; Vector: pT7T3D-PacI; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCGGATCGAAC 3' and 5' GTTGGATCGG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
ORIGIN

Alignment Scores:

Pred. No.:	963	Length:	270
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-102 (1-187) x BX106716 (1-270)

```
Qy         76 GlySerCysLeuAlaSerArgLys 83
              |||||||||||||||||||||||
Db         47 GGGTCATGCCTGGCCAGCAGAAAG 70
```

RESULT 72
AQ313634
LOCUS AQ313634 270 bp DNA linear GSS 04-MAY-1999
DEFINITION RPCI11-96B3.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-96B3,

```
          genomic survey sequence.
CCESSION  AQ313634
'ERSION   AQ313634.1  GI:4045097
'EYWORDS  GSS.
OURCE     Homo sapiens (human)
 ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
EFERENCE  1  (bases 1 to 270)
 AUTHORS  Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
          Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
 TITLE    Use of human BAC End Sequences for Sequence-Ready Map Building
 JOURNAL  Unpublished (1998)
'OMMENT   Other_GSSs: RPCI11-96B3.TV
          Contact: Shaying Zhao, William Nierman, Mark Adams
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: hbe@tigr.org
          Clones are derived from the human BAC library RPCI-11. For BAC
          library availability, please contact Pieter de Jong
          (pieter@dejong.med.buffalo.edu). Clones may be purchased from
          BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
          Research Genetics (info@resgen.com). BAC end search page:
          http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
          Seq primer: SP6
          Class: BAC ends.
EATURES             Location/Qualifiers
    source          1. .270
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="GDB:7536506"
                    /db_xref="taxon:9606"
                    /clone="RPCI-11-96B3"
                    /sex="Male"
                    /cell_type="Lymphocytes"
                    /clone_lib="RPCI-11"
                    /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                    RPCI11 Human Male BAC Library"
RIGIN

lignment Scores:
red. No.:               963             Length:         270
core:                   8.00            Matches:        8
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             4.3%            Indels:         0
B:                      11              Gaps:           0

'S-10-821-670A-102 (1-187) x AQ313634 (1-270)

y          88 ThrThrLeuCysLeuSerSerIle 95
              |||||||||||||||||||||||||
b         107 ACAACTTTATGCCTTTCTTCTATA 130

ESULT 73
'L398698
OCUS        CL398698                272 bp    DNA     linear   GSS 05-MAR-2004
EFINITION   ZMMBBb0400M17r ZMMBBb (HindIII) Zea mays genomic clone
            ZMMBBb0400M17 3', genomic survey sequence.
CCESSION    CL398698
ERSION      CL398698.1  GI:45204217
EYWORDS     GSS.
OURCE       Zea mays
 ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
EFERENCE    1  (bases 1 to 272)
 AUTHORS    Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 TITLE      Sequencing of the maize genome at PGIR (2003c)
 JOURNAL    Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
            Class: BAC ends
            High quality sequence start: 77.
FEATURES             Location/Qualifiers
     source          1. .272
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBb0400M17"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBb (HindIII)"
                     /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Alignment Scores:
Pred. No.:              969             Length:         272
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.3%            Indels:         0
DB:                     13              Gaps:           0

US-10-821-670A-102 (1-187) x CL398698 (1-272)

Qy          69 GluIleSerLeuIleThrAsnGly 76
               |||||||||||||||||||||||
Db         113 GAGATTTCCCTTATCACTAATGGA 136

RESULT 74
DR380792
LOCUS       DR380792                276 bp    mRNA    linear   EST 29-JAN-2006
DEFINITION  987564 CERES-149 Arabidopsis thaliana cDNA clone 145523 3', mRNA
            sequence.
ACCESSION   DR380792
VERSION     DR380792.1  GI:86085033
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 276)
  AUTHORS   Alexandrov,N.N., Troukhan,M.E., Brover,V.V., Tatarinova,T.,
            Lu,Y.-P., Flavell,R.B. and Feldmann,K.A.
  TITLE     Features of Arabidopsis genes and genome discovered using
            full-length cDNAs
  JOURNAL   Plant Mol. Biol. 60 (1), 71-87 (2006)
COMMENT     Contact: Alexandrov NN
            Ceres, Inc
            1535 Rancho Conejo Blvd., Thousand Oaks, CA 91320, USA
            Tel: (805) 376-6539
            Fax: (805) 498-1002
            Email: nalexandrov@ceres-inc.com.
FEATURES             Location/Qualifiers
     source          1. .276
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Mixed, WS and Landsberg erecta"
                     /db_xref="taxon:3702"
                     /clone="145523"
                     /tissue_type="Mixed floral buds, roots (9:1)"
```

```
                     /clone_lib="CERES-149"
ORIGIN

Alignment Scores:
Pred. No.:                 982           Length:         276
Score:                     8.00          Matches:        8
Percent Similarity:        100.0%        Conservative:   0
Best Local Similarity:     100.0%        Mismatches:     0
Query Match:               4.3%          Indels:         0
DB:                        10            Gaps:           0

US-10-821-670A-102 (1-187) x DR380792 (1-276)

Qy        166 LeuLeuHisAlaPheArgIleArg 173
              |||||||||||||||||||||||
Db         45 CTGCTACATGCCTTTCGAATCCGT 68

RESULT 75
DY123482
LOCUS       DY123482                280 bp    mRNA    linear   EST 01-FEB-2006
DEFINITION  001212BAMA009031HT BAMA Bos taurus cDNA, mRNA sequence.
ACCESSION   DY123482
VERSION     DY123482.1  GI:86317657
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 280)
  AUTHORS   McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
            Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
            Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C.,
            McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
            Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
            Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
            Atkinson,P.
  TITLE     AgResearch, Genesis and Primary Industry Victoria Bovine EST
            project
  JOURNAL   Unpublished (2006)
COMMENT     Contact: Maqbool N
            AgResearch Ltd.
            Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
            Mosgiel, New Zealand
            Email: nauman.maqbool@agresearch.co.nz.
FEATURES             Location/Qualifiers
     source          1. .280
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="Muscle"
                     /clone_lib="BAMA"
                     /note="Vector: pBK-CMV; Bovine Muscle cDNA library"
ORIGIN

Alignment Scores:
Pred. No.:                 994           Length:         280
Score:                     8.00          Matches:        8
Percent Similarity:        100.0%        Conservative:   0
Best Local Similarity:     100.0%        Mismatches:     0
Query Match:               4.3%          Indels:         0
DB:                        10            Gaps:           0

US-10-821-670A-102 (1-187) x DY123482 (1-280)

Qy        136 GlnAlaLeuAsnValAsnSerVal 143
              |||||||||||||||||||||||
Db         67 CAGGCTCTGAATGTAAATAGCGTG 90

RESULT 76
CW284805/c
LOCUS       CW284805                284 bp    DNA     linear   GSS 31-OCT-2004
DEFINITION  104_761_11409991_148_35493_018 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 11409991, genomic survey
            sequence.
ACCESSION   CW284805
VERSION     CW284805.1  GI:55000993
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 284)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
  PUBMED    15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 761  row: o  column: 07
            Seq primer: SWfor Forward
            Class: methylation filtered
            High quality sequence stop: 284.
FEATURES             Location/Qualifiers
     source          1. .284
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="11409991"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:                 1.01e+03      Length:         284
Score:                     8.00          Matches:        8
Percent Similarity:        100.0%        Conservative:   0
Best Local Similarity:     100.0%        Mismatches:     0
Query Match:               4.3%          Indels:         0
DB:                        13            Gaps:           0

US-10-821-670A-102 (1-187) x CW284805 (1-284)

Qy        171 ArgIleArgAlaValThrIleAsn 178
              |||||||||||||||||||||||
Db        134 AGGATAAGGGCAGTCACTATTAAT 111

RESULT 77
DR111969/c
LOCUS       DR111969                291 bp    mRNA    linear   EST 14-JUN-2005
DEFINITION  RTS1_25_A01.b1_A029 Roots minus sulfur Pinus taeda cDNA clone
            RTS1_25_A01_A029 3', mRNA sequence.
ACCESSION   DR111969
VERSION     DR111969.1  GI:67686779
KEYWORDS    EST.
SOURCE      Pinus taeda (loblolly pine)
  ORGANISM  Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1  (bases 1 to 291)
```

```
 AUTHORS   Pratt,L., Cordonnier-Pratt,M.M., Lorenz,W.W., Zimmermann,C. and
           Dean,J.F.D.
 TITLE     An EST database from sulfur-deficient loblolly pine (Pinus taeda)
           roots
 JOURNAL   Unpublished (2005)
OMMENT     Other_ESTs: RTS1_25_A01.g1_A029
           Contact: Cordonnier-Pratt MM
           Laboratory for Genomics and Bioinformatics
           The University of Georgia, Department of Plant Biology
           Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
           Tel: 706 542 1860
           Fax: 706 583 0210
           Email: mmpratt@uga.edu
           RNA prepared and library constructed by W. Walter Lorenz (School of
           Forest Resources, University of Georgia); plant material prepared
           by Craig Zimmermann (School of Forest Resources, University of
           Georgia) using rooted cuttings provided by the Forest Biology
           Research Cooperative (FBRC) and the CCLONES project a the
           University of Florida; sequencing done in the Laboratory for
           Genomics and Bioinformatics, University of Georgia. Sequence ends
           have been trimmed to exclude vector and regions below Phred quality
           16. Three-prime sequences are presented as their reverse complement
           and have been trimmed to exclude polyA.
           Seq primer: M13-21 (TGTAAAACGACGGCCAGT)
           POLYA=Yes.
'EATURES             Location/Qualifiers
     source          1. .291
                     /organism="Pinus taeda"
                     /mol_type="mRNA"
                     /strain="3 CCLONES"
                     /db_xref="taxon:3352"
                     /clone="RTS1_25_A01_A029"
                     /lab_host="DH10B-T1 phage-resistant E. coli"
                     /clone_lib="Roots minus sulfur"
                     /note="Organ: Root; Vector: pSL1180; Site_1: EcoRI;
                     Site_2: XhoI; The library was prepared from polyA+ RNA
                     from the roots of 1-year-old loblolly pine (Pinus taeda)
                     cuttings that were rooted and then planted in washed sand.
                     The rooted cuttings were maintained for 136 days (July 25
                     2003 harvest) under ambient conditions in a local
                     greenhouse. They were kept on a weekly regimen of 0.5x
                     nutrient-complete Hoagland's solution and supplemented
                     with additional water sufficient to maintain a 15% soil
                     moisture content. Starting five weeks prior to harvesting
                     roots for mRNA preparation, the weekly fertilizer regimen
                     for the potted trees was modified to omit sulfur from the
                     0.5x Hoagland's solution (5 applications). For two days
                     prior to starting the modified fertilizer regimen, pots
                     were flushed extensively with water to reduce residual
                     levels of sulfur. Double-stranded cDNA was cloned
                     unidirectionally into pSL1180. Inserts can be excised with
                     EcoRI (5' end) and XhoI (3' end)."
RIGIN

lignment Scores:
red. No.:              1.03e+03      Length:        291
core:                  8.00          Matches:       8
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            4.3%          Indels:        0
B:                     9             Gaps:          0

'S-10-821-670A-102 (1-187) x DR111969 (1-291)

y         16 IleSerAsnThrLeuGlnLysAla 23
             ||||||||||||||||||||||||
b        164 ATTTCCAATACCCTCCAAAAGGCC 141

ESULT 78
G883630/c
OCUS       BG883630               298 bp    mRNA    linear   EST 30-MAY-2001
'EFINITION fp27g12.y1 zebrafish gridded kidney Danio rerio cDNA clone
           IMAGE:4744534 5' similar to SW:ACTM_STYPL Q00214 ACTIN, MUSCLE. ;,
           mRNA sequence.
ACCESSION  BG883630
VERSION    BG883630.1  GI:14260722
KEYWORDS   EST.
SOURCE     Danio rerio (zebrafish)
  ORGANISM Danio rerio
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
           Cypriniformes; Cyprinidae; Danio.
REFERENCE  1  (bases 1 to 298)
  AUTHORS  Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
           Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
           Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
           Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
           Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
           Waterston,R. and Wilson,R.
  TITLE    WashU Zebrafish EST Project 1998
  JOURNAL  Unpublished (1998)
COMMENT    Other_ESTs: fp27g12.x1
           Contact: Stephen L. Johnson
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: zbrafish@watson.wustl.edu
           cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
           Washington University Genome Sequencing Center Clone distribution:
           Genome Systems, St. Louis, Missouri (web address:
           www.genomesystems.com) (email contact: info@genomesystems.com) and
           Research Genetics, Huntsville, Alabama (web address:
           www.resgen.com) (email contact: info@resgen.com) and
           RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
           www.rzpd.de)
           Trace considered overall poor quality
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .298
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:4744534"
                     /sex="mixed"
                     /tissue_type="kidney pooled from 300 wild type adults"
                     /lab_host="XLOLR"
                     /clone_lib="zebrafish gridded kidney"
                     /note="Organ: kidney; Vector: pBK-CMV; Site_1: EcoRI;
                     Site_2: XhoI; Oligo dT cDNA library constructed from mRNA
                     pooled from pooled kidney  tissue from 300 adult
                     zebrafish."
ORIGIN

Alignment Scores:
Pred. No.:              1.05e+03      Length:        298
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.3%          Indels:        0
DB:                     2             Gaps:          0

US-10-821-670A-102 (1-187) x BG883630 (1-298)

Qy         72 LeuIleThrAsnGlySerCysLeu 79
              |||||||||||||||||||||||
Db         40 CTCATCACCAACGGTAGCTGTCTT 17

RESULT 79
BF947586
LOCUS      BF947586               305 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION QV2-NN0045-291000-447-d01 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF947586
VERSION    BF947586.1  GI:12364861
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 305)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
    PUBMED  10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-NN0045-
            291000-447-d01&t3=2000-10-29&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 305.
FEATURES              Location/Qualifiers
     source           1. .305
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /dev_stage="Adult"
                      /clone_lib="NN0045"
                      /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                      Site_2: SmaI; A mini-library was made by cloning products
                      derived from  ORESTES PCR (U.S. Letters Patent application
                      No. 196,716 -  Ludwig Institute for Cancer Research)
                      profiles into  the pUC 18 vector. Reverse transcription of
                      tissue mRNA and cDNA amplification were performed under
                      low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                1.07e+03        Length:          305
Score:                    8.00            Matches:         8
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              4.3%            Indels:          0
DB:                       2               Gaps:            0

US-10-821-670A-102 (1-187) x BF947586 (1-305)

Qy        134 LeuLeuGlnAlaLeuAsnValAsn 141
              |||||||||||||||||||||||
Db         13 TTATTACAGGCTCTCAATGTGAAT 36

RESULT 80
DY190750/c
LOCUS       DY190750                309 bp    mRNA    linear   EST 02-FEB-2006
DEFINITION  000929BEMN024688HT BEMN Bos taurus cDNA, mRNA sequence.
ACCESSION   DY190750
VERSION     DY190750.1  GI:86394850
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 309)
  AUTHORS   McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
            Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
            Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C.,
            McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
            Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
            Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
            Atkinson,P.
  TITLE     AgResearch, Genesis and Primary Industry Victoria Bovine EST
            project
  JOURNAL   Unpublished (2006)
COMMENT     Contact: Maqbool N
            AgResearch Ltd.
            Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
            Mosgiel, New Zealand
            Email: nauman.maqbool@agresearch.co.nz.
FEATURES              Location/Qualifiers
     source           1. .309
                      /organism="Bos taurus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /tissue_type="Life Tech Normalised library"
                      /clone_lib="BEMN"
                      /note="Vector: pCMV-Sport6; Life Tech Normalised library"
ORIGIN

Alignment Scores:
Pred. No.:                1.08e+03        Length:          309
Score:                    8.00            Matches:         8
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              4.3%            Indels:          0
DB:                       10              Gaps:            0

US-10-821-670A-102 (1-187) x DY190750 (1-309)

Qy         89 ThrLeuCysLeuSerSerIleTyr 96
              |||||||||||||||||||||||
Db        240 ACATTATGTCTTAGCTCTATATAC 217

RESULT 81
Z43509
LOCUS       Z43509                  310 bp    mRNA    linear   EST 11-NOV-1994
DEFINITION  HSC1EA031 normalized infant brain cDNA Homo sapiens cDNA clone
            c-1ea03, mRNA sequence.
ACCESSION   Z43509
VERSION     Z43509.1  GI:571096
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 310)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
    PUBMED  7757816
COMMENT     Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1ea03
            Seq primer: (-21)M13_universal.
FEATURES              Location/Qualifiers
     source           1. .310
                      /organism="Homo sapiens"
```

```
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="c-1ea03"
                     /sex="Female"
                     /tissue_type="total brain"
                     /dev_stage="3 months old"
                     /clone_lib="normalized infant brain cDNA"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI; sex=Female; dev_stage=3 months old;
                     isolate=muscular atrophy patient;  tissue_type=total
                     brain;  total mRNA was oligo-(dT) primed and directionally
                     cloned 5' -> 3' into the  HindIII -> NotI sites of the
                     lafmid BA vector. Clone library from B.Soares,  Psychiatry
                     Dept. Columbia University, USA.  Normalization_method:
                     Bento Soares, P.N.A.S in press"
RIGIN

lignment Scores:
red. No.:                1.09e+03        Length:         310
core:                    8.00            Matches:        8
ercent Similarity:       100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              4.3%            Indels:         0
B:                       10              Gaps:           0

S-10-821-670A-102 (1-187) x Z43509 (1-310)

y         133 GluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||
b         242 GAATTGCTGCAGGCATTAAATGTA 265

ESULT 82
X722217/c
OCUS       BX722217                320 bp    mRNA    linear   EST 18-NOV-2003
EFINITION  BX722217 XGC-tadpole Xenopus tropicalis cDNA clone TTpA072f15 3',
           mRNA sequence.
CCESSION   BX722217
ERSION     BX722217.1  GI:38394958
EYWORDS    EST.
OURCE      Xenopus tropicalis (western clawed frog)
 ORGANISM  Xenopus tropicalis
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
           Xenopodinae; Xenopus; Silurana.
EFERENCE   1  (bases 1 to 320)
 AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
 TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL   Unpublished (2003)
OMMENT     Contact: Croning MDR
           Sanger Institute
           Hinxton, Cambridgeshire, CB10 1SA, UK
           Email: trop@sanger.ac.uk
           Sanger Xenopus tropicalis EST project 2001
           TROPICALIS_SEQUENCE_ID: TTpA072f15.q1kaT7
           Sequencing primer: T7
           This sequence is from a Xenopus Gene Collection (XGC) library
           constructed by Nigel Garrett.
           cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
           embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
           EcoRI at the 5' end and NotI at the 3' end.
           Vector: pCS107; Site_1: EcoRI; Site_2: NotI
           Host: Escherichia coli DH10B.
EATURES                Location/Qualifiers
    source             1. .320
                       /organism="Xenopus tropicalis"
                       /mol_type="mRNA"
                       /db_xref="taxon:8364"
                       /clone="TTpA072f15"
                       /dev_stage="tadpole (stage 35-40)"
                       /lab_host="E. coli DH10B"
                       /clone_lib="XGC-tadpole"
                       /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                       was oligo dT primed from 5ug of poly A+ RNA from tadpole
                       embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                       with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

Alignment Scores:
Pred. No.:               1.12e+03        Length:         320
Score:                   8.00            Matches:        8
Percent Similarity:      100.0%          Conservative:   0
Best Local Similarity:   100.0%          Mismatches:     0
Query Match:             4.3%            Indels:         0
DB:                      4               Gaps:           0

US-10-821-670A-102 (1-187) x BX722217 (1-320)

Qy          65 LeuAlaSerArgGluIleSerLeu 72
               |||||||||||||||||||||||
Db         283 CTTGCAAGCAGGGAGATTAGTTTG 260

RESULT 83
AW828155/c
LOCUS       AW828155                320 bp    mRNA    linear   EST 10-MAY-2001
DEFINITION  ra67c01.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
            cDNA 5' similar to SW:ENOB_MOUSE P21550 BETA ENOLASE ;, mRNA
            sequence.
ACCESSION   AW828155
VERSION     AW828155.1  GI:7921941
KEYWORDS    EST.
SOURCE      Meloidogyne incognita (southern root-knot nematode)
  ORGANISM  Meloidogyne incognita
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
REFERENCE   1  (bases 1 to 320)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
            Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
            Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
            Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
            Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Uma Rao and David Bird
            (david_bird@ncsu.edu) at North Carolina State University. DNA
            Sequencing by: Washington University Genome Sequencing Center St.
            Louis.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 171.
FEATURES              Location/Qualifiers
     source           1. .320
                      /organism="Meloidogyne incognita"
                      /mol_type="mRNA"
                      /db_xref="taxon:6306"
                      /dev_stage="enriched for 2nd stage juveniles"
                      /lab_host="XLORL"
                      /clone_lib="Bird-Rao Meloidogyne incognita J2"
                      /note="Vector: ZAP express - pBKCMV (Stratagene); Site_1:
                      EcoRI; Site_2: XhoI; Oligo (dT) primed library.  cDNA was
                      contructed and cloned  unidirectionally into the vector
                      within the 5' EcoRI and  3' XhoI sites.  This library was
                      constructed by Dr. Uma Rao  and Dr. David Bird at North
                      Carolina state University."
ORIGIN

Alignment Scores:
Pred. No.:               1.12e+03        Length:         320
Score:                   8.00            Matches:        8
```

```
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.3%            Indels:        0
DB:                     7               Gaps:          0

US-10-821-670A-102 (1-187) x AW828155 (1-320)

Qy         71 SerLeuIleThrAsnGlySerCys 78
              ||||||||||||||||||||||||
Db        152 TCCCTCATCACCAACGGCAGTTGC 129

RESULT 84
BM133293/c
LOCUS       BM133293                323 bp    mRNA    linear   EST 07-MAY-2003
DEFINITION  NXLV_002_B09_F NXLV (Nsf Xylem Late wood Vertical) Pinus taeda cDNA
            clone NXLV_002_B09 5', mRNA sequence.
ACCESSION   BM133293
VERSION     BM133293.1  GI:17140144
KEYWORDS    EST.
SOURCE      Pinus taeda (loblolly pine)
  ORGANISM  Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1  (bases 1 to 323)
  AUTHORS   Sederoff,R.
  TITLE     Molecular Basis of Wood Formation in the Pine Megagenome
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Sederoff, Ron
            Forest Biotechnology
            North Carolina State University
            840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
            NC 27695, USA
            Tel: 919 515 7800
            Fax: 919 515 7801
            Email: ron_sederoff@ncsu.edu, jerri_johnson@ncsu.edu
            Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further
            information.
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .323
                     /organism="Pinus taeda"
                     /mol_type="mRNA"
                     /strain="Coastal plain loblolly pine from North Carolina"
                     /db_xref="taxon:3352"
                     /clone="NXLV_002_B09"
                     /tissue_type="primary xylem"
                     /dev_stage="late wood"
                     /lab_host="XL1-Blue"
                     /clone_lib="NXLV (Nsf Xylem Late wood Vertical)"
                     /note="Vector: pTriplEx; Site_1: EcoRI; The library is
                     from late (summer-August) wood, taken from below the crown
                     of a 20 year old tree. The harvested xylem tissue was on
                     the the cusp between transitional and mature wood. NOTE:
                     The sequences contain a 'cDNA adapter' between the EcoRI
                     site and the start of the EST. The adapter sequence is
                     'AATTCGGCCATTATGGCC'."
ORIGIN

Alignment Scores:
Pred. No.:              1.13e+03        Length:        323
Score:                  8.00            Matches:       8
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.3%            Indels:        0
DB:                     2               Gaps:          0

US-10-821-670A-102 (1-187) x BM133293 (1-323)

Qy         10 GlnThrLeuLeuArgAlaIleSer 17
              |||||||||||||||||||||||
Db        181 CAAACATTACTAAGAGCAATTTCC 158

RESULT 85
DX058631/c
LOCUS       DX058631                323 bp    DNA     linear   GSS 10-JAN-2006
DEFINITION  KBrB064E12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrB064E12, genomic survey
            sequence.
ACCESSION   DX058631
VERSION     DX058631.1  GI:84752927
KEYWORDS    GSS.
SOURCE      Brassica rapa subsp. pekinensis
  ORGANISM  Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 323)
  AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
  TITLE     End sequence of Brassica rapa BamHI (KBrB) BAC clone
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@rda.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
            KBrB064E12
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .323
                     /organism="Brassica rapa subsp. pekinensis"
                     /mol_type="genomic DNA"
                     /cultivar="Chiifu"
                     /sub_species="pekinensis"
                     /db_xref="taxon:51351"
                     /clone="KBrB064E12"
                     /lab_host="E.coli DH10B"
                     /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                     /note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
                     pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                     by Yong-Pyo Lim (CNU)."
ORIGIN

Alignment Scores:
Pred. No.:              1.13e+03        Length:        323
Score:                  8.00            Matches:       8
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            4.3%            Indels:        0
DB:                     14              Gaps:          0

US-10-821-670A-102 (1-187) x DX058631 (1-323)

Qy         54 LeuProLeuGluLeuThrMetAsn 61
              |||||||||||||||||||||||
Db         38 CTTCCATTGGAACTGACTATGAAT 15

RESULT 86
BM148903
LOCUS       BM148903                326 bp    mRNA    linear   EST 30-NOV-2001
DEFINITION  TCAAP2E5272 Pediatric acute myelogenous leukemia cell (FAB M1)
            Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP5272, mRNA
            sequence.
ACCESSION   BM148903
VERSION     BM148903.1  GI:17170039
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```

```
EFERENCE   1  (bases 1 to 326)
 AUTHORS   Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
           Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
 TITLE     Pediatric Leukemia cDNA Sequencing Project (2001)
 JOURNAL   Unpublished (2001)
OMMENT     Contact: Dr. Judith F. Margolin
           Texas Children's Cancer Center and Human Genome Sequencing Center
           at Baylor College of Medicine
           1102 Bates, MC3-3320 Houston, TX 77030, USA
           Tel: 832-824-4536
           Fax: 832-825-4038
           Email: clones@txccc.org
           Seq primer: M13 primer.
EATURES             Location/Qualifiers
    source          1. .326
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="TCAAP5272"
                    /sex="male"
                    /tissue_type="leukopheresis"
                    /cell_type="myeloid cell"
                    /dev_stage="pediatric 6 years"
                    /lab_host="DH10B"
                    /clone_lib="Pediatric acute myelogenous leukemia cell (FAB
                    M1) Baylor-HGSC project=TCAA"
                    /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
                    First strand cDNA was primed with an anchored
                    XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGCAGGAGGAG(T)VN
                    3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
                    was primed with a BamH1-dC primer
                    [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3'].
                    Double-stranded cDNA was then digested with BamH1 and XhoI
                    and directionally cloned into the BamH1 and Sa1I sites of
                    lambda pSB vector. Library went through one round of
                    normalization. Library was constructed by Wei Yu at RIKEN
                    of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
                    Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M,
                    Schneider C, Hayashizaki Y, High efficiency selection of
                    full-length cDNA by improved biotinylated cap trapper.,
                    DNA Res 4: 1, 61-6, Feb 28, 1997)"
RIGIN

lignment Scores:
red. No.:              1.14e+03        Length:         326
core:                  8.00            Matches:        8
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            4.3%            Indels:         0
B:                     2               Gaps:           0

S-10-821-670A-102 (1-187) x BM148903 (1-326)

y          76 GlySerCysLeuAlaSerArgLys 83
              |||||||||||||||||||||
b           8 GGGTCATGCCTGGCCAGCAGAAAG 31

ESULT 87
N091358/c
OCUS       DN091358                333 bp    mRNA    linear   EST 14-FEB-2005
EFINITION  JGI_CABE4215.rev NIH_XGC_tropOva1 Xenopus tropicalis cDNA clone
           IMAGE:7822680 3', mRNA sequence.
CCESSION   DN091358
ERSION     DN091358.1  GI:59758462
EYWORDS    EST.
OURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM Xenopus tropicalis
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
           Xenopodinae; Xenopus; Silurana.
EFERENCE   1  (bases 1 to 333)
  AUTHORS  Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
           Brokstein,P. and Lindquist,E.A.
  TITLE    DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL  Unpublished (2004)
COMMENT    Other_ESTs: JGI_CABE4215.fwd
           Contact: Lindquist,E.A., Richardson,P.
           DOE Joint Genome Institute
           2800 Mitchell Drive, Walnut Creek, CA 94598, USA
           Tel: 925 296 5600
           Fax: 925 296 5710
           Email: cdna@jgi-psf.org
           Tissue Procurement: Robert M. Grainger
           cDNA Library Preparation: Bruce Blumberg Laboratory, University of
           California, Irvine
           DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
           Clone Distribution: I.M.A.G.E. Consortium/LLNL:
           http://image.llnl.gov
           Naming Conventions: EST name is generated by the concatenation of
           the JGI Clone Id and the direction of sequencing. The suffix '.rev'
           indicates a reverse sequencing read of the insert. It does not
           necessarily reflect the orientation of the insert.
           Poly-A: Based upon the presence of a run of 14 or more T residues
           at the beginning of the sequence, this clone was polyadenylated.
           The resulting Poly-T sequence has been removed.
           Plate: CABE 0041  row: n  column: 22
           High quality sequence stop: 319
           POLYA=Yes.
FEATURES            Location/Qualifiers
     source         1. .333
                    /organism="Xenopus tropicalis"
                    /mol_type="mRNA"
                    /strain="N6 (Nigerian 6th generation inbred)"
                    /db_xref="taxon:8364"
                    /clone="IMAGE:7822680"
                    /sex="Female"
                    /tissue_type="Ovary"
                    /dev_stage="Adult"
                    /lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
                    /clone_lib="NIH_XGC_tropOva1"
                    /note="Vector: pCS107; Site_1: EcoRI; Site_2: XhoI; The
                    library was prepared from 5 ug of poly A+ RNA by oligo-dT
                    priming
                    (5'-ACTAGTGCGGCCGCCTAGGCCTCGAGTTTTTTTTTTTTTTTTV-3') and
                    Stratascript reverse transcriptase. After ligation of
                    EcoRI adapters (5'-AATTCGGCACGAGG-3') followed by kinasing
                    adapters and by XhoI digestion, the cDNA was size selected
                    by chromatography on Sepharose CL-2B columns and fractions
                    containing cDNAs larger than 1000 bp were ligated into
                    EcoRI/XhoI-digested pCS107. Reference for library
                    construction: Current Genomics 4, 635-644. Library
                    constructed by Michelle Tabb and Bruce Blumberg (Dept of
                    Developmental and Cell Biology, University of California,
                    Irvine)."
ORIGIN

Alignment Scores:
Pred. No.:             1.16e+03        Length:         333
Score:                 8.00            Matches:        8
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           4.3%            Indels:         0
DB:                    9               Gaps:           0

US-10-821-670A-102 (1-187) x DN091358 (1-333)

Qy          65 LeuAlaSerArgGluIleSerLeu 72
               |||||||||||||||||||||||
Db         245 CTTGCAAGCAGGGAGATTAGTTTG 222

RESULT 88
DV663472/c
LOCUS      DV663472                334 bp    mRNA    linear   EST 09-NOV-2005
DEFINITION CGN-151 Pericarp Coffea canephora cDNA clone cccp24n9 5', mRNA
           sequence.
ACCESSION  DV663472
```

```
VERSION     DV663472.1  GI:81289278
KEYWORDS    EST.
SOURCE      Coffea canephora
  ORGANISM  Coffea canephora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
            Coffea.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Lin,C., Mueller,L.A., McCarthy,J., Crouzillat,D., Petiard,V. and
            Tanksley,S.D.
  TITLE     Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep
            Sequencing of Seed and Cherry Transcripts
  JOURNAL   Theoretical and Applied Genetics (2005) In press
COMMENT     Contact: Steven D. Tanksley
            Department of Plant Breeding
            Cornell University
            248 Emerson Hall, Ithaca, NY 14853
            Tel: 607 255 1673
            Fax: 607 255 6683
            Email: sdt4@cornell.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Sol
            Genome Network website (http://www.sgn.cornell.edu)
            Plate: 24  row: n  column: 9
            Seq primer: M13R
            High quality sequence stop: 334.
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Coffea canephora"
                     /mol_type="mRNA"
                     /db_xref="taxon:49390"
                     /clone="cccp24n9"
                     /tissue_type="pericarp"
                     /dev_stage="All developmental stages"
                     /clone_lib="Pericarp"
                     /note="Vector: pBSSK-; Site_1: ECoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:                1.16e+03       Length:         334
Score:                    8.00           Matches:        8
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              4.3%           Indels:         0
DB:                       10             Gaps:           0

US-10-821-670A-102 (1-187) x DV663472 (1-334)

Qy          6 LeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||
Db         57 CTTAACCATTCCCAAACCCTTCTC 34

RESULT 89
DV663813/c
LOCUS       DV663813                334 bp    mRNA    linear   EST 09-NOV-2005
DEFINITION  CGN-632 Pericarp Coffea canephora cDNA clone cccp20a18 5', mRNA
            sequence.
ACCESSION   DV663813
VERSION     DV663813.1  GI:81289619
KEYWORDS    EST.
SOURCE      Coffea canephora
  ORGANISM  Coffea canephora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
            Coffea.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Lin,C., Mueller,L.A., McCarthy,J., Crouzillat,D., Petiard,V. and
            Tanksley,S.D.
  TITLE     Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep
            Sequencing of Seed and Cherry Transcripts
  JOURNAL   Theoretical and Applied Genetics (2005) In press
COMMENT     Contact: Steven D. Tanksley
            Department of Plant Breeding
            Cornell University
            248 Emerson Hall, Ithaca, NY 14853
            Tel: 607 255 1673
            Fax: 607 255 6683
            Email: sdt4@cornell.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Sol
            Genome Network website (http://www.sgn.cornell.edu)
            Plate: 20  row: a  column: 18
            Seq primer: M13R
            High quality sequence stop: 334.
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Coffea canephora"
                     /mol_type="mRNA"
                     /db_xref="taxon:49390"
                     /clone="cccp20a18"
                     /tissue_type="pericarp"
                     /dev_stage="All developmental stages"
                     /clone_lib="Pericarp"
                     /note="Vector: pBSSK-; Site_1: ECoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:                1.16e+03       Length:         334
Score:                    8.00           Matches:        8
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              4.3%           Indels:         0
DB:                       10             Gaps:           0

US-10-821-670A-102 (1-187) x DV663813 (1-334)

Qy          6 LeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||
Db         57 CTTAACCATTCCCAAACCCTTCTC 34

RESULT 90
DV672452/c
LOCUS       DV672452                334 bp    mRNA    linear   EST 15-NOV-2005
DEFINITION  CGN-8068 Pericarp Coffea canephora cDNA clone cccp8d5 5', mRNA
            sequence.
ACCESSION   DV672452
VERSION     DV672452.1  GI:82445832
KEYWORDS    EST.
SOURCE      Coffea canephora
  ORGANISM  Coffea canephora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
            Coffea.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Lin,C., Mueller,L.A., McCarthy,J., Crouzillat,D., Petiard,V. and
            Tanksley,S.D.
  TITLE     Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep
            Sequencing of Seed and Cherry Transcripts
  JOURNAL   Theoretical and Applied Genetics (2005) In press
COMMENT     Contact: Steven D. Tanksley
            Department of Plant Breeding
            Cornell University
            248 Emerson Hall, Ithaca, NY 14853
            Tel: 607 255 1673
            Fax: 607 255 6683
            Email: sdt4@cornell.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Sol
            Genome Network website (http://www.sgn.cornell.edu)
            Plate: 8  row: d  column: 5
            Seq primer: M13R
            High quality sequence stop: 334.
FEATURES             Location/Qualifiers
```

```
    source          1. .334
                    /organism="Coffea canephora"
                    /mol_type="mRNA"
                    /db_xref="taxon:49390"
                    /clone="cccp8d5"
                    /tissue_type="pericarp"
                    /dev_stage="All developmental stages"
                    /clone_lib="Pericarp"
                    /note="Vector: pBSSK-; Site_1: ECoRI; Site_2: XhoI"
RIGIN

lignment Scores:
red. No.:               1.16e+03        Length:         334
core:                   8.00            Matches:        8
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             4.3%            Indels:         0
B:                      10              Gaps:           0

S-10-821-670A-102 (1-187) x DV672452 (1-334)

y          6 LeuAsnHisSerGlnThrLeuLeu 13
             |||||||||||||||||||||||
b         57 CTTAACCATTCCCAAACCCTTCTC 34

ESULT 91
V673948/c
OCUS        DV673948                334 bp    mRNA    linear   EST 15-NOV-2005
EFINITION   CGN-10251 Pericarp Coffea canephora cDNA clone cccp6o24 5', mRNA
            sequence.
CCESSION    DV673948
ERSION      DV673948.1  GI:82447328
EYWORDS     EST.
OURCE       Coffea canephora
 ORGANISM   Coffea canephora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
            Coffea.
EFERENCE    1  (bases 1 to 334)
 AUTHORS    Lin,C., Mueller,L.A., McCarthy,J., Crouzillat,D., Petiard,V. and
            Tanksley,S.D.
 TITLE      Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep
            Sequencing of Seed and Cherry Transcripts
 JOURNAL    Theoretical and Applied Genetics (2005) In press
OMMENT      Contact: Steven D. Tanksley
            Department of Plant Breeding
            Cornell University
            248 Emerson Hall, Ithaca, NY 14853
            Tel: 607 255 1673
            Fax: 607 255 6683
            Email: sdt4@cornell.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Sol
            Genome Network website (http://www.sgn.cornell.edu)
            Plate: 6  row: o  column: 24
            Seq primer: M13R
            High quality sequence stop: 334.
EATURES             Location/Qualifiers
    source          1. .334
                    /organism="Coffea canephora"
                    /mol_type="mRNA"
                    /db_xref="taxon:49390"
                    /clone="cccp6o24"
                    /tissue_type="pericarp"
                    /dev_stage="All developmental stages"
                    /clone_lib="Pericarp"
                    /note="Vector: pBSSK-; Site_1: ECoRI; Site_2: XhoI"
RIGIN

lignment Scores:
red. No.:               1.16e+03        Length:         334
core:                   8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.3%            Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-102 (1-187) x DV673948 (1-334)

Qy          6 LeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||
Db         57 CTTAACCATTCCCAAACCCTTCTC 34

RESULT 92
DV674662/c
LOCUS       DV674662                334 bp    mRNA    linear   EST 15-NOV-2005
DEFINITION  CGN-11317 Pericarp Coffea canephora cDNA clone cccp8g10 5', mRNA
            sequence.
ACCESSION   DV674662
VERSION     DV674662.1  GI:82448042
KEYWORDS    EST.
SOURCE      Coffea canephora
  ORGANISM  Coffea canephora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
            Coffea.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Lin,C., Mueller,L.A., McCarthy,J., Crouzillat,D., Petiard,V. and
            Tanksley,S.D.
  TITLE     Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep
            Sequencing of Seed and Cherry Transcripts
  JOURNAL   Theoretical and Applied Genetics (2005) In press
COMMENT     Contact: Steven D. Tanksley
            Department of Plant Breeding
            Cornell University
            248 Emerson Hall, Ithaca, NY 14853
            Tel: 607 255 1673
            Fax: 607 255 6683
            Email: sdt4@cornell.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Sol
            Genome Network website (http://www.sgn.cornell.edu)
            Plate: 8  row: g  column: 10
            Seq primer: M13R
            High quality sequence stop: 334.
FEATURES            Location/Qualifiers
     source         1. .334
                    /organism="Coffea canephora"
                    /mol_type="mRNA"
                    /db_xref="taxon:49390"
                    /clone="cccp8g10"
                    /tissue_type="pericarp"
                    /dev_stage="All developmental stages"
                    /clone_lib="Pericarp"
                    /note="Vector: pBSSK-; Site_1: ECoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:              1.16e+03        Length:         334
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.3%            Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-102 (1-187) x DV674662 (1-334)

Qy          6 LeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||
Db         57 CTTAACCATTCCCAAACCCTTCTC 34

RESULT 93
DV678489/c
LOCUS       DV678489                334 bp    mRNA    linear   EST 15-NOV-2005
```

```
)EFINITION  CGN-16277 Pericarp Coffea canephora cDNA clone cccp29n14 5', mRNA
            sequence.
ACCESSION   DV678489
VERSION     DV678489.1  GI:82451869
KEYWORDS    EST.
SOURCE      Coffea canephora
  ORGANISM  Coffea canephora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
            Coffea.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Lin,C., Mueller,L.A., McCarthy,J., Crouzillat,D., Petiard,V. and
            Tanksley,S.D.
  TITLE     Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep
            Sequencing of Seed and Cherry Transcripts
  JOURNAL   Theoretical and Applied Genetics (2005) In press
COMMENT     Contact: Steven D. Tanksley
            Department of Plant Breeding
            Cornell University
            248 Emerson Hall, Ithaca, NY 14853
            Tel: 607 255 1673
            Fax: 607 255 6683
            Email: sdt4@cornell.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Sol
            Genome Network website (http://www.sgn.cornell.edu)
            Plate: 29  row: n  column: 14
            Seq primer: M13R
            High quality sequence stop: 334.
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Coffea canephora"
                     /mol_type="mRNA"
                     /db_xref="taxon:49390"
                     /clone="cccp29n14"
                     /tissue_type="pericarp"
                     /dev_stage="All developmental stages"
                     /clone_lib="Pericarp"
                     /note="Vector: pBSSK-; Site_1: ECoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:                1.16e+03        Length:         334
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.3%            Indels:         0
DB:                       10              Gaps:           0

US-10-821-670A-102 (1-187) x DV678489 (1-334)

Qy          6 LeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||
Db         57 CTTAACCATTCCCAAACCCTTCTC 34

RESULT 94
DV678500/c
LOCUS       DV678500                334 bp    mRNA    linear   EST 15-NOV-2005
DEFINITION  CGN-16295 Pericarp Coffea canephora cDNA clone cccp8g7 5', mRNA
            sequence.
ACCESSION   DV678500
VERSION     DV678500.1  GI:82451880
KEYWORDS    EST.
SOURCE      Coffea canephora
  ORGANISM  Coffea canephora
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
            Coffea.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Lin,C., Mueller,L.A., McCarthy,J., Crouzillat,D., Petiard,V. and
            Tanksley,S.D.
  TITLE     Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep
            Sequencing of Seed and Cherry Transcripts
  JOURNAL   Theoretical and Applied Genetics (2005) In press
COMMENT     Contact: Steven D. Tanksley
            Department of Plant Breeding
            Cornell University
            248 Emerson Hall, Ithaca, NY 14853
            Tel: 607 255 1673
            Fax: 607 255 6683
            Email: sdt4@cornell.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Sol
            Genome Network website (http://www.sgn.cornell.edu)
            Plate: 8  row: g  column: 7
            Seq primer: M13R
            High quality sequence stop: 334.
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Coffea canephora"
                     /mol_type="mRNA"
                     /db_xref="taxon:49390"
                     /clone="cccp8g7"
                     /tissue_type="pericarp"
                     /dev_stage="All developmental stages"
                     /clone_lib="Pericarp"
                     /note="Vector: pBSSK-; Site_1: ECoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:                1.16e+03        Length:         334
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.3%            Indels:         0
DB:                       10              Gaps:           0

US-10-821-670A-102 (1-187) x DV678500 (1-334)

Qy          6 LeuAsnHisSerGlnThrLeuLeu 13
              |||||||||||||||||||||||
Db         57 CTTAACCATTCCCAAACCCTTCTC 34

RESULT 95
CN153290
LOCUS       CN153290                337 bp    mRNA    linear   EST 02-APR-2004
DEFINITION  940391 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
ACCESSION   CN153290
VERSION     CN153290.1  GI:46167720
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 337)
  AUTHORS   Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
            Nonneman,D.J., Wray,J.E. and Keele,J.W.
  TITLE     Porcine EST collection using a normalized library constructed from
            embryos representing early developmental stages
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: TMW8047  row: K  column: 7
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES             Location/Qualifiers
     source          1. .337
```

```
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 4PIG"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with combined RNA from day-10, day-13,
                     day-15, day-25, and day-30 whole embryos."
RIGIN

lignment Scores:
red. No.:              1.17e+03       Length:        337
core:                  8.00           Matches:       8
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            4.3%           Indels:        0
B:                     8              Gaps:          0

S-10-821-670A-102 (1-187) x CN153290 (1-337)

y          12 LeuLeuArgAlaIleSerAsnThr 19
              ||||||||||||||||||||||
b         262 TTGTTAAGGGCCATCTCAAACACA 285

ESULT 96
'N155402/c
OCUS        CN155402                  337 bp    mRNA    linear   EST 02-APR-2004
EFINITION   942695 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
CCESSION    CN155402
'ERSION     CN155402.1  GI:46169832
'EYWORDS    EST.
'OURCE      Sus scrofa (pig)
 ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
EFERENCE    1  (bases 1 to 337)
 AUTHORS    Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
            Nonneman,D.J., Wray,J.E. and Keele,J.W.
 TITLE      Porcine EST collection using a normalized library constructed from
            embryos representing early developmental stages
 JOURNAL    Unpublished (2003)
OMMENT      Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: TMW8047  row: K  column: 7
            Seq primer: GTAATACGACTCACTATAGGG.
EATURES             Location/Qualifiers
     source         1. .337
                    /organism="Sus scrofa"
                    /mol_type="mRNA"
                    /db_xref="taxon:9823"
                    /tissue_type="pooled"
                    /lab_host="DH10B"
                    /clone_lib="MARC 4PIG"
                    /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                    Library made with combined RNA from day-10, day-13,
                    day-15, day-25, and day-30 whole embryos."
RIGIN

lignment Scores:
red. No.:              1.17e+03       Length:        337
core:                  8.00           Matches:       8
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            4.3%           Indels:        0
B:                     8              Gaps:          0

US-10-821-670A-102 (1-187) x CN155402 (1-337)

Qy         12 LeuLeuArgAlaIleSerAsnThr 19
              ||||||||||||||||||||||
Db         76 TTGTTAAGGGCCATCTCAAACACA 53

RESULT 97
AZ772692
LOCUS       AZ772692                  344 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0583I18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0583I18 R, genomic survey sequence.
ACCESSION   AZ772692
VERSION     AZ772692.1  GI:12896270
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 344)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0583  row: I  column: 18
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 344.
FEATURES            Location/Qualifiers
     source         1. .344
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0583I18"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
ORIGIN
```

```
Alignment Scores:
Pred. No.:                1.19e+03        Length:         344
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.3%            Indels:         0
DB:                       11              Gaps:           0

US-10-821-670A-102 (1-187) x AZ772692 (1-344)

Qy          92 LeuSerSerIleTyrGluAspLeu 99
               |||||||||||||||||||||||
Db         291 CTATCTTCCATATATGAGGATCTC 314

RESULT 98
BE710882/c
LOCUS       BE710882                345 bp    mRNA    linear   EST 12-SEP-2000
DEFINITION  QV1-HT0638-150500-200-f08 HT0638 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE710882
VERSION     BE710882.1  GI:10099147
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 345)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  PUBMED    10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV1-HT0638-150
            500-200-f08&t3=2000-05-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 5
            High quality sequence stop: 345.
FEATURES             Location/Qualifiers
     source          1. .345
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0638"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                1.2e+03         Length:         345
Score:                    8.00            Matches:        8
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.3%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x BE710882 (1-345)

Qy         146 ProGlnAsnSerSerLeuGluGlu 153
               |||||||||||||||||||||||
Db         345 CCCCAGAATTCTTCATTAGAGGAA 322

RESULT 99
CK690084
LOCUS       CK690084                351 bp    mRNA    linear   EST 30-MAR-2004
DEFINITION  ZF101-P00051-DEPE-F_F01 GISZF001_ra Danio rerio cDNA clone
            IMAGE:7153347 5', mRNA sequence.
ACCESSION   CK690084
VERSION     CK690084.1  GI:42442420
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Wei,C., Mathavan,S., Thoreau,H., Lim,L., Lee,C. and Ruan,Y.
  TITLE     Genome Institute of Singapore, Zebrafish Gene Collection
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Ruan Y
            Cloning and Sequencing
            Genome Institute of Singapore
            60 Biopolis Street, #02-01, Genome, Singapore 138672
            Tel: +65 6478 8073
            Fax: +65 6478 9059
            Email: ruanyj@gis.a-star.edu.sg
            GIS Clone ID: ZF101-P00051-BR2_F01
            PCR PRimers
            FORWARD: M13
            BACKWARD: M13
            Plate: ZF101-P00051-BR2  row: F  column: 01
            Seq primer: CCGCATAACTTGTATAGCA
            High quality sequence stop: 351.
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /strain="Singapore local strain"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:7153347"
                     /tissue_type="Embryo"
                     /dev_stage="7 Different embryonic Stages(From just
                     fertilized Embryos to 72 hours just hatched baby fish)"
                     /lab_host="DH10B"
                     /clone_lib="GISZF001_ra"
                     /note="Vector: pDNR-LIB; Site_1: Sfi A (GGCCATTACGGCC);
                     Site_2: Sfi B (GGCCGAGGCGGCC); Priming method: Sfi-(dT)30
                     Primed ; Priming sequence:
                     5.ATTCTAGAGGCCGAGGCGGCCGACATG(T)30VN ; Directionally
                     cloned,  5' cloning site: Sfi A site GGCCATTACGGCC ;  5'
                     linker/adaptor sequence: 5.AAGCAGTGGTATCAACGCAGAGTGGCC ;
                     3' cloning site: Sfi B site GGCCGAGGCGGCC ;  3'
                     linker/adaptor sequence: same as the priming sequence ;
                     Average insert size: 2kb ; For PCR insert analysis: Use
                     M13 Forward and reverse primers ; Library Amplified ;
                     Recombinants (inserts): 98% ; Library complexity: 5x106 ;
                     Full-length construction (method): SMART, a Clontech
                     method The pooled tissue RNA was collected and used to
                     construct full length enriched cDNA library and also
                     served as template to synthesize complex first strand cDNA
                     probe. Two high density colony arrays were made from over
                     110K cDNA clones and hybridized with the probes. Low
                     intensity clones were selected as they represented rare
                     expressed clones. The hybridization intensities for all
                     clones span from 0 to 1.8 million counts and the low
                     abundant class ranged from 0 to 13,000."
```

```
RIGIN

lignment Scores:
red. No.:               1.21e+03        Length:         351
core:                   8.00            Matches:        8
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             4.3%            Indels:         0
B:                      5               Gaps:           0

S-10-821-670A-102 (1-187) x CK690084 (1-351)

y          8 HisSerGlnThrLeuLeuArgAla 15
             ||||||||||||||||||||||||
b         57 CATTCTCAAACTCTATTGAGAGCA 80

ESULT 100
Y098863/c
OCUS       BY098863                352 bp    mRNA    linear   EST 07-DEC-2002
EFINITION  BY098863 RIKEN full-length enriched, 13 days embryo whole body Mus
           musculus cDNA clone K630123P18 5', mRNA sequence.
CCESSION   BY098863
ERSION     BY098863.1  GI:26209480
EYWORDS    EST.
OURCE      Mus musculus (house mouse)
 ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
EFERENCE   1  (bases 1 to 352)
 AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
           Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
           Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
           Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
           Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
           Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
           Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
           Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
           Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
           Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
           Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
           Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
           Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
           Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
           Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
           Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
           Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
           Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
           Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
           Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
           Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
           Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
           Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
           Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
           Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
           Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
           Rogers,J., Birney,E. and Hayashizaki,Y.
 TITLE     Analysis of the mouse transcriptome based on functional annotation
           of 60,770 full-length cDNAs
 JOURNAL   Nature 420, 563-573 (2002)
  PUBMED   12466851
OMMENT     Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
           Sciences Center(GSC), Yokohama Institute
           The Institute of Physical and Chemical Research (RIKEN)
           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
           Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
           Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
           Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
           Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
           Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
           Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
           Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
           prepare full-length cDNA libraries for rapid discovery of new
           genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
           sequencing pipeline with 384 multicapillary sequencer. Genome Res.
           10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
           encyclopedia: real-time sequence clustering for construction of a
           nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
           Encyclopedia Project of Genome Exploration Research Group in Riken
           Genomic Sciences Center and Genome Science Laboratory in RIKEN.
           Division of Experimental Animal Research in Riken contributed to
           prepare mouse tissues.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
           further details.
FEATURES             Location/Qualifiers
     source          1. .352
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="K630123P18"
                     /tissue_type="whole body"
                     /dev_stage="13 days embryo"
                     /clone_lib="RIKEN full-length enriched, 13 days embryo
                     whole body"
ORIGIN

Alignment Scores:
Pred. No.:              1.22e+03        Length:         352
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.3%            Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-102 (1-187) x BY098863 (1-352)

Qy         75 AsnGlySerCysLeuAlaSerArg 82
              |||||||||||||||||||||||
Db        306 AACGGCTCCTGCCTTGCGAGCCGG 283


Search completed: June 10, 2006, 16:34:40
Job time : 2608.08 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

)M protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:23:11 ; Search time 453.088 Seconds
(without alignments)
4316.416 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 187
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size: 1

Total number of hits satisfying chosen parameters: 10484871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110446_27507/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rng -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US10821670_@CGN_1_1_1666_@runat_07062006_110446_27507 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	187	100.0	561	6	ABK99001	Abk99001 Feline in
c	2	187	100.0	561	6	ABK99002	Abk99002 Feline in
	3	187	100.0	561	14	ADV34751	Adv34751 Feline N-
c	4	187	100.0	561	14	ADV34753	Adv34753 Feline N-
	5	187	100.0	591	6	ABK98948	Abk98948 Feline in
c	6	187	100.0	591	6	ABK98949	Abk98949 Feline in
	7	187	100.0	591	14	ADV34688	Adv34688 Feline si
c	8	187	100.0	591	14	ADV34690	Adv34690 Feline si
c	9	187	100.0	666	6	ABK98947	Abk98947 Feline in
	10	187	100.0	666	6	ABK98946	Abk98946 Feline in
	11	187	100.0	666	14	ADV34685	Adv34685 Feline si
c	12	187	100.0	666	14	ADV34687	Adv34687 Feline si
c	13	187	100.0	1533	6	ABK98954	Abk98954 Feline in
	14	187	100.0	1533	6	ABK98953	Abk98953 Feline in
c	15	187	100.0	1533	14	ADV34697	Adv34697 Feline si
	16	187	100.0	1533	14	ADV34695	Adv34695 Feline si
	17	187	100.0	1599	6	ABK98950	Abk98950 Feline in
c	18	187	100.0	1599	6	ABK98951	Abk98951 Feline in
	19	187	100.0	1599	14	ADV34691	Adv34691 Feline si
c	20	187	100.0	1599	14	ADV34693	Adv34693 Feline si
	21	185	98.9	591	2	AAV56629	Aav56629 Feline FL
	22	185	98.9	689	2	AAV56641	Aav56641 Feline FL
	23	185	98.9	1441	2	AAV56628	Aav56628 Feline FL
	24	69	36.9	679	4	AAF26097	Aaf26097 Feline fi
	25	59	31.6	660	5	AAD15219	Aad15219 Modified
	26	59	31.6	660	5	AAD15214	Aad15214 Modified
	27	59	31.6	660	5	AAD15218	Aad15218 Modified
	28	56	29.9	660	5	AAD15215	Aad15215 Modified
	29	54	28.9	639	4	AAF26098	Aaf26098 Plasmid p
	30	54	28.9	669	4	AAF26083	Aaf26083 Feline IL
	31	54	28.9	669	4	AAF26086	Aaf26086 Feline IL
	32	54	28.9	4201	4	AAF26077	Aaf26077 Feline IL
	33	52	27.8	591	2	AAX18179	Aax18179 Canine ma
c	34	52	27.8	591	6	ABK98958	Abk98958 Canine in
	35	52	27.8	591	6	ABK98957	Abk98957 Canine in
	36	52	27.8	591	14	ADV34701	Adv34701 Canine si
c	37	52	27.8	591	14	ADV34703	Adv34703 Canine si
	38	52	27.8	666	6	ABK98955	Abk98955 Canine in
c	39	52	27.8	666	6	ABK98956	Abk98956 Canine in
c	40	52	27.8	666	14	ADV34700	Adv34700 Canine si
	41	52	27.8	666	14	ADV34698	Adv34698 Canine si
	42	52	27.8	669	2	AAV13818	Aav13818 Canine IL
	43	52	27.8	669	2	AAV13819	Aav13819 Canine IL
	44	52	27.8	669	2	AAX03163	Aax03163 Nucleic a
	45	52	27.8	669	2	AAX03153	Aax03153 Nucleic a
	46	52	27.8	669	2	AAX35616	Aax35616 Nucleic a
	47	52	27.8	669	2	AAX35626	Aax35626 Nucleic a
	48	52	27.8	669	4	AAI64389	Aai64389 Canine co
	49	52	27.8	669	4	AAI64379	Aai64379 Canine co
	50	52	27.8	669	11	ADZ25701	Adz25701 Canine in
	51	52	27.8	1282	2	AAX18178	Aax18178 Canine fu
	52	52	27.8	1455	6	ABK99003	Abk99003 Canine in
c	53	52	27.8	1455	6	ABK99004	Abk99004 Canine in
c	54	52	27.8	1455	14	ADV34756	Adv34756 Canine si
	55	52	27.8	1455	14	ADV34754	Adv34754 Canine si
	56	52	27.8	1533	6	ABK98967	Abk98967 Canine in
c	57	52	27.8	1533	6	ABK98968	Abk98968 Canine in
c	58	52	27.8	1533	14	ADV34718	Adv34718 Canine si
	59	52	27.8	1533	14	ADV34716	Adv34716 Canine si
	60	52	27.8	1599	6	ABK98965	Abk98965 Canine in
c	61	52	27.8	1599	6	ABK98966	Abk98966 Canine in
c	62	52	27.8	1599	14	ADV34715	Adv34715 Canine si
	63	52	27.8	1599	14	ADV34713	Adv34713 Canine si
	64	50	26.7	669	13	ADT04852	Adt04852 Canine in
	65	43	23.0	666	5	AAD15212	Aad15212 Modified
	66	42	22.5	554	2	AAT50757	Aat50757 Partial s
	67	40	21.4	703	3	AAA70708	Aaa70708 Bovine in
	68	39	20.9	660	5	AAD15213	Aad15213 Modified
	69	39	20.9	660	5	AAD15216	Aad15216 Modified
	70	39	20.9	660	5	AAD15220	Aad15220 Modified
	71	37	19.8	660	5	AAD15217	Aad15217 Modified
	72	31	16.6	666	5	AAD15211	Aad15211 Modified
	73	29	15.5	201	13	ADQ41825	Adq41825 Myocardia
	74	29	15.5	201	13	ADQ41824	Adq41824 Myocardia
	75	29	15.5	201	13	ADQ41835	Adq41835 Myocardia

76	29	15.5	201	13	ADQ41829	Adq41829 Myocardia
77	29	15.5	201	13	ADQ41838	Adq41838 Myocardia
78	29	15.5	201	13	ADQ41833	Adq41833 Myocardia
79	29	15.5	630	12	ADF77258	Adf77258 Human IL-
80	29	15.5	657	12	ADG39431	Adg39431 Human CLM
81	29	15.5	660	2	AAQ97485	Aaq97485 Human int
82	29	15.5	660	2	AAV07274	Aav07274 Human Int
83	29	15.5	660	2	AAV07218	Aav07218 DNA encod
84	29	15.5	660	2	AAZ40408	Aaz40408 Human int
85	29	15.5	660	2	AAZ40407	Aaz40407 Human int
86	29	15.5	660	2	AAZ40409	Aaz40409 Human int
87	29	15.5	660	5	AAD15221	Aad15221 Human cyt
88	29	15.5	660	6	AAL44226	Aal44226 Human int
89	29	15.5	660	6	ACC47589	Acc47589 Human int
90	29	15.5	660	12	ADF77245	Adf77245 Human IL-
91	29	15.5	660	12	ADF77257	Adf77257 Human IL-
92	29	15.5	660	12	ADF77246	Adf77246 Human IL-
93	29	15.5	660	12	ADF77244	Adf77244 Human IL-
94	29	15.5	683	4	AAF26096	Aaf26096 Human pG-
95	29	15.5	702	12	ADP88401	Adp88401 Human int
96	29	15.5	721	2	AAQ67880	Aaq67880 EPV 42 kD
97	29	15.5	721	2	AAZ08515	Aaz08515 Vaccinia
98	29	15.5	721	13	ADR21891	Adr21891 Vaccinia
99	29	15.5	761	10	ADK98708	Adk98708 Human int
100	29	15.5	761	10	ADK98706	Adk98706 Human int
101	29	15.5	762	2	AAV83207	Aav83207 Interleuk
102	29	15.5	762	3	AAA35201	Aaa35201 Human ade
103	29	15.5	762	3	AAF21323	Aaf21323 Human low
104	29	15.5	762	10	ABZ97017	Abz97017 Human nuc
105	29	15.5	762	11	ABD20866	Abd20866 Human pul
106	29	15.5	762	12	ADO07654	Ado07654 Human int
107	29	15.5	762	13	ADS88021	Ads88021 Tumour tr
108	29	15.5	762	14	ADV42511	Adv42511 Human psy
109	29	15.5	823	10	ACD26420	Acd26420 cDNA enco
110	29	15.5	856	2	AAQ12150	Aaq12150 Cytotoxic
111	29	15.5	856	2	AAT77850	Aat77850 35 kDa su
112	29	15.5	856	2	AAT97970	Aat97970 35 kDa su
113	29	15.5	856	2	AAV00402	Aav00402 35 kDa su
114	29	15.5	856	2	AAV37772	Aav37772 Cytotoxic
115	29	15.5	856	12	ADG39389	Adg39389 Human cyt
116	29	15.5	856	12	ADO03760	Ado03760 Human CLM
117	29	15.5	889	13	ADU04652	Adu04652 Human ext
118	29	15.5	1026	3	AAZ40020	Aaz40020 Human p35
119	29	15.5	1026	8	ACA61266	Aca61266 DNA encod
120	29	15.5	1026	11	ADI31715	Adi31715 Human cDN
121	29	15.5	1026	13	ADS83782	Ads83782 Human lym
122	29	15.5	1172	8	ACC42373	Acc42373 Human ext
123	29	15.5	1200	8	ACF64408	Acf64408 Human IL1
124	29	15.5	1287	4	AAF76882	Aaf76882 DNA encod
125	29	15.5	1289	8	ACC42375	Acc42375 Human ext
126	29	15.5	1316	2	AAT63621	Aat63621 Interleuk
127	29	15.5	1316	6	AAD41639	Aad41639 Human int
128	29	15.5	1364	2	AAT48099	Aat48099 Human int
129	29	15.5	1364	2	AAV42536	Aav42536 Human int
130	29	15.5	1364	2	AAV15228	Aav15228 Heterodim
131	29	15.5	1364	3	AAZ28863	Aaz28863 Human int
132	29	15.5	1364	4	AAF56281	Aaf56281 IL-12 vac
133	29	15.5	1384	15	AEF92723	Aef92723 Human int
134	29	15.5	1396	2	AAQ24371	Aaq24371 Natural k
135	29	15.5	1444	12	ACF57533	Acf57533 Human IL1
136	29	15.5	1444	12	ADJ62891	Adj62891 Human int
137	29	15.5	1444	12	ADN12152	Adn12152 Interleuk
138	29	15.5	1444	14	ADY15785	Ady15785 DNA encod
139	29	15.5	1444	14	ADZ26544	Adz26544 Human IL1
140	29	15.5	1444	14	AEB56478	Aeb56478 Radiochem
141	29	15.5	1494	12	ADQ59495	Adq59495 Human can
142	29	15.5	1526	12	ADQ59549	Adq59549 Human can
143	29	15.5	1532	13	ADQ38388	Adq38388 Human SNP
144	29	15.5	1532	14	ADZ13866	Adz13866 Human can
145	29	15.5	1607	13	ADQ38387	Adq38387 Human SNP
146	29	15.5	1607	14	ADZ13864	Adz13864 Human can
147	29	15.5	2300	3	AAA92406	Aaa92406 Human int
148	29	15.5	2336	14	AEE03207	Aee03207 Human int
149	29	15.5	2390	12	ADM29103	Adm29103 Human int
150	29	15.5	3205	14	AEB48820	Aeb48820 Monoclona
151	29	15.5	4521	3	AAA35204	Aaa35204 Human ade
152	29	15.5	4521	3	AAF21326	Aaf21326 Human low
153	29	15.5	4521	10	ABZ97020	Abz97020 Human nuc
154	29	15.5	4521	11	ABD20869	Abd20869 Human pul
155	29	15.5	5013	14	AEA40941	Aea40941 T-DNA reg
156	29	15.5	5686	2	AAZ40415	Aaz40415 Plasmid p
157	29	15.5	5686	12	ADF77239	Adf77239 Human IL-
158	29	15.5	6139	3	AAZ40023	Aaz40023 Interleuk
159	29	15.5	8578	6	AAD31546	Aad31546 pIRES-hB7
160	29	15.5	8578	6	AAD31545	Aad31545 pIRES-hB7
161	29	15.5	8608	6	AAD31548	Aad31548 pIRES-hB7
162	29	15.5	8623	6	AAD31547	Aad31547 pIRES-hB7
163	29	15.5	8629	6	AAD31552	Aad31552 pIRES-IL1
164	29	15.5	8638	6	AAD31549	Aad31549 pIRES-hB7
165	29	15.5	8644	6	AAD31551	Aad31551 pIRES-IL1
166	29	15.5	8659	6	AAD31550	Aad31550 pIRES-IL1
167	29	15.5	11441	6	AAL44225	Aal44225 Human int
168	29	15.5	11453	10	ADG25152	Adg25152 Vector pS
169	29	15.5	11569	10	ADG25150	Adg25150 Vector pA
170	29	15.5	27277	12	ADQ59494	Adq59494 Human can
171	29	15.5	27277	14	ADZ13863	Adz13863 Human can
172	28	15.0	700	8	ACF64405	Acf64405 Human IL1
173	26	13.9	79	2	AAV56639	Aav56639 Feline FL
174	26	13.9	79	2	AAX18181	Aax18181 Primer fo
175	25	13.4	666	2	AAT50758	Aat50758 Sequence
176	23	12.3	71	4	AAF26092	Aaf26092 Feline IL
177	23	12.3	71	4	AAF26099	Aaf26099 Feline Il
178	20	10.7	201	13	ADQ41830	Adq41830 Myocardia
179	20	10.7	201	13	ADQ41821	Adq41821 Myocardia
180	20	10.7	700	8	ACF64406	Acf64406 Human IL1
181	20	10.7	700	8	ACF64407	Acf64407 Human IL1
182	18	9.6	76	4	AAF26100	Aaf26100 Feline Il
c 183	18	9.6	76	4	AAF26093	Aaf26093 Feline IL
c 184	18	9.6	76	4	AAF26090	Aaf26090 Feline IL
185	13	7.0	60	6	ABN39662	Abn39662 Human spl
186	13	7.0	660	2	AAV31481	Aav31481 Human int
187	13	7.0	660	2	AAZ40421	Aaz40421 Human int
188	13	7.0	660	12	ADF77255	Adf77255 Human IL-
c 189	12	6.4	36	2	AAV56640	Aav56640 Feline FL
c 190	12	6.4	36	2	AAX18182	Aax18182 Primer fo
191	10	5.3	39	6	ABK98991	Abk98991 Synthetic
192	10	5.3	39	14	ADV34741	Adv34741 Feline IL
193	10	5.3	582	4	AAF76877	Aaf76877 Mature mu
194	10	5.3	660	2	AAX78396	Aax78396 IL-12p35
195	10	5.3	660	2	AAX25946	Aax25946 Interleuk
196	10	5.3	713	2	AAT35199	Aat35199 Mouse int
197	10	5.3	1231	12	ADQ59492	Adq59492 Human can
198	10	5.3	1265	2	AAV28473	Aav28473 Murine in
199	10	5.3	1265	8	ACA61264	Aca61264 DNA encod
200	10	5.3	1273	14	ADZ13861	Adz13861 Murine ca

ALIGNMENTS

RESULT 1
ABK99001
ID ABK99001 standard; cDNA; 561 BP.
XX
AC ABK99001;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-N561 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.

```
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69315.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 92-93; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.92e-184       Length:         561
Score:                    187.00          Matches:        187
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       6               Gaps:           0

US-10-821-670A-102 (1-187) x ABK99001 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 2
ABK99002/c
ID   ABK99002 standard; cDNA; 561 BP.
XX
AC   ABK99002;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12nFeIL-12p35-N561 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 94; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.92e-184       Length:         561
Score:                    187.00          Matches:        187
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
```

```
:B:                    6              Gaps:          0

:S-10-821-670A-102 (1-187) x ABK99002 (1-561)

:y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

:y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

:y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

:y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

:y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

:y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

:y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

:y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

:y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

:y        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
:b         21 ATGAGCTATCTGAATGCTTCC 1

:ESULT 3
:DV34751
:D   ADV34751 standard; cDNA; 561 BP.
:X
:C   ADV34751;
:X
:T   24-FEB-2005  (first entry)
:X
:E   Feline N-terminal single chain IL-12p35 cDNA, nFeIL-12p35-N561.
:X
:W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
:W   infectious disease; antimicrobial; gene; ss.
:X
:S   Felis catus.
:X
:H   Key             Location/Qualifiers
:T   CDS             1. .561
:T                   /*tag=  a
:T                   /product= "PFeIL-12p35-N187 protein"
:T                   /partial
:T                   /note= "No start and stop codon"
:X
:N   US2004248261-A1.
:X
:D   09-DEC-2004.
:X
:F   09-APR-2004; 2004US-00821670.
:X
:R   04-AUG-2000; 2000US-0223016P.
```

```
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34752.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 101; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.92e-184       Length:          561
Score:                    187.00          Matches:         187
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-102 (1-187) x ADV34751 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
```

```
Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 4
ADV34753/c
ID   ADV34753 standard; cDNA; 561 BP.
XX
AC   ADV34753;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p35 complementary DNA, nFeIL-12p35-N561.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Disclosure; SEQ ID NO 103; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein complementary DNA.
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.92e-184       Length:          561
Score:                    187.00          Matches:         187
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-102 (1-187) x ADV34753 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 5
ABK98948
ID   ABK98948 standard; cDNA; 591 BP.
XX
AC   ABK98948;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-591 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69305.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 56-57; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
```

```
:C   multimeric forms of these proteins, an antibody against these proteins,
:C   or an inhibitor identified by its ability to inhibit the activity of
:C   these proteins, can be used to treat or prevent autoimmune diseases,
:C   allergic reactions, infectious diseases, tumour development, inflammatory
:C   diseases and/or graft rejection in animals. The present nucleic acid
:C   sequence represents a feline interleukin 12 DNA sequence, as described in
:C   the invention
:X
:Q   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

:lignment Scores:
:red. No.:              7.28e-184      Length:        591
:core:                  187.00         Matches:       187
:ercent Similarity:     100.0%         Conservative:  0
:est Local Similarity:  100.0%         Mismatches:    0
:uery Match:            100.0%         Indels:        0
:B:                     6              Gaps:          0

:S-10-821-670A-102 (1-187) x ABK98948 (1-591)

:y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

:y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

:y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

:y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

:y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

:y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

:y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

:y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

:y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:b        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

:y        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
:b        571 ATGAGCTATCTGAATGCTTCC 591

ESULT 6
BK98949/c
:D   ABK98949 standard; cDNA; 591 BP.
:X
:C   ABK98949;
:X
:T   21-OCT-2002  (first entry)
:X
:E   Feline interleukin-12 nFeIL-12p35-591 complementary strand.
:X
:W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
:W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
:W   tumour development; inflammatory disease; graft rejection; ss.
```

```
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 58; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.28e-184      Length:        591
Score:                  187.00         Matches:       187
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     6              Gaps:          0

US-10-821-670A-102 (1-187) x ABK98949 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202
```

```
Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 7
ADV34688
ID ADV34688 standard; cDNA; 591 BP.
XX
AC ADV34688;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .591
FT   /*tag= a
FT   /product= "PFeIL-12p35 197 protein"
FT   /partial
FT   /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34689.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 35; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p35 subunit
CC protein encoding cDNA.
XX
SQ Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.28e-184	Length:	591
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-102 (1-187) x ADV34688 (1-591)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591
```

RESULT 8
ADV34690/c
ID ADV34690 standard; DNA; 591 BP.
XX
AC ADV34690;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.

```
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2005-020565/02.
X
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
T   vaccine against infectious diseases in feline animals.
X
S   Example 3; SEQ ID NO 37; 103pp; English.
X
C   The present invention relates to the feline interleukin (IL)-12p35 or p40
C   subunit protein and their encoding nucleic acid molecules and a nucleic
C   acid linker. The invention also provides the feline caspase (casp)-1,
C   feline IL-18 single chain and canine IL-12 single chain proteins and
C   their nucleic acid molecules. The nucleic acid molecule is useful in
C   preparing a vaccine against infectious diseases in feline animals. The
C   present sequence is the feline single chain mature IL-12p35 subunit
C   complementary DNA.
X
Q   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.28e-184       Length:         591
Score:                  187.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x ADV34690 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 9
ABK98947/c
ID   ABK98947 standard; cDNA; 666 BP.
XX
AC   ABK98947;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 56; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.18e-184       Length:         666
Score:                  187.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-102 (1-187) x ABK98947 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442
```

```
Qy          41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy         141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy         161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy         181 MetSerTyrLeuAsnAlaSer 187
               |||||||||||||||||||
Db          21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 10
ABK98946
ID ABK98946 standard; cDNA; 666 BP.
XX
AC ABK98946;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69304.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 54-55; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.18e-184	Length:	666
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x ABK98946 (1-666)

```
Qy           1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy          21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy          41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy         141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy         161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy         181 MetSerTyrLeuAsnAlaSer 187
               |||||||||||||||||||
Db         646 ATGAGCTATCTGAATGCTTCC 666
```

RESULT 11
ADV34685
ID ADV34685 standard; cDNA; 666 BP.
XX
AC ADV34685;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX

```
W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W   infectious disease; antimicrobial; gene; ss.
X
S   Felis catus.
X
H   Key             Location/Qualifiers
T   CDS             1. .666
T                   /*tag=  a
T                   /product= "PFeIL-12p35 222 protein "
T                   /partial
T                   /note= "No stop codon"
X
N   US2004248261-A1.
X
D   09-DEC-2004.
X
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2005-020565/02.
R   P-PSDB; ADV34686.
X
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
T   vaccine against infectious diseases in feline animals.
X
S   Claim 23; SEQ ID NO 32; 103pp; English.
X
C   The present invention relates to the feline interleukin (IL)-12p35 or p40
C   subunit protein and their encoding nucleic acid molecules and a nucleic
C   acid linker. The invention also provides the feline caspase (casp)-1,
C   feline IL-18 single chain and canine IL-12 single chain proteins and
C   their nucleic acid molecules. The nucleic acid molecule is useful in
C   preparing a vaccine against infectious diseases in feline animals. The
C   present sequence is the feline single chain IL-12p35 subunit protein
C   encoding full-length cDNA.
X
Q   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

lignment Scores:
red. No.:               8.18e-184       Length:         666
core:                   187.00          Matches:        187
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             100.0%          Indels:         0
B:                      14              Gaps:           0

S-10-821-670A-102 (1-187) x ADV34685 (1-666)

y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy       101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy       121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy       141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy       161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy       181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
Db       646 ATGAGCTATCTGAATGCTTCC 666

RESULT 12
ADV34687/c
ID   ADV34687 standard; DNA; 666 BP.
XX
AC   ADV34687;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 34; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.18e-184       Length:         666
```

```
Score:                  187.00        Matches:       187
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            100.0%        Indels:        0
DB:                     14            Gaps:          0

US-10-821-670A-102 (1-187) x ADV34687 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 13
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.84e-183     Length:        1533
Score:                  187.00        Matches:       187
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            100.0%        Indels:        0
DB:                     6             Gaps:          0

US-10-821-670A-102 (1-187) x ABK98954 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22
```

```
y       181 MetSerTyrLeuAsnAlaSer 187
            |||||||||||||||||||
b        21 ATGAGCTATCTGAATGCTTCC 1

ESULT 14
BK98953
D   ABK98953 standard; cDNA; 1533 BP.
X
C   ABK98953;
X
T   21-OCT-2002  (first entry)
X
E   Feline interleukin-12 nFeIL-12-1533 coding strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; gene; ss.
X
S   Felis catus.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
X
R   04-AUG-2000; 2000US-0223016P.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2002-573554/61.
R   P-PSDB; ABG69307.
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Claim 6; Page 63-64; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a feline interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.84e-183      Length:          1533
core:                  187.00         Matches:         187
ercent Similarity:     100.0%         Conservative:    0
est Local Similarity:  100.0%         Mismatches:      0
uery Match:            100.0%         Indels:          0
B:                     6              Gaps:            0

S-10-821-670A-102 (1-187) x ABK98953 (1-1533)

y         1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy        21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy       101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy       121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy       141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy       161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy       181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||
Db      1513 ATGAGCTATCTGAATGCTTCC 1533

RESULT 15
ADV34697/c
ID   ADV34697 standard; DNA; 1533 BP.
XX
AC   ADV34697;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
```

```
:C   The present invention relates to the feline interleukin (IL)-12p35 or p40
:C   subunit protein and their encoding nucleic acid molecules and a nucleic
:C   acid linker. The invention also provides the feline caspase (casp)-1,
:C   feline IL-18 single chain and canine IL-12 single chain proteins and
:C   their nucleic acid molecules. The nucleic acid molecule is useful in
:C   preparing a vaccine against infectious diseases in feline animals. The
:C   present sequence is the feline single chain IL-12 complementary DNA.
:X
:Q   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

\lignment Scores:
>red. No.:              1.84e-183      Length:         1533
>core:                  187.00         Matches:        187
>ercent Similarity:     100.0%         Conservative:   0
>est Local Similarity:  100.0%         Mismatches:     0
>uery Match:            100.0%         Indels:         0
>B:                     14             Gaps:           0

>S-10-821-670A-102 (1-187) x ADV34697 (1-1533)

>y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

>y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

>y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

>y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

>y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

>y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

>y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

>y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

>y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>b         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

>y        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
>b         21 ATGAGCTATCTGAATGCTTCC 1

<ESULT 16
\DV34695
:D   ADV34695 standard; cDNA; 1533 BP.
<X
\C   ADV34695;
<X
>T   24-FEB-2005  (first entry)
<X
>E   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
<X
<W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
<W   infectious disease; antimicrobial; gene; ss.
<X
```

```
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.84e-183      Length:         1533
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-102 (1-187) x ADV34695 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

y        181 MetSerTyrLeuAsnAlaSer 187
                ||||||||||||||||||||
b       1513 ATGAGCTATCTGAATGCTTCC 1533
```

ESULT 17
BK98950
D ABK98950 standard; cDNA; 1599 BP.
X
C ABK98950;
X
T 21-OCT-2002 (first entry)
X
E Feline interleukin-12 nFeIL-12-1599 coding strand.
X
W Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W tumour development; inflammatory disease; graft rejection; gene; ss.
X
S Felis catus.
X
N US2002052030-A1.
X
D 02-MAY-2002.
X
F 27-JUL-2001; 2001US-00917265.
X
R 04-AUG-2000; 2000US-0223016P.
X
A (WOND/) WONDERLING R S.
A (BORO/) BOROUGHS K L.
X
I Wonderling RS, Boroughs KL;
X
R WPI; 2002-573554/61.
R P-PSDB; ABG69306.
X
T Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T chain and canine IL-12 single chain proteins, useful for treating and
T preventing autoimmune diseases, inflammatory diseases and/or graft
T rejection in animals.
X
S Claim 6; Page 58-60; 106pp; English.
X
C The present invention discloses new feline interleukin 18 (IL-18), feline
C caspase-1, feline IL-12 single chain and canine IL-12 single chain
C proteins. A composition comprising a feline IL-18, feline caspase-1,
C feline IL-12 single chain or canine IL-12 single chain proteins, a
C nucleic acid encoding these proteins, mimetopes of these proteins,
C multimeric forms of these proteins, an antibody against these proteins,
C or an inhibitor identified by its ability to inhibit the activity of
C these proteins, can be used to treat or prevent autoimmune diseases,
C allergic reactions, infectious diseases, tumour development, inflammatory
C diseases and/or graft rejection in animals. The present nucleic acid
C sequence represents a feline interleukin 12 DNA sequence, as described in
C the invention
X
Q Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.91e-183	Length:	1599
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x ABK98950 (1-1599)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599
```

RESULT 18
ABK98951/c
ID ABK98951 standard; cDNA; 1599 BP.
XX
AC ABK98951;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.

```
CX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
CX
PI   Wonderling RS,  Boroughs KL;
CX
DR   WPI; 2002-573554/61.
CX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
CX
PS   Claim 6; Page 61-62; 106pp; English.
CX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
CX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.91e-183      Length:          1599
Score:                    187.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       6              Gaps:            0

US-10-821-670A-102 (1-187) x ABK98951 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 19
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.91e-183      Length:          1599
Score:                    187.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       14             Gaps:            0

US-10-821-670A-102 (1-187) x ADV34691 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

y        181 MetSerTyrLeuAsnAlaSer 187
                ||||||||||||||||||||
b       1579 ATGAGCTATCTGAATGCTTCC 1599

ESULT 20
DV34693/c
D   ADV34693 standard; DNA; 1599 BP.
X
C   ADV34693;
X
T   24-FEB-2005  (first entry)
X
E   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
X
W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W   infectious disease; antimicrobial; ds.
X
S   Felis catus.
X
N   US2004248261-A1.
X
D   09-DEC-2004.
X
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2005-020565/02.
X
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
T   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.91e-183       Length:          1599
Score:                    187.00          Matches:         187
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-102 (1-187) x ADV34693 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
                ||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 21
AAV56629
ID   AAV56629 standard; cDNA; 591 BP.
XX
AC   AAV56629;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA mature transcript.
XX
```

```
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76176.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 23; Page 59; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.58e-182      Length:          591
Score:                    185.00         Matches:         185
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              98.9%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AAV56629 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsn 185
              |||||||||||||||
Db        571 ATGAGCTACCTGAAT 585

RESULT 22
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                9.96e-182      Length:          689
Score:                    185.00         Matches:         185
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              98.9%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AAV56641 (1-689)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

y          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

y          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

y         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

y         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

y         141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

y         161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

y         181 MetSerTyrLeuAsn 185
                ||||||||||||||||
b         652 ATGAGCTACCTGAAT 666

ESULT 23
AV56628
D   AAV56628 standard; cDNA; 1441 BP.
X
C   AAV56628;
X
T   23-NOV-1998  (first entry)
X
E   Feline FLAFp35 cDNA.
X
W   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
W   T lymphocyte cell; autoimmune disease; ds.
X
S   Felis catus.
X
H   Key             Location/Qualifiers
T   CDS             133. .811
T                   /*tag= a
T   sig_peptide     133. .217
T                   /*tag= b
T   mat_peptide     218. .808
T                   /*tag= c
T                   /product= "FLAFp35"
T                   /note= "feline cytokine"
X
N   WO9746583-A1.
X
D   11-DEC-1997.
X
F   29-MAY-1997;   97WO-JP001824.
X
R   04-JUN-1996;   96JP-00165249.
X
A   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
X
I   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
X
R   WPI; 1998-042118/04.
R   P-PSDB; AAW76175.
X
T   Novel feline cytokine protein - useful for treating feline auto:immune
T   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
X
PS  Claim 22; Page 57-58; 94pp; Japanese.
X
CC  This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC  protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC  which can potentiate the cytotoxic activity of feline cytotoxic T
CC  lymphocyte cells. Such proteins are used for treatment of feline
CC  autoimmune diseases e.g. as caused by feline herpes virus or feline
CC  calcivirus
XX
SQ  Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.04e-181       Length:         1441
Score:                  185.00          Matches:        185
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            98.9%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AAV56628 (1-1441)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 427

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 487

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 547

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 607

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 667

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 727

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 787

Qy        181 MetSerTyrLeuAsn 185
                ||||||||||||||||
Db        788 ATGAGCTACCTGAAT 802

RESULT 24
AAF26097
ID  AAF26097 standard; DNA; 679 BP.
XX
AC  AAF26097;
XX
DT  24-APR-2001  (first entry)
XX
DE  Feline fil12p35a DNA.
XX
KW  Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
```

```
CW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
CW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
CX
OS   Felis sp.
CX
PN   WO200104155-A2.
CX
PD   18-JAN-2001.
CX
PF   08-JUL-2000; 2000WO-DE002263.
CX
PR   08-JUL-1999;   99CH-00001259.
CX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
CX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
CX
DR   WPI; 2001-147178/15.
CX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
CX
PS   Disclosure; Fig 2; 35pp; German.
CX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
CX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.33e-61        Length:         679
Score:                    69.00           Matches:        69
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              36.9%           Indels:         0
DB:                       4               Gaps:           0

US-10-821-670A-102 (1-187) x AAF26097 (1-679)

Qy         79 LeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAsp 98
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 399

Qy         99 LeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLys 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 459

Qy        119 ArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeu 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 519

Qy        139 AsnValAsnSerValThrValProGln 147
              |||||||||||||||||||||||||||
Db        520 AATGTCAACAGTGTGACTGTGCCACAG 546

RESULT 25
AAD15219
ID   AAD15219 standard; DNA; 660 BP.
XX
AC   AAD15219;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-157.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08612.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 181 A; 178 C; 144 G; 157 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.93e-51        Length:         660
Score:                    59.00           Matches:        59
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              31.6%           Indels:         0
DB:                       5               Gaps:           0
```

```
S-10-821-670A-102 (1-187) x AAD15219 (1-660)

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 89
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

y         90 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

y        110 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        424 AATGCAAAGCTGTTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

ESULT 26
AD15214
D   AAD15214 standard; DNA; 660 BP.
X
C   AAD15214;
X
T   01-NOV-2001  (first entry)
X
E   Modified human cytokine p35 encoding DNA from clone R2-631.
X
W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
W   p35; mutant; ds.
X
S   Homo sapiens.
S   Synthetic.
X
H   Key             Location/Qualifiers
T   CDS             1. .660
T                   /*tag=  a
T                   /product= "Modified p35 protein precursor"
T   sig_peptide     1. .66
T                   /*tag=  b
T   mat_peptide     67. .657
T                   /*tag=  c
T                   /product= "Mature modified p35 protein"
X
N   WO200140257-A2.
X
D   07-JUN-2001.
X
F   30-NOV-2000; 2000WO-US032664.
X
R   02-DEC-1999;   99US-0169035P.
R   28-NOV-2000; 2000US-00725324.
X
A   (MAXY-) MAXYGEN INC.
X
I   Leong SR,  Punnonen J;
X
R   WPI; 2001-502381/55.
R   P-PSDB; AAE08607.
X
T   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
T   and p35 polypeptides), useful for treating various diseases e.g. diabetic
T   retinopathy and cancer.
X
S   Claim 87; Page 139; 223pp; English.
X
C   The invention relates to nucleic acids encoding modified cytokine
C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
C   gamma induction activities. The polypeptides and polynucleotides of the
C   invention are useful for treating various diseases e.g. bacterial
C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
C   vaccinated host's cell-mediated immunity for protective response to a
C   pathogen. The present sequence is a modified human p35 protein encoding
CC  DNA
XX
SQ  Sequence 660 BP; 182 A; 178 C; 142 G; 158 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.93e-51        Length:          660
Score:                    59.00           Matches:         59
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              31.6%           Indels:          0
DB:                       5               Gaps:            0

US-10-821-670A-102 (1-187) x AAD15214 (1-660)

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

Qy         90 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy        110 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 27
AAD15218
ID  AAD15218 standard; DNA; 660 BP.
XX
AC  AAD15218;
XX
DT  01-NOV-2001  (first entry)
XX
DE  Modified human cytokine p35 encoding DNA from clone R2-162.
XX
KW  Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW  diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW  p35; mutant; ds.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .660
FT                  /*tag=  a
FT                  /product= "Modified p35 protein precursor"
FT  sig_peptide     1. .66
FT                  /*tag=  b
FT  mat_peptide     67. .657
FT                  /*tag=  c
FT                  /product= "Mature modified p35 protein"
XX
PN  WO200140257-A2.
XX
PD  07-JUN-2001.
XX
PF  30-NOV-2000; 2000WO-US032664.
XX
PR  02-DEC-1999;   99US-0169035P.
PR  28-NOV-2000; 2000US-00725324.
XX
PA  (MAXY-) MAXYGEN INC.
XX
PI  Leong SR,  Punnonen J;
XX
DR  WPI; 2001-502381/55.
DR  P-PSDB; AAE08611.
XX
PT  Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT  and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT  retinopathy and cancer.
XX
```

```
)S   Claim 87; Page 140; 223pp; English.
(X
:C   The invention relates to nucleic acids encoding modified cytokine
:C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
:C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
:C   gamma induction activities. The polypeptides and polynucleotides of the
:C   invention are useful for treating various diseases e.g. bacterial
:C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
:C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
:C   vaccinated host's cell-mediated immunity for protective response to a
:C   pathogen. The present sequence is a modified human p35 protein encoding
:C   DNA
(X
;Q   Sequence 660 BP; 182 A; 180 C; 144 G; 154 T; 0 U; 0 Other;

\lignment Scores:
)red. No.:                2.93e-51       Length:         660
;core:                    59.00          Matches:        59
)ercent Similarity:       100.0%         Conservative:   0
}est Local Similarity:    100.0%         Mismatches:     0
)uery Match:              31.6%          Indels:         0
)B:                       5              Gaps:           0

JS-10-821-670A-102 (1-187) x AAD15218 (1-660)

)y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 89
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACAACC 363

)y          90 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 109
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

)y         110 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

(ESULT 28
\AD15215
:D   AAD15215 standard; DNA; 660 BP.
(X
\C   AAD15215;
(X
)T   01-NOV-2001  (first entry)
(X
)E   Modified human cytokine p35 encoding DNA from clone R2-613.
(X
(W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
(W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
(W   p35; mutant; ds.
(X
)S   Homo sapiens.
)S   Synthetic.
(X
'H   Key             Location/Qualifiers
'T   CDS             1. .660
'T                   /*tag=  a
'T                   /product= "Modified p35 protein precursor"
'T   sig_peptide     1. .66
'T                   /*tag=  b
'T   mat_peptide     67. .657
'T                   /*tag=  c
'T                   /product= "Mature modified p35 protein"
(X
)N   WO200140257-A2.
(X
)D   07-JUN-2001.
(X
)F   30-NOV-2000; 2000WO-US032664.
(X
)R   02-DEC-1999;   99US-0169035P.
)R   28-NOV-2000; 2000US-00725324.
(X
```

```
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08608.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139-140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 190 A; 171 C; 137 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.75e-48       Length:         660
Score:                    56.00          Matches:        56
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              29.9%          Indels:         0
DB:                       5              Gaps:           0

US-10-821-670A-102 (1-187) x AAD15215 (1-660)

Qy          73 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu 92
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         313 ATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTT 372

Qy          93 SerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLys 112
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         373 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 432

Qy         113 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 128
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         433 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 29
AAF26098
ID   AAF26098 standard; DNA; 639 BP.
XX
AC   AAF26098;
XX
DT   24-APR-2001  (first entry)
XX
DE   Plasmid pMOL-fIL12 p35 DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Synthetic.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
```

```
A   (UYZU-) UNIV ZUERICH.
A   (REGC ) UNIV CALIFORNIA.
X
I   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
X
R   WPI; 2001-147178/15.
X
T   Recombinant feline interleukin-12, useful as immunostimulant and for
T   treating e.g. viral infections in cats, and related nucleic acid
T   constructs.
X
S   Disclosure; Fig 2; 35pp; German.
X
C   This invention describes a novel feline interleukin-12 (fIL-12)
C   polypeptide (I) that is expressed, by recombinant gene expression in
C   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
C   of subunits p35 and p40. These proteins are formed so that, in equimolar
C   concentrations and in presence of an immunizing antigen, they can be
C   administered to carnivores, particularly domestic cats. The invention
C   also describes a nucleic acid construct (II) encoding fIL-12 containing
C   sequences at least 95% identical with the p40- and p35-encoding sequences
C   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
C   as immunostimulants for immunization against infectious diseases and/or
C   for treating infections or tumors in felines, especially domestic cats.
C   The products of the invention have immunostimulatory, antiviral and
C   antitumor activity. Nucleic acid constructs that encode (II) are useful
C   as adjuvants for prophylactic immunization against viral diseases and for
C   treating diseases associated with a Th1 defect. IL-12 induces synthesis
C   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
C   is useful for carnivores, and particularly domestic cats in the
C   following: (i) as immunostimulant, for preventative or therapeutic use;
C   and (ii) treating tumors and autoimmune diseases, or diseases associated
C   with a Th1 defect, especially pre-existing infections by feline immune
C   deficiency virus (FIV), feline leukemia virus and corona virus
X
Q   Sequence 639 BP; 189 A; 166 C; 133 G; 151 T; 0 U; 0 Other;

lignment Scores:
red. No.:               4.28e-46        Length:         639
core:                   54.00           Matches:        54
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             28.9%           Indels:         0
B:                      4               Gaps:           0

S-10-821-670A-102 (1-187) x AAF26098 (1-639)

y          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         293 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 352

y         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         353 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 412

y         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
              |||||||||||||||||||||||||||||||||||||||||||
b         413 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 454

ESULT 30
AF26083
D   AAF26083 standard; DNA; 669 BP.
X
C   AAF26083;
X
T   24-APR-2001  (first entry)
X
E   Feline IL-12p35 encoding DNA SEQ ID 4.
X
W   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
W   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
X
S   Felis sp.
X
PN  WO200104280-A2.
XX
PD  18-JAN-2001.
XX
PF  08-JUL-2000; 2000WO-DE002262.
XX
PR  08-JUL-1999;  99CH-00001258.
XX
PA  (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA  (UYZU-) UNIV ZUERICH.
XX
PI  Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR  WPI; 2001-147190/15.
XX
PT  Vaccine for treating or preventing lentivirus infection in cats, contains
PT  nucleic acid sequence encoding viral protein under control of eukaryotic
PT  promoter.
XX
PS  Claim 14; Page 37; 37pp; German.
XX
CC  This invention describes a novel vaccine (A) for prevention or treatment
CC  of lentivirus infection in felines which comprises an immunizing nucleic
CC  acid sequence (I) that contains, or comprises, at least part of a gene
CC  encoding a protein (II) of the virus, under control of a eukaryotic
CC  promoter functional in the relevant animal. (II) is especially the
CC  envelope (env) protein. The invention also describes (1) vaccine (A)
CC  containing an immunizing protein, or fragment, from a lentivirus plus at
CC  least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC  lentivirus protein, or fragment, especially derived from feline immune
CC  deficiency virus (FIV), by expressing the corresponding nucleic acid
CC  sequence in a host cell. The products of the invention have antiviral
CC  activity. The vaccine (A) and related protein-based vaccines, are
CC  particularly used to treat or prevent lentivirus infections in domestic
CC  cats, especially feline immune deficiency virus (FIV). Vaccination with
CC  (A) allows differentiation between vaccinated and infected animals, from
CC  the antibody status. The vaccines may be formulated with an adjuvant
CC  (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC  immune response, particularly a Th1 response
XX
SQ  Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.48e-46        Length:         669
Score:                  54.00           Matches:        54
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            28.9%           Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-102 (1-187) x AAF26083 (1-669)

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
              |||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507

RESULT 31
AAF26086
ID  AAF26086 standard; DNA; 669 BP.
XX
AC  AAF26086;
XX
DT  24-APR-2001  (first entry)
XX
```

)E Feline IL-12p35 encoding DNA.
:X
:W Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
:W immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
:W Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
:X
)S Felis sp.
:X
)N WO200104155-A2.
:X
)D 18-JAN-2001.
:X
)F 08-JUL-2000; 2000WO-DE002263.
:X
)R 08-JUL-1999; 99CH-00001259.
:X
)A (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
)A (UYZU-) UNIV ZUERICH.
)A (REGC) UNIV CALIFORNIA.
:X
)I Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
:X
)R WPI; 2001-147178/15.
:X
)T Recombinant feline interleukin-12, useful as immunostimulant and for
)T treating e.g. viral infections in cats, and related nucleic acid
)T constructs.
:X
)S Claim 3; Page 31; 35pp; German.
:X
:C This invention describes a novel feline interleukin-12 (fIL-12)
:C polypeptide (I) that is expressed, by recombinant gene expression in
:C eukaryotic or prokaryotic cells, in the form of both polypeptide chains
:C of subunits p35 and p40. These proteins are formed so that, in equimolar
:C concentrations and in presence of an immunizing antigen, they can be
:C administered to carnivores, particularly domestic cats. The invention
:C also describes a nucleic acid construct (II) encoding fIL-12 containing
:C sequences at least 95% identical with the p40- and p35-encoding sequences
:C (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
:C as immunostimulants for immunization against infectious diseases and/or
:C for treating infections or tumors in felines, especially domestic cats.
:C The products of the invention have immunostimulatory, antiviral and
:C antitumor activity. Nucleic acid constructs that encode (II) are useful
:C as adjuvants for prophylactic immunization against viral diseases and for
:C treating diseases associated with a Th1 defect. IL-12 induces synthesis
:C of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
:C is useful for carnivores, and particularly domestic cats in the
:C following: (i) as immunostimulant, for preventative or therapeutic use;
:C and (ii) treating tumors and autoimmune diseases, or diseases associated
:C with a Th1 defect, especially pre-existing infections by feline immune
:C deficiency virus (FIV), feline leukemia virus and corona virus
:X
;Q Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.48e-46	Length:	669
Score:	54.00	Matches:	54
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	28.9%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-102 (1-187) x AAF26086 (1-669)

```
Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
              ||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507
```

RESULT 32
AAF26077
ID AAF26077 standard; DNA; 4201 BP.
XX
AC AAF26077;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Disclosure; Page 31-33; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.66e-45	Length:	4201
Score:	54.00	Matches:	54
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	28.9%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-102 (1-187) x AAF26077 (1-4201)

```
Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3392 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 3451
```

```
y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       3452 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 3511

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
             |||||||||||||||||||||||||||||||||||||||||||
b       3512 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 3553

ESULT 33
AX18179
D   AAX18179 standard; cDNA; 591 BP.
X
C   AAX18179;
X
T   07-MAY-1999  (first entry)
X
E   Canine mature CLAF p35 subunit coding sequence.
X
W   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
W   viral disease; canine distemper; canine parvovirus; autoimmune disease;
W   canine infectious hepatitis; ds.
X
S   Canis sp.
X
N   WO9855511-A1.
X
D   10-DEC-1998.
X
F   26-MAY-1998;   98WO-JP002295.
X
R   03-JUN-1997;   97JP-00161936.
X
A   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
X
I   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
X
R   WPI; 1999-070260/06.
R   P-PSDB; AAW74325.
X
T   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
T   is useful for treatment of viral and autoimmune diseases in dogs.
X
S   Claim 8; Page 34-35; 51pp; Japanese.
X
C   This sequence encodes the canine lymphocyte activation factor (CLAF) of
C   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
C   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
C   recognising it may be used in the treatment of viral diseases in dogs
C   (such as canine distemper, canine parvovirus and canine infectious
C   hepatitis). The antibodies may also be used in isolation of CLAF from
C   culture of the transformant host cells by affinity chromatography. The
C   p40 homodimer can be used for the treatment of autoimmune diseases in
C   dogs
X
Q   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

lignment Scores:
red. No.:              4.68e-44       Length:        591
core:                  52.00          Matches:       52
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            27.8%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-102 (1-187) x AAX18179 (1-591)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||
Db       238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 34
ABK98958/c
ID   ABK98958 standard; cDNA; 591 BP.
XX
AC   ABK98958;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-591 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 70; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             4.68e-44       Length:        591
Score:                 52.00          Matches:       52
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           27.8%          Indels:        0
DB:                    6              Gaps:          0

US-10-821-670A-102 (1-187) x ABK98958 (1-591)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415
```

```
)y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

)y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
)b        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

!ESULT 35
\BK98957
:D   ABK98957 standard; cDNA; 591 BP.
:X
\C   ABK98957;
:X
)T   21-OCT-2002  (first entry)
:X
)E   Canine interleukin-12 nCaIL-12p35-591 coding strand.
:X
:W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
:W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
:W   tumour development; inflammatory disease; graft rejection; gene; ss.
:X
)S   Canis familiaris.
:X
)N   US2002052030-A1.
:X
)D   02-MAY-2002.
:X
)F   27-JUL-2001; 2001US-00917265.
:X
)R   04-AUG-2000; 2000US-0223016P.
:X
)A   (WOND/) WONDERLING R S.
)A   (BORO/) BOROUGHS K L.
:X
)I   Wonderling RS,  Boroughs KL;
:X
)R   WPI; 2002-573554/61.
)R   P-PSDB; ABG69309.
:X
)T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
)T   chain and canine IL-12 single chain proteins, useful for treating and
)T   preventing autoimmune diseases, inflammatory diseases and/or graft
)T   rejection in animals.
:X
)S   Claim 1; Page 69; 106pp; English.
:X
:C   The present invention discloses new feline interleukin 18 (IL-18), feline
:C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
:C   proteins. A composition comprising a feline IL-18, feline caspase-1,
:C   feline IL-12 single chain or canine IL-12 single chain proteins, a
:C   nucleic acid encoding these proteins, mimetopes of these proteins,
:C   multimeric forms of these proteins, an antibody against these proteins,
:C   or an inhibitor identified by its ability to inhibit the activity of
:C   these proteins, can be used to treat or prevent autoimmune diseases,
:C   allergic reactions, infectious diseases, tumour development, inflammatory
:C   diseases and/or graft rejection in animals. The present nucleic acid
:C   sequence represents a canine interleukin 12 DNA sequence, as described in
:C   the invention
:X
;Q   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

\lignment Scores:
?red. No.:              4.68e-44        Length:         591
;core:                  52.00           Matches:        52
?ercent Similarity:     100.0%          Conservative:   0
3est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            27.8%           Indels:         0
)B:                     6               Gaps:           0

JS-10-821-670A-102 (1-187) x ABK98957 (1-591)

)y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 36
ADV34701
ID   ADV34701 standard; cDNA; 591 BP.
XX
AC   ADV34701;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PCaIL-12P35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34702.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 49; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.68e-44        Length:         591
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            27.8%           Indels:         0
```

```
B:                    14            Gaps:          0

S-10-821-670A-102 (1-187) x ADV34701 (1-591)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||
b        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

ESULT 37
DV34703/c
D   ADV34703 standard; DNA; 591 BP.
X
C   ADV34703;
X
T   24-FEB-2005  (first entry)
X
E   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 591.
X
W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W   infectious disease; antimicrobial; ds.
X
S   Canis familiaris.
X
N   US2004248261-A1.
X
D   09-DEC-2004.
X
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2005-020565/02.
X
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
T   vaccine against infectious diseases in feline animals.
X
S   Example 4; SEQ ID NO 51; 103pp; English.
X
C   The present invention relates to the feline interleukin (IL)-12p35 or p40
C   subunit protein and their encoding nucleic acid molecules and a nucleic
C   acid linker. The invention also provides the feline caspase (casp)-1,
C   feline IL-18 single chain and canine IL-12 single chain proteins and
C   their nucleic acid molecules. The nucleic acid molecule is useful in
C   preparing a vaccine against infectious diseases in feline animals. The
C   present sequence is the canine single chain IL-12p35 subunit
C   complementary DNA.
X
Q   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

lignment Scores:
red. No.:              4.68e-44        Length:         591
core:                  52.00           Matches:        52
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            27.8%           Indels:         0
B:                     14              Gaps:           0

S-10-821-670A-102 (1-187) x ADV34703 (1-591)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||
Db       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 38
ABK98955
ID   ABK98955 standard; cDNA; 666 BP.
XX
AC   ABK98955;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69308.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 67-68; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             5.25e-44        Length:         666
Score:                 52.00           Matches:        52
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           27.8%           Indels:         0
```

```
)B:                    6              Gaps:          0

)S-10-821-670A-102 (1-187) x ABK98955 (1-666)

)y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

)y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

)y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
)b        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

(ESULT 39
(BK98956/c
:D   ABK98956 standard; cDNA; 666 BP.
:X
(C   ABK98956;
:X
)T   21-OCT-2002  (first entry)
:X
)E   Canine interleukin-12 nCaIL-12p35-66 complementary strand.
:X
:W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
:W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
:W   tumour development; inflammatory disease; graft rejection; ss.
:X
)S   Canis familiaris.
:X
)N   US2002052030-A1.
:X
)D   02-MAY-2002.
:X
)F   27-JUL-2001; 2001US-00917265.
:X
)R   04-AUG-2000; 2000US-0223016P.
:X
)A   (WOND/) WONDERLING R S.
)A   (BORO/) BOROUGHS K L.
:X
)I   Wonderling RS,  Boroughs KL;
:X
)R   WPI; 2002-573554/61.
:X
)T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
)T   chain and canine IL-12 single chain proteins, useful for treating and
)T   preventing autoimmune diseases, inflammatory diseases and/or graft
)T   rejection in animals.
:X
)S   Disclosure; Page 68-69; 106pp; English.
:X
:C   The present invention discloses new feline interleukin 18 (IL-18), feline
:C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
:C   proteins. A composition comprising a feline IL-18, feline caspase-1,
:C   feline IL-12 single chain or canine IL-12 single chain proteins, a
:C   nucleic acid encoding these proteins, mimetopes of these proteins,
:C   multimeric forms of these proteins, an antibody against these proteins,
:C   or an inhibitor identified by its ability to inhibit the activity of
:C   these proteins, can be used to treat or prevent autoimmune diseases,
:C   allergic reactions, infectious diseases, tumour development, inflammatory
:C   diseases and/or graft rejection in animals. The present nucleic acid
:C   sequence represents a canine interleukin 12 DNA sequence, as described in
:C   the invention
:X
(Q   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

lignment Scores:
)red. No.:              5.25e-44       Length:        666
(core:                  52.00          Matches:       52
)ercent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     6              Gaps:          0

US-10-821-670A-102 (1-187) x ABK98956 (1-666)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 40
ADV34700/c
ID   ADV34700 standard; DNA; 666 BP.
XX
AC   ADV34700;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 48; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.25e-44       Length:        666
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     14             Gaps:          0
```

```
S-10-821-670A-102 (1-187) x ADV34700 (1-666)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
b        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

ESULT 41
DV34698
D   ADV34698 standard; cDNA; 666 BP.
X
C   ADV34698;
X
T   24-FEB-2005  (first entry)
X
E   Canine single chain IL-12p35 full-length cDNA, nCaIL-12p35 666.
X
W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W   infectious disease; antimicrobial; gene; ss.
X
S   Canis familiaris.
X
H   Key             Location/Qualifiers
T   CDS             1. .666
T                   /*tag=  a
T                   /product= "PCaIL-12p222 protein"
T                   /partial
T                   /note= "No stop codon"
X
N   US2004248261-A1.
X
D   09-DEC-2004.
X
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2005-020565/02.
R   P-PSDB; ADV34699.
X
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
T   vaccine against infectious diseases in feline animals.
X
S   Example 4; SEQ ID NO 46; 103pp; English.
X
C   The present invention relates to the feline interleukin (IL)-12p35 or p40
C   subunit protein and their encoding nucleic acid molecules and a nucleic
C   acid linker. The invention also provides the feline caspase (casp)-1,
C   feline IL-18 single chain and canine IL-12 single chain proteins and
C   their nucleic acid molecules. The nucleic acid molecule is useful in
C   preparing a vaccine against infectious diseases in feline animals. The
C   present sequence is the canine single chain IL-12p35 subunit protein
C   encoding full-length cDNA.
X
Q   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

lignment Scores:
red. No.:              5.25e-44       Length:        666
```

```
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     14             Gaps:          0

US-10-821-670A-102 (1-187) x ADV34698 (1-666)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 42
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.27e-44       Length:        669
Score:                  52.00          Matches:       52
```

```
)ercent Similarity:     100.0%          Conservative:  0
}est Local Similarity:  100.0%          Mismatches:    0
}uery Match:            27.8%           Indels:        0
)B:                     2               Gaps:          0

}S-10-821-670A-102 (1-187) x AAV13818 (1-669)

}y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

}y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

}y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
)b        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

(ESULT 43
\AV13819
:D   AAV13819 standard; cDNA to mRNA; 669 BP.
:X
\C   AAV13819;
:X
)T   14-MAY-1998  (first entry)
:X
)E   Canine IL-12 P35 subunit cDNA.
:X
:W   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
:W   antiviral; vaccine adjuvant; ds.
:X
)S   Canis sp.
:X
'H   Key             Location/Qualifiers
'T   CDS             1. .669
'T                   /*tag=  a
'T                   /product= "interleukin-12_P35_subunit"
:X
'N   JP10036397-A.
:X
'D   10-FEB-1998.
:X
'F   08-NOV-1996;   96JP-00296789.
:X
'R   08-NOV-1995;   95JP-00289729.
'R   23-MAY-1996;   96JP-00128104.
:X
'A   (TORA ) TORAY IND INC.
:X
)R   WPI; 1998-174914/16.
)R   P-PSDB; AAW41793.
:X
'T   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
'T   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
'T   activities are expected.
:X
'S   Claim 11; Page 11-12; 12pp; Japanese.
:X
:C   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
:C   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
:C   antiviral activating factor and the expression of class II MHC molecules
:C   in canine tumour cells, stimulating proliferation of canine blastogenic
:C   lymphocytes and activating canine leukocytes to inhibit canine tumour
:C   cells. The canine IL-12 can be used in veterinary medicines, e.g.
:C   antitumour, antivirus and vaccine adjuvant activities are expected
:X
}Q   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 U; 0 Other;

\lignment Scores:
'red. No.:              5.27e-44        Length:        669
}core:                  52.00           Matches:       52
'ercent Similarity:     100.0%          Conservative:  0
```

```
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            27.8%           Indels:        0
DB:                     2               Gaps:          0

US-10-821-670A-102 (1-187) x AAV13819 (1-669)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 44
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
```

```
C   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
C   and hair loss; infections; dog Parvovirus infection and distemper virus,
C   cat plaque virus infection and feline leukaemia, and allergic diseases,
C   e.g. pollinosis
X
Q   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

lignment Scores:
red. No.:              5.27e-44       Length:        669
core:                  52.00          Matches:       52
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            27.8%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-102 (1-187) x AAX03163 (1-669)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
b        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

ESULT 45
AX03153
D   AAX03153 standard; cDNA to mRNA; 669 BP.
X
C   AAX03153;
X
T   30-MAR-1999  (first entry)
X
E   Nucleic acid encoding canine interleukin 12.
X
W   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
W   skin disease; viral infection; allergic disease; breast tumour;
W   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
W   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
W   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
W   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
W   dog Parvovirus infection; distemper virus; cat plaque virus infection;
W   feline leukaemia; allergy; pollinosis; ds.
X
S   Canis sp.
X
H   Key             Location/Qualifiers
T   CDS             1. .669
T                   /*tag=  a
T                   /product= "interleukin_12"
X
N   WO9851327-A1.
X
D   19-NOV-1998.
X
F   07-MAY-1998;   98WO-JP002031.
X
R   16-MAY-1997;   97JP-00127690.
X
A   (TORA ) TORAY IND INC.
X
I   Okano F,  Satoh M,  Yamada K;
X
R   WPI; 1999-070100/06.
R   P-PSDB; AAW84372.
X
T   New therapeutic and prophylactic agents - comprise genetically-engineered
T   canine interleukin 12, used to treat, e.g. canine and feline
T   immunological diseases.
XX
PS  Claim 1; Page 26-27; 45pp; Japanese.
XX
CC  The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC  IL-12 protein can be used in therapeutic or prophylactic agents. The
CC  agents can be used to prevent and treat canine and feline immunological
CC  diseases including dog and cat tumours, skin diseases, viral infections
CC  and allergic diseases, especially tumours, breast tumour, oesinophilic
CC  granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC  pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC  diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC  skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC  and hair loss; infections; dog Parvovirus infection and distemper virus,
CC  cat plaque virus infection and feline leukaemia, and allergic diseases,
CC  e.g. pollinosis
XX
SQ  Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             5.27e-44       Length:        669
Score:                 52.00          Matches:       52
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           27.8%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-102 (1-187) x AAX03153 (1-669)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 46
AAX35616
ID  AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC  AAX35616;
XX
DT  09-JUL-1999  (first entry)
XX
DE  Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW  Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW  tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS  Canis sp.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .669
FT                  /*tag=  a
XX
PN  JP11106350-A.
XX
PD  20-APR-1999.
XX
PF  15-MAY-1998;   98JP-00133345.
XX
PR  16-MAY-1997;   97JP-00127690.
PR  07-AUG-1997;   97JP-00213755.
XX
PA  (TORA ) TORAY IND INC.
XX
DR  WPI; 1999-308068/26.
DR  P-PSDB; AAY02340.
XX
```

```
)T   A prevention and treating agent containing interleukin 12 (CaIL12) - for
)T   prevention and treatment of dog and cat immune diseases.
:X
)S   Claim 1; Page 13; 16pp; Japanese.
:X
:C   The present sequence encodes canine interleukin-12 (IL-12). The
:C   specification describes a method for the prevention and treatment of dog
:C   and cat immune diseases. The treatment used an agent comprising dog IL-12
:C   (CaIL12) proteins to form a heterodimer. The agent is useful for
:C   preventing and treating dog and cat immune diseases, including tumours,
:C   skin diseases, infectious diseases and allergic diseases
:X
)Q   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
)red. No.:                5.27e-44        Length:         669
)core:                    52.00           Matches:        52
)ercent Similarity:       100.0%          Conservative:   0
)est Local Similarity:    100.0%          Mismatches:     0
)uery Match:              27.8%           Indels:         0
)B:                       2               Gaps:           0

)S-10-821-670A-102 (1-187) x AAX35616 (1-669)

)y          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

)y          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

)y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
)b         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

(ESULT 47
\AX35626
:D   AAX35626 standard; cDNA to mRNA; 669 BP.
:X
\C   AAX35626;
:X
)T   09-JUL-1999  (first entry)
:X
)E   Nucleic acid encoding canine Interleukin-12 (IL-12).
:X
:W   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
:W   tumour; skin disease; infectious disease; allergic disease; ds.
:X
)S   Canis sp.
:X
)H   Key             Location/Qualifiers
)T   CDS             1. .669
)T                   /*tag=  a
:X
)N   JP11106350-A.
:X
)D   20-APR-1999.
:X
)F   15-MAY-1998;   98JP-00133345.
:X
)R   16-MAY-1997;   97JP-00127690.
)R   07-AUG-1997;   97JP-00213755.
:X
)A   (TORA ) TORAY IND INC.
:X
)R   WPI; 1999-308068/26.
)R   P-PSDB; AAY02343.
:X
)T   A prevention and treating agent containing interleukin 12 (CaIL12) - for
)T   prevention and treatment of dog and cat immune diseases.
:X
)S   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.27e-44        Length:         669
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x AAX35626 (1-669)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 48
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "Canine protein #4"
FT   sig_peptide     1. .75
FT                   /*tag=  b
FT   mat_peptide     76. .666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 18; 21pp; Japanese.
```

```
X
C   The present invention relates to a method for the preparation of a highly
C   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
C   the activity of IL12 is contacted to an ion exchanging carrier and/or a
C   pigment carrier to get IL12 and/or a protein inhibiting the activity of
C   IL12. The protein is used as a preventive agent for dog immunopathy. The
C   present sequence was used in the method of the present invention
X
Q   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

lignment Scores:
red. No.:              5.27e-44       Length:         669
core:                  52.00          Matches:        52
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            27.8%          Indels:         0
B:                     4              Gaps:           0

S-10-821-670A-102 (1-187) x AAI64389 (1-669)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
b        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

ESULT 49
AI64379
D   AAI64379 standard; DNA; 669 BP.
X
C   AAI64379;
X
T   23-NOV-2001  (first entry)
X
E   Canine coding sequence #2.
X
W   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
X
S   Canis familiaris.
X
H   Key             Location/Qualifiers
T   CDS             1. .669
T                   /*tag=  a
T                   /product= "Canine protein #2"
T   sig_peptide     1. .75
T                   /*tag=  b
T   mat_peptide     76. .666
T                   /*tag=  c
X
N   JP2001161378-A.
X
D   19-JUN-2001.
X
F   26-SEP-2000; 2000JP-00292946.
X
R   01-OCT-1999;   99JP-00281234.
X
A   (TORA ) TORAY IND INC.
X
R   WPI; 2001-592466/67.
R   P-PSDB; AAG66481.
X
T   Preparation of a highly pure protein, interleukin 12, a protein
T   inhibiting the activity of interleukin 12, and a treating agent and a
T   treating method for immunopathy of mammalian.
X
S   Claim 6; Page 15; 21pp; Japanese.
```

```
XX
CC  The present invention relates to a method for the preparation of a highly
CC  pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC  the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC  pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC  IL12. The protein is used as a preventive agent for dog immunopathy. The
CC  present sequence was used in the method of the present invention
XX
SQ  Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             5.27e-44       Length:         669
Score:                 52.00          Matches:        52
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           27.8%          Indels:         0
DB:                    4              Gaps:           0

US-10-821-670A-102 (1-187) x AAI64379 (1-669)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 50
ADZ25701
ID  ADZ25701 standard; cDNA; 669 BP.
XX
AC  ADZ25701;
XX
DT  16-JUN-2005  (first entry)
XX
DE  Canine interleukin 12 P35 encoding cDNA SEQ ID NO:6.
XX
KW  interleukin-12; antiviral; gene; ss.
XX
OS  Canis sp.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .669
FT                  /*tag=  b
FT                  /product= "interleukin-12 P40"
FT  sig_peptide     1. .75
FT                  /*tag=  a
FT  mat_peptide     76. .666
FT                  /*tag=  c
FT                  /product= "interleukin-12 P40"
XX
PN  JP2003284585-A.
XX
PD  07-OCT-2003.
XX
PF  28-MAR-2002; 2002JP-00090161.
XX
PR  28-MAR-2002; 2002JP-00090161.
XX
PA  (TORA ) TORAY IND INC.
XX
DR  WPI; 2003-885430/82.
DR  P-PSDB; ADZ25703.
XX
PT  Large scale production of interleukin-12 for pharmaceutical applications,
PT  comprises infecting an insect cell with a recombinant virus containing
PT  gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT  of insect cell.
```

```
XX
DS   Example; SEQ ID NO 6; 8pp; Japanese.
XX
CC   The invention related to the large scale production of interleukin-12 (IL
CC   -12), which involves infecting an insect cell with a recombinant virus
CC   containing a gene encoding IL-12, and producing IL-12 by carrying out
CC   spinner culture of insect cell. The method is useful for producing IL-12,
CC   preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC   present sequence encodes canine IL-12 P35, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.27e-44        Length:         669
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       11              Gaps:           0

US-10-821-670A-102 (1-187) x ADZ25701 (1-669)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 51
AAX18178
ID   AAX18178 standard; cDNA; 1282 BP.
XX
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                9.92e-44        Length:         1282
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x AAX18178 (1-1282)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         258 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 317

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         318 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 377

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         378 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 413

RESULT 52
ABK99003
ID   ABK99003 standard; cDNA; 1455 BP.
XX
AC   ABK99003;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-1455 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69316.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 94-95; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
```

```
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a canine interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.12e-43        Length:         1455
core:                  52.00           Matches:        52
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            27.8%           Indels:         0
B:                     6               Gaps:           0

S-10-821-670A-102 (1-187) x ABK99003 (1-1455)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
b        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

ESULT 53
BK99004/c
D   ABK99004 standard; cDNA; 1455 BP.
X
C   ABK99004;
X
T   21-OCT-2002  (first entry)
X
E   Canine interleukin-12 nCaIL-12p35-1455 complementary strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; ss.
X
S   Canis familiaris.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
X
R   04-AUG-2000; 2000US-0223016P.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2002-573554/61.
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Example 4; Page 96; 106pp; English.
X
```

```
CC  The present invention discloses new feline interleukin 18 (IL-18), feline
CC  caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC  proteins. A composition comprising a feline IL-18, feline caspase-1,
CC  feline IL-12 single chain or canine IL-12 single chain proteins, a
CC  nucleic acid encoding these proteins, mimetopes of these proteins,
CC  multimeric forms of these proteins, an antibody against these proteins,
CC  or an inhibitor identified by its ability to inhibit the activity of
CC  these proteins, can be used to treat or prevent autoimmune diseases,
CC  allergic reactions, infectious diseases, tumour development, inflammatory
CC  diseases and/or graft rejection in animals. The present nucleic acid
CC  sequence represents a canine interleukin 12 DNA sequence, as described in
CC  the invention
XX
SQ  Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.12e-43        Length:         1455
Score:                 52.00           Matches:        52
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           27.8%           Indels:         0
DB:                    6               Gaps:           0

US-10-821-670A-102 (1-187) x ABK99004 (1-1455)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db       912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

RESULT 54
ADV34756/c
ID  ADV34756 standard; DNA; 1455 BP.
XX
AC  ADV34756;
XX
DT  24-FEB-2005  (first entry)
XX
DE  Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 1455.
XX
KW  DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW  infectious disease; antimicrobial; ds.
XX
OS  Canis familiaris.
XX
PN  US2004248261-A1.
XX
PD  09-DEC-2004.
XX
PF  09-APR-2004; 2004US-00821670.
XX
PR  04-AUG-2000; 2000US-0223016P.
PR  27-JUL-2001; 2001US-00917265.
XX
PA  (WOND/) WONDERLING R S.
PA  (BORO/) BOROUGHS K L.
XX
PI  Wonderling RS,  Boroughs KL;
XX
DR  WPI; 2005-020565/02.
XX
PT  New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT  p40 subunit protein and a nucleic acid linker, useful in preparing a
PT  vaccine against infectious diseases in feline animals.
XX
PS  Example 4; SEQ ID NO 106; 103pp; English.
```

```
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.12e-43      Length:          1455
Score:                    52.00         Matches:         52
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              27.8%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-102 (1-187) x ADV34756 (1-1455)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

RESULT 55
ADV34754
ID   ADV34754 standard; cDNA; 1455 BP.
XX
AC   ADV34754;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 1455.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             232. .900
FT                   /*tag= a
FT                   /product= "PCaIL-12p35 222 protein"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34755.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 104; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.12e-43      Length:          1455
Score:                    52.00         Matches:         52
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              27.8%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-102 (1-187) x ADV34754 (1-1455)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

RESULT 56
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69314.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
```

```
X
S   Claim 6; Page 83-85; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a canine interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.18e-43      Length:        1533
core:                  52.00         Matches:       52
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            27.8%         Indels:        0
B:                     6             Gaps:          0

S-10-821-670A-102 (1-187) x ABK98967 (1-1533)

y          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

y          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
b        1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

ESULT 57
BK98968/c
D   ABK98968 standard; cDNA; 1533 BP.
X
C   ABK98968;
X
T   21-OCT-2002  (first entry)
X
E   Canine interleukin-12 nCaIL-12-1533 complementary strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; ss.
X
S   Canis familiaris.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
X
R   04-AUG-2000; 2000US-0223016P.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2002-573554/61.
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
```

```
PT  preventing autoimmune diseases, inflammatory diseases and/or graft
PT  rejection in animals.
XX
PS  Claim 6; Page 86-87; 106pp; English.
XX
CC  The present invention discloses new feline interleukin 18 (IL-18), feline
CC  caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC  proteins. A composition comprising a feline IL-18, feline caspase-1,
CC  feline IL-12 single chain or canine IL-12 single chain proteins, a
CC  nucleic acid encoding these proteins, mimetopes of these proteins,
CC  multimeric forms of these proteins, an antibody against these proteins,
CC  or an inhibitor identified by its ability to inhibit the activity of
CC  these proteins, can be used to treat or prevent autoimmune diseases,
CC  allergic reactions, infectious diseases, tumour development, inflammatory
CC  diseases and/or graft rejection in animals. The present nucleic acid
CC  sequence represents a canine interleukin 12 DNA sequence, as described in
CC  the invention
XX
SQ  Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.18e-43      Length:        1533
Score:                 52.00         Matches:       52
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           27.8%         Indels:        0
DB:                    6             Gaps:          0

US-10-821-670A-102 (1-187) x ABK98968 (1-1533)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 58
ADV34718/c
ID  ADV34718 standard; DNA; 1533 BP.
XX
AC  ADV34718;
XX
DT  24-FEB-2005  (first entry)
XX
DE  Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW  DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW  infectious disease; antimicrobial; ds.
XX
OS  Canis familiaris.
XX
PN  US2004248261-A1.
XX
PD  09-DEC-2004.
XX
PF  09-APR-2004; 2004US-00821670.
XX
PR  04-AUG-2000; 2000US-0223016P.
PR  27-JUL-2001; 2001US-00917265.
XX
PA  (WOND/) WONDERLING R S.
PA  (BORO/) BOROUGHS K L.
XX
PI  Wonderling RS,  Boroughs KL;
XX
DR  WPI; 2005-020565/02.
XX
```

```
>T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
>T   p40 subunit protein and a nucleic acid linker, useful in preparing a
>T   vaccine against infectious diseases in feline animals.
;X
>S   Example 4; SEQ ID NO 68; 103pp; English.
;X
;C   The present invention relates to the feline interleukin (IL)-12p35 or p40
;C   subunit protein and their encoding nucleic acid molecules and a nucleic
;C   acid linker. The invention also provides the feline caspase (casp)-1,
;C   feline IL-18 single chain and canine IL-12 single chain proteins and
;C   their nucleic acid molecules. The nucleic acid molecule is useful in
;C   preparing a vaccine against infectious diseases in feline animals. The
;C   present sequence is the canine single chain IL-12 complementary DNA.
;X
;Q   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

\lignment Scores:
>red. No.:              1.18e-43      Length:        1533
;core:                  52.00         Matches:       52
>ercent Similarity:     100.0%        Conservative:  0
;est Local Similarity:  100.0%        Mismatches:    0
)uery Match:            27.8%         Indels:        0
)B:                     14            Gaps:          0

)S-10-821-670A-102 (1-187) x ADV34718 (1-1533)

)y          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

)y          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

)y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
)b         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

(ESULT 59
\DV34716
:D   ADV34716 standard; cDNA; 1533 BP.
;X
\C   ADV34716;
;X
>T   24-FEB-2005  (first entry)
;X
>E   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
;X
;W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
;W   infectious disease; antimicrobial; gene; ss.
;X
>S   Canis familiaris.
;X
'H   Key             Location/Qualifiers
'T   CDS             1. .1533
'T                   /*tag=  a
'T                   /product= "PCaIL-12 511 protein"
'T                   /partial
'T                   /note= "No start and stop codon"
;X
>N   US2004248261-A1.
;X
>D   09-DEC-2004.
;X
>F   09-APR-2004; 2004US-00821670.
;X
>R   04-AUG-2000; 2000US-0223016P.
>R   27-JUL-2001; 2001US-00917265.
;X
>A   (WOND/) WONDERLING R S.
>A   (BORO/) BOROUGHS K L.
;X
>I   Wonderling RS,  Boroughs KL;

XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.18e-43      Length:        1533
Score:                  52.00         Matches:       52
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            27.8%         Indels:        0
DB:                     14            Gaps:          0

US-10-821-670A-102 (1-187) x ADV34716 (1-1533)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db        1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 60
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69313.
```

```
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Claim 6; Page 79-80; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a canine interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.23e-43      Length:        1599
core:                  52.00         Matches:       52
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            27.8%         Indels:        0
B:                     6             Gaps:          0

S-10-821-670A-102 (1-187) x ABK98965 (1-1599)

y          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

y          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
b        1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

ESULT 61
BK98966/c
D   ABK98966 standard; cDNA; 1599 BP.
X
C   ABK98966;
X
T   21-OCT-2002  (first entry)
X
E   Canine interleukin-12 nCaIL-12-1599 complementary strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; ss.
X
S   Canis familiaris.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
X
R   04-AUG-2000; 2000US-0223016P.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
```

```
XX
DR  WPI; 2002-573554/61.
XX
PT  Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT  chain and canine IL-12 single chain proteins, useful for treating and
PT  preventing autoimmune diseases, inflammatory diseases and/or graft
PT  rejection in animals.
XX
PS  Claim 6; Page 82-83; 106pp; English.
XX
CC  The present invention discloses new feline interleukin 18 (IL-18), feline
CC  caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC  proteins. A composition comprising a feline IL-18, feline caspase-1,
CC  feline IL-12 single chain or canine IL-12 single chain proteins, a
CC  nucleic acid encoding these proteins, mimetopes of these proteins,
CC  multimeric forms of these proteins, an antibody against these proteins,
CC  or an inhibitor identified by its ability to inhibit the activity of
CC  these proteins, can be used to treat or prevent autoimmune diseases,
CC  allergic reactions, infectious diseases, tumour development, inflammatory
CC  diseases and/or graft rejection in animals. The present nucleic acid
CC  sequence represents a canine interleukin 12 DNA sequence, as described in
CC  the invention
XX
SQ  Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.23e-43      Length:        1599
Score:                 52.00         Matches:       52
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           27.8%         Indels:        0
DB:                    6             Gaps:          0

US-10-821-670A-102 (1-187) x ABK98966 (1-1599)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 62
ADV34715/c
ID  ADV34715 standard; DNA; 1599 BP.
XX
AC  ADV34715;
XX
DT  24-FEB-2005  (first entry)
XX
DE  Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW  DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW  infectious disease; antimicrobial; ds.
XX
OS  Canis familiaris.
XX
PN  US2004248261-A1.
XX
PD  09-DEC-2004.
XX
PF  09-APR-2004; 2004US-00821670.
XX
PR  04-AUG-2000; 2000US-0223016P.
PR  27-JUL-2001; 2001US-00917265.
XX
PA  (WOND/) WONDERLING R S.
PA  (BORO/) BOROUGHS K L.
```

```
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.23e-43      Length:          1599
Score:                    52.00         Matches:         52
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              27.8%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-102 (1-187) x ADV34713 (1-1599)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db        1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 64
ADT04852
ID   ADT04852 standard; DNA; 669 BP.
XX
AC   ADT04852;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p35 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
```

```
CX
PI   Wonderling RS,  Boroughs KL;
CX
DR   WPI; 2005-020565/02.
CX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
CX
PS   Example 4; SEQ ID NO 63; 103pp; English.
CX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
CX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.23e-43      Length:          1599
Score:                    52.00         Matches:         52
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              27.8%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-102 (1-187) x ADV34715 (1-1599)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 63
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
CX
AC   ADV34713;
CX
DT   24-FEB-2005  (first entry)
CX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
CX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
CX
OS   Canis familiaris.
CX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
CX
PN   US2004248261-A1.
CX
PD   09-DEC-2004.
CX
PF   09-APR-2004; 2004US-00821670.
CX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
```

```
T   Novel gene vector for expression in insect useful for expression of
T   foreign gene such as dog interleukin 12 gene, comprises two promoters.
X
S   Claim 4; SEQ ID NO 8; 13pp; Japanese.
X
C   The invention relates to a novel gene vector for expression in an insect
C   comprising at least two promoters, particularly the polyhedrin promoter
C   and p10 promoter. The vector contains at least two types of foreign
C   protein expression gene and the gene product of the vector is produced
C   using a gene recombinant baculovirus, particularly a recombinant silkworm
C   nuclear polyhedrosis virus. The baculovirus is proliferated in a
C   silkworm. The vector of the invention may be useful for expression of a
C   foreign gene, such as canine interleukin 12. Within the vector, two types
C   of foreign protein expression genes are integrated simultaneously for
C   their simultaneous expression. The current sequence is that of the canine
C   interleukin-12 (IL-12) p35 DNA of the invention.
X
Q   Sequence 669 BP; 183 A; 177 C; 145 G; 164 T; 0 U; 0 Other;

lignment Scores:
red. No.:              6.21e-42        Length:         669
core:                  50.00           Matches:        50
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            26.7%           Indels:         0
B:                     13              Gaps:           0

S-10-821-670A-102 (1-187) x ADT04852 (1-669)

y         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAG 258

y         52 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

y         72 LeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||
b        319 TTGATAACTAACGGGAGTTGCCTGGCCTCT 348

ESULT 65
AD15212
D   AAD15212 standard; DNA; 666 BP.
X
C   AAD15212;
X
T   01-NOV-2001  (first entry)
X
E   Modified human cytokine p35 encoding DNA from clone R2-146.
X
W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
W   p35; mutant; ds.
X
S   Homo sapiens.
S   Synthetic.
X
H   Key             Location/Qualifiers
T   CDS             1. .666
T                   /*tag=  a
T                   /product= "Modified p35 protein precursor"
T   sig_peptide     1. .75
T                   /*tag=  b
T   mat_peptide     76. .663
T                   /*tag=  c
T                   /product= "Mature modified p35 protein"
X
N   WO200140257-A2.
X
D   07-JUN-2001.
X
F   30-NOV-2000; 2000WO-US032664.
XX
PR  02-DEC-1999;  99US-0169035P.
PR  28-NOV-2000; 2000US-00725324.
XX
PA  (MAXY-) MAXYGEN INC.
XX
PI  Leong SR,  Punnonen J;
XX
DR  WPI; 2001-502381/55.
DR  P-PSDB; AAE08605.
XX
PT  Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT  and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT  retinopathy and cancer.
XX
PS  Claim 87; Page 139; 223pp; English.
XX
CC  The invention relates to nucleic acids encoding modified cytokine
CC  polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC  cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC  gamma induction activities. The polypeptides and polynucleotides of the
CC  invention are useful for treating various diseases e.g. bacterial
CC  infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC  polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC  vaccinated host's cell-mediated immunity for protective response to a
CC  pathogen. The present sequence is a modified human p35 protein encoding
CC  DNA
XX
SQ  Sequence 666 BP; 186 A; 179 C; 141 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.1e-34         Length:         666
Score:                 43.00           Matches:        43
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           23.0%           Indels:         0
DB:                    5               Gaps:           0

US-10-821-670A-102 (1-187) x AAD15212 (1-666)

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAG 402

Qy        101 MetTyrGln 103
              |||||||||
Db        403 ATGTACCAG 411

RESULT 66
AAT50757
ID  AAT50757 standard; cDNA; 554 BP.
XX
AC  AAT50757;
XX
DT  17-OCT-2003  (revised)
DT  24-SEP-1997  (first entry)
XX
DE  Partial sequence of ovine IL-12 35 kD sununit cDNA.
XX
KW  Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW  livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW  immunosuppression; allergy; reproductive system; growth; early maturity;
KW  antibody; diagnosis; immunopotentiator;
KW  early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW  secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.
XX
OS  Ovis aries.
XX
PN  WO9700321-A1.
```

```
XX
DT   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-AU000360.
XX
PR   14-JUN-1995;   95AU-00003502.
PR   27-OCT-1995;   95AU-00006244.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Seow H,  Wood P;
XX
DR   WPI; 1997-077528/07.
DR   P-PSDB; AAW08481.
XX
PT   Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT   adjuvants and to treat or prevent microbial infections in livestock.
XX
PS   Claim 8; Page 43-44; 78pp; English.
XX
CC   The sequences given in AAT50757-59 encode ovine interleukin-12 (IL-12) 35
CC   kD subunit (partial and full length sequence) and the 40 kD subunit.
CC   Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC   livestock (esp. cows and sheep), particularly where the animals are
CC   stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC   adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC   subunit or synthetic peptide vaccines). They may also be used to treat
CC   cancer, immunosuppression and allergy, to enhance/suppress the
CC   reproductive system and to promote growth or early maturity. Optionally
CC   interleukin can be delivered from constructs or delivery cells and
CC   antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC   infection. The interleukins are immunopotentiators, especially IL-5
CC   promotes growth of early haematopoietic progenitor cells and generation
CC   of cytotoxic cells from thymocytes, also it stimulates production and
CC   secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC   induces production of gamma-interferon by, and proliferation of, T and NK
CC   cells and increases the (non-)specific cytolytic lymphocyte response. The
CC   genetic constructs can also be used for in vitro production of IL-5 or -
CC   12. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 554 BP; 159 A; 144 C; 124 G; 127 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                9.97e-34        Length:         554
Score:                    42.00           Matches:        42
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              22.5%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-102 (1-187) x AAT50757 (1-554)

Qy          17 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 36
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          96 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 155

Qy          37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         156 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 215

Qy          57 GluLeu 58
               ||||||
Db         216 GAATTA 221

RESULT 67
AAT70708
ID   AAA70708 standard; DNA; 703 BP.
XX
AC   AAA70708;
XX
DT   15-DEC-2000  (first entry)
XX
DE   Bovine interleukin-12 p35 subunit gene.
XX
KW   Antiinfective; bovine; interleukin 12; IL12; heterodimer; infection; ss.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .677
FT                   /*tag=  a
FT                   /product= "IL-12 p35 subunit"
XX
PN   JP2000157274-A.
XX
PD   13-JUN-2000.
XX
PF   20-NOV-1998;   98JP-00331052.
XX
PR   20-NOV-1998;   98JP-00331052.
XX
PA   (DAUC ) DAIICHI PHARM CO LTD.
XX
DR   WPI; 2000-468201/41.
DR   P-PSDB; AAB15391.
XX
PT   Preparation of bovine interleukin 12 comprising using a vector containing
PT   the gene encoding it, useful for the prevention and treatment of chronic
PT   and opportunistic infections.
XX
PS   Example 1; Page 8-9; 11pp; Japanese.
XX
CC   The invention relates to a method for the preparation of bovine
CC   interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35 and p40
CC   subunits. BoIL12 is produced by introducing into a host cell, recombinant
CC   vectors containing genes encoding the p35 and p40 subunits. This sequence
CC   represents the coding region for the bovine IL12 p35 subunit. Interleukin
CC   12 is used for the prevention and treatment of chronic infections and
CC   opportunistic infections
XX
SQ   Sequence 703 BP; 188 A; 194 C; 157 G; 164 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.48e-31        Length:         703
Score:                    40.00           Matches:        40
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              21.4%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x AAA70708 (1-703)

Qy          19 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 38
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         168 ACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 227

Qy          39 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         228 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 287

RESULT 68
AAD15213
ID   AAD15213 standard; DNA; 660 BP.
XX
AC   AAD15213;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-796.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
```

```
X
H   Key             Location/Qualifiers
T   CDS             1. .660
T                   /*tag=  a
T                   /product= "Modified p35 protein precursor"
T   sig_peptide     1. .66
T                   /*tag=  b
T   mat_peptide     67. .657
T                   /*tag=  c
T                   /product= "Mature modified p35 protein"
X
N   WO200140257-A2.
X
D   07-JUN-2001.
X
F   30-NOV-2000; 2000WO-US032664.
X
R   02-DEC-1999;   99US-0169035P.
R   28-NOV-2000; 2000US-00725324.
X
A   (MAXY-) MAXYGEN INC.
X
I   Leong SR,  Punnonen J;
X
R   WPI; 2001-502381/55.
R   P-PSDB; AAE08606.
X
T   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
T   and p35 polypeptides), useful for treating various diseases e.g. diabetic
T   retinopathy and cancer.
X
S   Claim 87; Page 139; 223pp; English.
X
C   The invention relates to nucleic acids encoding modified cytokine
C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
C   gamma induction activities. The polypeptides and polynucleotides of the
C   invention are useful for treating various diseases e.g. bacterial
C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
C   vaccinated host's cell-mediated immunity for protective response to a
C   pathogen. The present sequence is a modified human p35 protein encoding
C   DNA
X
Q   Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.51e-30       Length:        660
core:                  39.00          Matches:       39
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            20.9%          Indels:        0
B:                     5              Gaps:          0

S-10-821-670A-102 (1-187) x AAD15213 (1-660)

y         20 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 39
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

y         40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

ESULT 69
AD15216
D   AAD15216 standard; DNA; 660 BP.
X
C   AAD15216;
X
T   01-NOV-2001  (first entry)
X
E   Modified human cytokine p35 encoding DNA from clone R2-571.
XX
KW  Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW  diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW  p35; mutant; ds.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .660
FT                  /*tag=  a
FT                  /product= "Modified p35 protein precursor"
FT  sig_peptide     1. .66
FT                  /*tag=  b
FT  mat_peptide     67. .657
FT                  /*tag=  c
FT                  /product= "Mature modified p35 protein"
XX
PN  WO200140257-A2.
XX
PD  07-JUN-2001.
XX
PF  30-NOV-2000; 2000WO-US032664.
XX
PR  02-DEC-1999;   99US-0169035P.
PR  28-NOV-2000; 2000US-00725324.
XX
PA  (MAXY-) MAXYGEN INC.
XX
PI  Leong SR,  Punnonen J;
XX
DR  WPI; 2001-502381/55.
DR  P-PSDB; AAE08609.
XX
PT  Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT  and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT  retinopathy and cancer.
XX
PS  Claim 87; Page 140; 223pp; English.
XX
CC  The invention relates to nucleic acids encoding modified cytokine
CC  polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC  cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC  gamma induction activities. The polypeptides and polynucleotides of the
CC  invention are useful for treating various diseases e.g. bacterial
CC  infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC  polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC  vaccinated host's cell-mediated immunity for protective response to a
CC  pathogen. The present sequence is a modified human p35 protein encoding
CC  DNA
XX
SQ  Sequence 660 BP; 184 A; 172 C; 141 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.51e-30       Length:        660
Score:                 39.00          Matches:       39
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           20.9%          Indels:        0
DB:                    5              Gaps:          0

US-10-821-670A-102 (1-187) x AAD15216 (1-660)

Qy        20 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 39
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy        40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 270

RESULT 70
AAD15220
```

```
:D   AAD15220 standard; DNA; 660 BP.
:X
\C   AAD15220;
:X
)T   01-NOV-2001  (first entry)
:X
)E   Modified human cytokine p35 encoding DNA from clone R1-4-87.
:X
:W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
:W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
:W   p35; mutant; ds.
:X
)S   Homo sapiens.
)S   Synthetic.
:X
'H   Key             Location/Qualifiers
'T   CDS             1. .660
'T                   /*tag=  a
'T                   /product= "Modified p35 protein precursor"
'T   sig_peptide     1. .66
'T                   /*tag=  b
'T   mat_peptide     67. .657
'T                   /*tag=  c
'T                   /product= "Mature modified p35 protein"
:X
)N   WO200140257-A2.
:X
)D   07-JUN-2001.
:X
)F   30-NOV-2000; 2000WO-US032664.
:X
)R   02-DEC-1999;   99US-0169035P.
)R   28-NOV-2000; 2000US-00725324.
:X
)A   (MAXY-) MAXYGEN INC.
:X
)I   Leong SR,  Punnonen J;
:X
)R   WPI; 2001-502381/55.
)R   P-PSDB; AAE08613.
:X
'T   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
'T   and p35 polypeptides), useful for treating various diseases e.g. diabetic
'T   retinopathy and cancer.
:X
)S   Claim 87; Page 140-141; 223pp; English.
:X
:C   The invention relates to nucleic acids encoding modified cytokine
:C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
:C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
:C   gamma induction activities. The polypeptides and polynucleotides of the
:C   invention are useful for treating various diseases e.g. bacterial
:C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
:C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
:C   vaccinated host's cell-mediated immunity for protective response to a
:C   pathogen. The present sequence is a modified human p35 protein encoding
:C   DNA
:X
;Q   Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

\lignment Scores:
'red. No.:              1.51e-30      Length:        660
;core:                  39.00         Matches:       39
'ercent Similarity:     100.0%        Conservative:  0
}est Local Similarity:  100.0%        Mismatches:    0
}uery Match:            20.9%         Indels:        0
)B:                     5             Gaps:          0

)S-10-821-670A-102 (1-187) x AAD15220 (1-660)

)y         20 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 39
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         40 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

RESULT 71
AAD15217
ID   AAD15217 standard; DNA; 660 BP.
XX
AC   AAD15217;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-555.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08610.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 173 C; 136 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.78e-28      Length:        660
Score:                  37.00         Matches:       37
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            19.8%         Indels:        0
```

```
B:                    5             Gaps:          0

S-10-821-670A-102 (1-187) x AAD15217 (1-660)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

y        169 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 185
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        601 GCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

ESULT 72
AD15211
D   AAD15211 standard; DNA; 666 BP.
X
C   AAD15211;
X
T   01-NOV-2001  (first entry)
X
E   Modified human cytokine p35 encoding DNA from clone R2-42.
X
W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
W   p35; mutant; ds.
X
S   Homo sapiens.
S   Synthetic.
X
H   Key             Location/Qualifiers
T   CDS             1. .666
T                   /*tag=  a
T                   /product= "Modified p35 protein precursor"
T   sig_peptide     1. .75
T                   /*tag=  b
T   mat_peptide     76. .663
T                   /*tag=  c
T                   /product= "Mature modified p35 protein"
X
N   WO200140257-A2.
X
D   07-JUN-2001.
X
F   30-NOV-2000; 2000WO-US032664.
X
R   02-DEC-1999;   99US-0169035P.
R   28-NOV-2000; 2000US-00725324.
X
A   (MAXY-) MAXYGEN INC.
X
I   Leong SR,  Punnonen J;
X
R   WPI; 2001-502381/55.
R   P-PSDB; AAE08604.
X
T   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
T   and p35 polypeptides), useful for treating various diseases e.g. diabetic
T   retinopathy and cancer.
X
S   Claim 87; Page 139; 223pp; English.
X
C   The invention relates to nucleic acids encoding modified cytokine
C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
C   gamma induction activities. The polypeptides and polynucleotides of the
C   invention are useful for treating various diseases e.g. bacterial
C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
C   vaccinated host's cell-mediated immunity for protective response to a
C   pathogen. The present sequence is a modified human p35 protein encoding
C   DNA
X
Q   Sequence 666 BP; 186 A; 181 C; 141 G; 158 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.94e-22        Length:         666
Score:                  31.00           Matches:        31
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            16.6%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-102 (1-187) x AAD15211 (1-666)

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

Qy         81 SerArgLysThrSerPheMetThrThrLeuCys 91
              |||||||||||||||||||||||||||||||
Db        343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGC 375

RESULT 73
ADQ41825
ID   ADQ41825 standard; DNA; 201 BP.
XX
AC   ADQ41825;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3488.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 3488; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
```

```
:C   nucleic acid molecule; a method of detecting a variant polypeptide; and a
:C   method for identifying an agent useful in treating or preventing
:C   myocardial infarction. The novel detection method has cardiant activity.
:C   The nucleic acids of the invention may be used in gene therapy. The
:C   method is useful in identifying an individual who has an increased or
:C   decreased risk for developing myocardial infarction and for preparing a
:C   composition for treating or preventing myocardial infarction. This
:C   polynucleotide sequence represents a transcript-based context sequence
:C   which flanks an SNP found in a human myocardial infarction-associated
:C   gene of the invention. Note: This sequence was not shown in the
:C   specification. The sequence has come from an electronic sequence listing
:C   downloaded from the WIPO website.
:X
;Q   Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

\lignment Scores:
'red. No.:              1.08e-20      Length:         201
;core:                  29.00         Matches:        29
'ercent Similarity:     100.0%        Conservative:   0
}est Local Similarity:  100.0%        Mismatches:     0
)uery Match:            15.5%         Indels:         0
)B:                     13            Gaps:           0

)S-10-821-670A-102 (1-187) x ADQ41825 (1-201)

)y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

)y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
)b         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

{ESULT 74
\DQ41824
:D   ADQ41824 standard; DNA; 201 BP.
{X
\C   ADQ41824;
{X
)T   18-NOV-2004  (first entry)
{X
)E   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3487.
{X
{W   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
{W   cardiant; gene therapy; human; ds.
{X
)S   Homo sapiens.
{X
'N   WO2004058052-A2.
{X
'D   15-JUL-2004.
{X
'F   22-DEC-2003; 2003WO-US040978.
{X
'R   20-DEC-2002; 2002US-0434778P.
'R   10-MAR-2003; 2003US-0453135P.
'R   30-APR-2003; 2003US-0466412P.
'R   23-SEP-2003; 2003US-0504955P.
{X
'A   (APPL-) APPLERA CORP.
{X
'I   Cargill M,  Devlin JJ,  Iakoubova O;
{X
)R   WPI; 2004-533949/51.
{X
'T   Identifying an individual who has an altered risk for developing
'T   myocardial infarction by detecting a single nucleotide polymorphism in
'T   the individual's nucleic acids.
{X
'S   Claim 7; SEQ ID NO 3487; 145pp; English.
{X
:C   The invention relates to a novel method for identifying an individual who
:C   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a transcript-based context sequence
CC   which flanks an SNP found in a human myocardial infarction-associated
CC   gene of the invention. Note: This sequence was not shown in the
CC   specification. The sequence has come from an electronic sequence listing
CC   downloaded from the WIPO website.
XX
SQ   Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              1.08e-20      Length:         201
Score:                  29.00         Matches:        29
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            15.5%         Indels:         0
DB:                     13            Gaps:           0

US-10-821-670A-102 (1-187) x ADQ41824 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 75
ADQ41835
ID   ADQ41835 standard; DNA; 201 BP.
XX
AC   ADQ41835;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3498.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
```

```
A   (APPL-) APPLERA CORP.
X
I   Cargill M,  Devlin JJ,  Iakoubova O;
X
R   WPI; 2004-533949/51.
X
T   Identifying an individual who has an altered risk for developing
T   myocardial infarction by detecting a single nucleotide polymorphism in
T   the individual's nucleic acids.
X
S   Claim 7; SEQ ID NO 3498; 145pp; English.
X
C   The invention relates to a novel method for identifying an individual who
C   has an altered risk for developing myocardial infarction. The method
C   comprises detecting a single nucleotide polymorphism (SNP) in any one of
C   the nucleotide sequences given in the specification in the individual's
C   nucleic acids, where the presence of the SNP is correlated with an
C   altered risk for myocardial infarction in the individual. The invention
C   further comprises: an isolated nucleic acid molecule comprising at least
C   8 contiguous nucleotides where one of the nucleotides is an SNP given in
C   the specification or its complement and encoding any one of the amino
C   acid sequences given in the specification; an isolated polypeptide
C   comprising an amino acid sequence given in the specification; an antibody
C   that specifically binds to the polypeptide or its antigen-binding
C   fragment; an amplified polynucleotide containing an SNP given in the
C   specification and which is between about 16 and 1000 nucleotides in
C   length; a kit for detecting an SNP in a nucleic acid, comprising the
C   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
C   nucleic acid molecule; a method of detecting a variant polypeptide; and a
C   method for identifying an agent useful in treating or preventing
C   myocardial infarction. The novel detection method has cardiant activity.
C   The nucleic acids of the invention may be used in gene therapy. The
C   method is useful in identifying an individual who has an increased or
C   decreased risk for developing myocardial infarction and for preparing a
C   composition for treating or preventing myocardial infarction. This
C   polynucleotide sequence represents a transcript-based context sequence
C   which flanks an SNP found in a human myocardial infarction-associated
C   gene of the invention. Note: This sequence was not shown in the
C   specification. The sequence has come from an electronic sequence listing
C   downloaded from the WIPO website.
X
Q   Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

lignment Scores:
red. No.:               1.08e-20        Length:         201
core:                   29.00           Matches:        29
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             15.5%           Indels:         0
B:                      13              Gaps:           0

S-10-821-670A-102 (1-187) x ADQ41835 (1-201)

y         149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

y         169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
b          72 GCTTTCAGAATTCGGGCAGTGACTATT 98

ESULT 76
DQ41829
D   ADQ41829 standard; DNA; 201 BP.
X
C   ADQ41829;
X
T   18-NOV-2004  (first entry)
X
E   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3492.
X
W   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
W   cardiant; gene therapy; human; ds.
XX
OS  Homo sapiens.
XX
PN  WO2004058052-A2.
XX
PD  15-JUL-2004.
XX
PF  22-DEC-2003; 2003WO-US040978.
XX
PR  20-DEC-2002; 2002US-0434778P.
PR  10-MAR-2003; 2003US-0453135P.
PR  30-APR-2003; 2003US-0466412P.
PR  23-SEP-2003; 2003US-0504955P.
XX
PA  (APPL-) APPLERA CORP.
XX
PI  Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR  WPI; 2004-533949/51.
XX
PT  Identifying an individual who has an altered risk for developing
PT  myocardial infarction by detecting a single nucleotide polymorphism in
PT  the individual's nucleic acids.
XX
PS  Claim 7; SEQ ID NO 3492; 145pp; English.
XX
CC  The invention relates to a novel method for identifying an individual who
CC  has an altered risk for developing myocardial infarction. The method
CC  comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC  the nucleotide sequences given in the specification in the individual's
CC  nucleic acids, where the presence of the SNP is correlated with an
CC  altered risk for myocardial infarction in the individual. The invention
CC  further comprises: an isolated nucleic acid molecule comprising at least
CC  8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC  the specification or its complement and encoding any one of the amino
CC  acid sequences given in the specification; an isolated polypeptide
CC  comprising an amino acid sequence given in the specification; an antibody
CC  that specifically binds to the polypeptide or its antigen-binding
CC  fragment; an amplified polynucleotide containing an SNP given in the
CC  specification and which is between about 16 and 1000 nucleotides in
CC  length; a kit for detecting an SNP in a nucleic acid, comprising the
CC  polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC  nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC  method for identifying an agent useful in treating or preventing
CC  myocardial infarction. The novel detection method has cardiant activity.
CC  The nucleic acids of the invention may be used in gene therapy. The
CC  method is useful in identifying an individual who has an increased or
CC  decreased risk for developing myocardial infarction and for preparing a
CC  composition for treating or preventing myocardial infarction. This
CC  polynucleotide sequence represents a transcript-based context sequence
CC  which flanks an SNP found in a human myocardial infarction-associated
CC  gene of the invention. Note: This sequence was not shown in the
CC  specification. The sequence has come from an electronic sequence listing
CC  downloaded from the WIPO website.
XX
SQ  Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              1.08e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     13              Gaps:           0

US-10-821-670A-102 (1-187) x ADQ41829 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
```

```
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 77
ADQ41838
ID   ADQ41838 standard; DNA; 201 BP.
XX
AC   ADQ41838;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3501.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 3501; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a transcript-based context sequence
CC   which flanks an SNP found in a human myocardial infarction-associated
CC   gene of the invention. Note: This sequence was not shown in the
CC   specification. The sequence has come from an electronic sequence listing
CC   downloaded from the WIPO website.
XX
SQ   Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              1.08e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     13              Gaps:           0

US-10-821-670A-102 (1-187) x ADQ41838 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 78
ADQ41833
ID   ADQ41833 standard; DNA; 201 BP.
XX
AC   ADQ41833;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3496.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 3496; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
```

```
C   The nucleic acids of the invention may be used in gene therapy. The
C   method is useful in identifying an individual who has an increased or
C   decreased risk for developing myocardial infarction and for preparing a
C   composition for treating or preventing myocardial infarction. This
C   polynucleotide sequence represents a transcript-based context sequence
C   which flanks an SNP found in a human myocardial infarction-associated
C   gene of the invention. Note: This sequence was not shown in the
C   specification. The sequence has come from an electronic sequence listing
C   downloaded from the WIPO website.
X
Q   Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

lignment Scores:
red. No.:               1.08e-20        Length:         201
core:                   29.00           Matches:        29
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             15.5%           Indels:         0
B:                      13              Gaps:           0

S-10-821-670A-102 (1-187) x ADQ41833 (1-201)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||
b         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

ESULT 79
DF77258
D   ADF77258 standard; DNA; 630 BP.
X
C   ADF77258;
X
T   26-FEB-2004  (first entry)
X
E   Human IL-12 p35 subunit optimised DNA #5.
X
W   ds; human; interferon alpha expression plasmid; tumour; IL-12.
X
S   Synthetic.
S   Homo sapiens.
X
N   US2003181405-A1.
X
D   25-SEP-2003.
X
F   29-APR-2002; 2002US-00136837.
X
R   12-MAR-1999;   99US-00268135.
X
A   (NORD/) NORDSTROM J L.
A   (PERI/) PERICLE F.
A   (ROLL/) ROLLAND A.
A   (RALS/) RALSTON R O.
X
I   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
X
R   WPI; 2004-020834/02.
X
T   A mammalian interferon alpha expression plasmid is useful in gene therapy
T   to deliver interferon alpha to cells to modulate tumor activity in the
T   treatment of cancer.
X
S   Disclosure; SEQ ID NO 27; 65pp; English.
X
C   The invention relates to a mammalian interferon alpha expression plasmid,
C   comprising a promoter and a synthetic 5' intron transcriptionally linked
C   with an interferon alpha coding sequence and a 3' untranslated region.
C   The mammalian interferon alpha expression plasmid is useful for treating
C   tumour growth. The present sequence is used in the exemplification of the
CC  present invention.
XX
SQ  Sequence 630 BP; 118 A; 234 C; 141 G; 137 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.28e-20        Length:         630
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     12              Gaps:           0

US-10-821-670A-102 (1-187) x ADF77258 (1-630)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       511 TCCTCCTTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGTTGTGCATCTTGTTGCAC 570

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||
Db       571 GCCTTCCGCATCCGCGCCGTCACCATC 597

RESULT 80
ADG39431
ID  ADG39431 standard; DNA; 657 BP.
XX
AC  ADG39431;
XX
DT  26-FEB-2004  (first entry)
XX
DE  Human CLMF 35 kDa subunit DNA.
XX
KW  human; cytotoxic lymphocyte maturation factor; CLMF;
KW  activated T-cell stimulator; natural killer cell stimulator;
KW  immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  CDS             67. .657
FT                  /*tag= a
FT                  /partial
FT                  /product= "CLMF 35 kDa subunit"
FT                  /note= "No start or stop codon given"
XX
PN  US2003204059-A1.
XX
PD  30-OCT-2003.
XX
PF  08-OCT-2002; 2002US-00267565.
XX
PR  22-DEC-1989;   89US-00455708.
PR  09-MAY-1990;   90US-00520935.
PR  27-AUG-1990;   90US-00572284.
PR  24-MAR-1992;   92US-00857023.
PR  02-MAR-1994;   94US-00205011.
PR  02-JUN-1995;   95US-00459151.
PR  22-SEP-1999;   99US-00401839.
XX
PA  (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI  Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI  Chizzonite RA,  Pan YE;
XX
DR  WPI; 2004-010534/01.
DR  P-PSDB; ADG39428.
XX
PT  Novel protein comprising cytotoxic lymphocyte maturation factor in
PT  substantially pure form or protein which exhibits cytotoxic lymphocyte
PT  maturation factor activity, useful as antitumor and immunoenhancing
PT  agent.
XX
PS  Claim 20; Page 29; 74pp; English.
```

```
CX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
CX
SQ   Sequence 657 BP; 186 A; 166 C; 139 G; 166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.42e-20      Length:          657
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       12            Gaps:            0

US-10-821-670A-102 (1-187) x ADG39431 (1-657)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 81
AAQ97485
ID   AAQ97485 standard; cDNA; 660 BP.
XX
AC   AAQ97485;
XX
DT   25-MAR-2003  (revised)
DT   22-DEC-1995  (first entry)
XX
DE   Human interleukin-12 35 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Wolf SF,  Sykes M;
XX
DR   WPI; 1995-269273/35.
DR   P-PSDB; AAR79187.
XX
PT   Control of graft versus host disease using interleukin 12 - partic.
PT   admin. at the time of bone marrow transplant.
XX
PS   Disclosure; Page 23-24; 32pp; English.
XX
CC   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC   12 is a heterodimeric cytokine which was originally identified as a
CC   factor which induces gamma-interferon from T cells and natural killer
CC   cells as set forth in PCT/US91/06332, published April 2 1992, and
CC   incorporated by reference. EP 433827, published June 26 1991, disclosed
CC   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC   is defined as a heterodimeric glycoprotein comprised of two covalently
CC   linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC   subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.43e-20      Length:          660
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-102 (1-187) x AAQ97485 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 82
AAV07274
ID   AAV07274 standard; cDNA; 660 BP.
XX
AC   AAV07274;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Human Interleukin-12 p35 gene.
XX
KW   IL-12 subunit; expression construct; treatment; asthma;
KW   microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "IL-12 p35"
FT                   /transl_except= (pos:58. .60,aa:Ser)
XX
PN   WO9817689-A2.
XX
PD   30-APR-1998.
XX
PF   10-OCT-1997;   97WO-US018779.
XX
PR   18-OCT-1996;   96US-0028676P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Freimark B,  Deshpande D;
XX
DR   WPI; 1998-261428/23.
DR   P-PSDB; AAV07274.
XX
PT   Constructs for expression of interleukin-12 sub-units - are used for
PT   delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT   infections and certain cancers.
XX
```

```
S   Claim 1; Page 34-35; 80pp; English.
X
C   The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
C   appropriate expression construct engineered into a plasmid. The plasmids
C   can provide for efficient expression of IL-12 subunits. The products can
C   be used for the treatment of asthma, microbial and viral infections and
C   certain cancers
X
Q   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

lignment Scores:
red. No.:              3.43e-20       Length:        660
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-102 (1-187) x AAV07274 (1-660)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b       601 GCTTTCAGAATTCGGGCAGTGACTATT 627

ESULT 83
AV07218
D   AAV07218 standard; DNA; 660 BP.
X
C   AAV07218;
X
T   12-AUG-1998  (first entry)
X
E   DNA encoding human interleukin-12 35kDa subunit.
X
W   Interleukin-12; IL-12; graft-versus-host disease;
W   GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
X
S   Homo sapiens.
X
H   Key             Location/Qualifiers
T   CDS             1. .660
T                   /*tag=  a
T                   /product= "Interleukin-12_35kDa_subunit"
X
N   US5756085-A.
X
D   26-MAY-1998.
X
F   30-APR-1996;   96US-00640386.
X
R   21-JAN-1994;   94US-00186529.
X
A   (GEMY ) GENETICS INST INC.
A   (GEHO ) GEN HOSPITAL CORP.
X
I   Sykes M,  Wolf SF;
X
R   WPI; 1998-321459/28.
R   P-PSDB; AAW51222.
X
T   Therapy of graft-versus-host disease - by administration of interleukin-
T   12 to maintain and/or promote graft-versus-leukaemia effects.
X
S   Disclosure; Col 23-24; 20pp; English.
X
C   The invention relates to a method for the treatment or prevention of
C   graft-versus-host disease (GVHD) which comprises the administration of
C   interleukin-12 (IL-12) at the time of bone-marrow transplantation to
C   maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC  0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC  the bone marrow transplant. IL-12 is administered daily until there is an
CC  improvement in the condition. Administration is oral, cutaneous,
CC  subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC  intravenous. The present sequence encodes the human interleukin-12 35kDa
CC  subunit
XX
SQ  Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             3.43e-20       Length:        660
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-102 (1-187) x AAV07218 (1-660)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
Db      601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 84
AAZ40408
ID  AAZ40408 standard; DNA; 660 BP.
XX
AC  AAZ40408;
XX
DT  15-FEB-2000  (first entry)
XX
DE  Human interleukin 12 p35 subunit optimised coding sequence.
XX
KW  Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW  promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW  cancer; ss.
XX
OS  Homo sapiens.
XX
PN  WO9947678-A2.
XX
PD  23-SEP-1999.
XX
PF  12-MAR-1999;   99WO-US005394.
XX
PR  19-MAR-1998;   98US-0078654P.
XX
PA  (GENE-) GENEMEDICINE INC.
XX
PI  Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR  WPI; 1999-562116/47.
DR  P-PSDB; AAY42488.
XX
PT  New plasmids containing an interferon-alpha coding sequence, used for the
PT  treatment of a mammalian condition or disease, particularly cancer.
XX
PS  Claim 11; Page 38-39; 137pp; English.
XX
CC  This sequence represents an optimised coding region for the human
CC  interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC  comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC  an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC  untranslated region (UTR). The plasmids can be used for treating a
CC  mammalian condition or disease, particularly cancer
XX
SQ  Sequence 660 BP; 147 A; 237 C; 180 G; 96 T; 0 U; 0 Other;

Alignment Scores:
```

```
Pred. No.:              3.43e-20        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AAZ40408 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

RESULT 85
AAZ40407
ID   AAZ40407 standard; DNA; 660 BP.
XX
AC   AAZ40407;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p35 subunit wild type coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9947678-A2.
XX
PD   23-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005394.
XX
PR   19-MAR-1998;   98US-0078654P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR   WPI; 1999-562116/47.
DR   P-PSDB; AAY42488.
XX
PT   New plasmids containing an interferon-alpha coding sequence, used for the
PT   treatment of a mammalian condition or disease, particularly cancer.
XX
PS   Claim 11; Page 38-39; 137pp; English.
XX
CC   This sequence represents the wild type coding region for the human
CC   interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC   untranslated region (UTR). The plasmids can be used for treating a
CC   mammalian condition or disease, particularly cancer
XX
SQ   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.43e-20        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AAZ40407 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

RESULT 86
AAZ40409
ID   AAZ40409 standard; DNA; 660 BP.
XX
AC   AAZ40409;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p35 subunit semi-optimised coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9947678-A2.
XX
PD   23-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005394.
XX
PR   19-MAR-1998;   98US-0078654P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR   WPI; 1999-562116/47.
DR   P-PSDB; AAY42488.
XX
PT   New plasmids containing an interferon-alpha coding sequence, used for the
PT   treatment of a mammalian condition or disease, particularly cancer.
XX
PS   Claim 11; Page 38-39; 137pp; English.
XX
CC   This sequence represents a semi-optimised coding region for the human
CC   interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC   untranslated region (UTR). The plasmids can be used for treating a
CC   mammalian condition or disease, particularly cancer
XX
SQ   Sequence 660 BP; 147 A; 242 C; 170 G; 101 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.43e-20        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x AAZ40409 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGGGCCGTGACCATC 627

RESULT 87
AAD15221
ID   AAD15221 standard; DNA; 660 BP.
```

```
X
C   AAD15221;
X
T   01-NOV-2001  (first entry)
X
E   Human cytokine p35 DNA.
X
W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
W   p35; ds.
X
S   Homo sapiens.
X
H   Key             Location/Qualifiers
T   CDS             1. .660
T                   /*tag=  a
T                   /product= "p35 protein precursor"
T   sig_peptide     1. .66
T                   /*tag=  b
T   mat_peptide     67. .657
T                   /*tag=  c
T                   /product= "Mature p35 protein"
X
N   WO200140257-A2.
X
D   07-JUN-2001.
X
F   30-NOV-2000; 2000WO-US032664.
X
R   02-DEC-1999;   99US-0169035P.
R   28-NOV-2000; 2000US-00725324.
X
A   (MAXY-) MAXYGEN INC.
X
I   Leong SR,  Punnonen J;
X
R   WPI; 2001-502381/55.
R   P-PSDB; AAE08614.
X
T   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
T   and p35 polypeptides), useful for treating various diseases e.g. diabetic
T   retinopathy and cancer.
X
S   Claim 91; Page 142; 223pp; English.
X
C   The invention relates to nucleic acids encoding modified cytokine
C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
C   gamma induction activities. The polypeptides and polynucleotides of the
C   invention are useful for treating various diseases e.g. bacterial
C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
C   vaccinated host's cell-mediated immunity for protective response to a
C   pathogen. The present sequence is human p35 protein encoding DNA
X
Q   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

lignment Scores:
red. No.:              3.43e-20       Length:        660
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     5              Gaps:          0

S-10-821-670A-102 (1-187) x AAD15221 (1-660)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
```

```
Db      601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 88
AAL44226
ID   AAL44226 standard; DNA; 660 BP.
XX
AC   AAL44226;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Human interleukin 12A (IL-12A) coding sequence.
XX
KW   Human; gene; ds; interleukin 12A; IL-12A; drug screening; AIDS; malaria;
KW   tuberculosis; cancer; haplotyping; genotyping; transgenic animal.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Human interleukin 12A (IL-12A)"
FT   variation       replace(142, A)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200229115-A1.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-US031656.
XX
PR   06-OCT-2000; 2000US-0238693P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Armstrong B,  Cappola G,  Choi JY,  Gilson CR,  Kliem SE,  Koshy B;
PI   Parks KE;
XX
DR   WPI; 2002-315865/35.
DR   P-PSDB; AAO15506.
XX
PT   New interleukin 12A (IL-12A) gene polymorphic variants, for studying the
PT   expression and function of IL-12A and screening candidate drugs for
PT   treating AIDS and cancer.
XX
PS   Claim 28; Fig 2; 72pp; English.
XX
CC   The invention comprises the amino acid and coding sequence of the human
CC   interleukin 12A (IL-12A) protein. Specifically the invention relates to
CC   the identification of polymorphisms within the human (IL-12A) gene
CC   sequence. The polymorphisms identified in the human IL-12A gene sequence
CC   are useful in studying the expression and function of IL-12A, and in
CC   screening drugs for the treatment of disorders such as AIDS, malaria,
CC   tuberculosis and cancer. The IL-12A polymorphisms may be used to
CC   haplotype and genotype the IL-12A gene of an individual. The IL-12A DNA
CC   sequences of the invention can be used to create transgenic animals for
CC   studying expression of the IL-12A isogenes in vivo. The present DNA
CC   sequence represents the coding sequence of the human interleukin 12A (IL-
CC   12A) gene
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             3.43e-20       Length:        660
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    6              Gaps:          0

US-10-821-670A-102 (1-187) x AAL44226 (1-660)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

)y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
)b        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

{ESULT 89
\CC47589
:D   ACC47589 standard; DNA; 660 BP.
:X
\C   ACC47589;
:X
)T   12-JUN-2003  (first entry)
:X
)E   Human interleukin 12 (hIL-12) P35 subunit gene.
:X
:W   Human; interleukin 12; hIL-12; baculovirus vector;
:W   recombinant production; AcNPV-hIL12;
:W   Autographa california nuclear polyhedrosis virus; tumour; cancer;
:W   infection; bacterial; viral; cytostatic; P35 subunit; gene; ds.
:X
)S   Homo sapiens.
:X
)N   CN1357622-A.
:X
)D   10-JUL-2002.
:X
)F   02-NOV-2001; 2001CN-00133631.
:X
)R   02-NOV-2001; 2001CN-00133631.
:X
)A   (UYWU-) UNIV WUHAN.
:X
)I   Meng X,  Xu J,  Yu Z;
:X
)R   WPI; 2002-741792/81.
:X
)T   Human interleukin-12 recombinant insect virus strain and its preparation.
:X
)S   Claim 4; Fig 6; 17pp; Chinese.
:X
:C   The invention relates to a recombinant baculovirus comprising DNA
:C   encoding human interleukin 12 (hIL-12) and methods for its preparation.
:C   The recombinant baculovirus strain is designated Autographa california
:C   nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
:C   contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
:C   (ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
:C   respectively under the control of the viral polyhedrin and P10 promoters.
:C   The baculovirus can be used in the recombinant production of human IL-12
:C   which is suitable for treating tumours and bacterial, viral and other
:C   infections. The present sequence represents the human IL-12 P35 subunit
:C   gene used in construction of the baculovirus vector of the invention
:X
)Q   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

\lignment Scores:
)red. No.:               3.43e-20       Length:        660
)core:                   29.00          Matches:       29
)ercent Similarity:      100.0%         Conservative:  0
)est Local Similarity:   100.0%         Mismatches:    0
)uery Match:             15.5%          Indels:        0
)B:                      6              Gaps:          0

)S-10-821-670A-102 (1-187) x ACC47589 (1-660)

)y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

)y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
)b        601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

```
RESULT 90
ADF77245
ID   ADF77245 standard; DNA; 660 BP.
XX
AC   ADF77245;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p35 subunit optimised DNA #1.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; SEQ ID NO 7; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 660 BP; 147 A; 237 C; 180 G; 96 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:               3.43e-20       Length:        660
Score:                   29.00          Matches:       29
Percent Similarity:      100.0%         Conservative:  0
Best Local Similarity:   100.0%         Mismatches:    0
Query Match:             15.5%          Indels:        0
DB:                      12             Gaps:          0

US-10-821-670A-102 (1-187) x ADF77245 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

RESULT 91
ADF77257
ID   ADF77257 standard; DNA; 660 BP.
XX
AC   ADF77257;
XX
DT   26-FEB-2004  (first entry)
```

```
·X
 E   Human IL-12 p35 subunit optimised DNA #4.
 X
 W   ds; human; interferon alpha expression plasmid; tumour; IL-12.
·X
 S   Synthetic.
 S   Homo sapiens.
·X
 N   US2003181405-A1.
 X
 D   25-SEP-2003.
·X
 F   29-APR-2002; 2002US-00136837.
·X
 R   12-MAR-1999;   99US-00268135.
·X
 A   (NORD/) NORDSTROM J L.
·A   (PERI/) PERICLE F.
 A   (ROLL/) ROLLAND A.
·A   (RALS/) RALSTON R O.
·X
 I   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
·X
 R   WPI; 2004-020834/02.
·X
 T   A mammalian interferon alpha expression plasmid is useful in gene therapy
 T   to deliver interferon alpha to cells to modulate tumor activity in the
 T   treatment of cancer.
·X
 S   Disclosure; SEQ ID NO 26; 65pp; English.
 X
 C   The invention relates to a mammalian interferon alpha expression plasmid,
 C   comprising a promoter and a synthetic 5' intron transcriptionally linked
 C   with an interferon alpha coding sequence and a 3' untranslated region.
 C   The mammalian interferon alpha expression plasmid is useful for treating
 C   tumour growth. The present sequence is used in the exemplification of the
 C   present invention.
 X
 Q   Sequence 660 BP; 197 A; 93 C; 82 G; 288 T; 0 U; 0 Other;

lignment Scores:
red. No.:              3.43e-20       Length:        660
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     12             Gaps:          0

S-10-821-670A-102 (1-187) x ADF77257 (1-660)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 TCTTCTTTAGAAGAACCTGATTTTTATAAAACTAAAATTAAATTATGTATTTTATTACAT 600

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||
b        601 GCTTTTCGTATTCGTGCTGTTACTATT 627

ESULT 92
DF77246
D   ADF77246 standard; DNA; 660 BP.
X
C   ADF77246;
X
T   26-FEB-2004  (first entry)
X
E   Human IL-12 p35 subunit optimised DNA #2.
X
W   ds; human; interferon alpha expression plasmid; tumour; IL-12.
X
S   Synthetic.
S   Homo sapiens.
X
```

```
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; SEQ ID NO 8; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 660 BP; 147 A; 242 C; 170 G; 101 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.43e-20       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     12             Gaps:          0

US-10-821-670A-102 (1-187) x ADF77246 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGGGCCGTGACCATC 627

RESULT 93
ADF77244
ID   ADF77244 standard; DNA; 660 BP.
XX
AC   ADF77244;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p35 subunit DNA.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
```

```
)A   (PERI/) PERICLE F.
)A   (ROLL/) ROLLAND A.
)A   (RALS/) RALSTON R O.
(X
)I   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
(X
)R   WPI; 2004-020834/02.
(X
)T   A mammalian interferon alpha expression plasmid is useful in gene therapy
)T   to deliver interferon alpha to cells to modulate tumor activity in the
)T   treatment of cancer.
(X
)S   Disclosure; SEQ ID NO 6; 65pp; English.
(X
:C   The invention relates to a mammalian interferon alpha expression plasmid,
:C   comprising a promoter and a synthetic 5' intron transcriptionally linked
:C   with an interferon alpha coding sequence and a 3' untranslated region.
:C   The mammalian interferon alpha expression plasmid is useful for treating
:C   tumour growth. The present sequence is used in the exemplification of the
:C   present invention.
(X
;Q   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

\lignment Scores:
)red. No.:                3.43e-20        Length:         660
;core:                    29.00           Matches:        29
)ercent Similarity:       100.0%          Conservative:   0
;est Local Similarity:    100.0%          Mismatches:     0
)uery Match:              15.5%           Indels:         0
)B:                       12              Gaps:           0

)S-10-821-670A-102 (1-187) x ADF77244 (1-660)

)y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

)y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
)b        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

(ESULT 94
\AF26096
:D   AAF26096 standard; DNA; 683 BP.
(X
\C   AAF26096;
(X
)T   24-APR-2001  (first entry)
(X
)E   Human pG-hIL12p DNA.
(X
(W   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
(W   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
(W   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
(X
)S   Homo sapiens.
(X
)N   WO200104155-A2.
(X
)D   18-JAN-2001.
(X
)F   08-JUL-2000; 2000WO-DE002263.
(X
)R   08-JUL-1999;   99CH-00001259.
(X
)A   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
)A   (UYZU-) UNIV ZUERICH.
)A   (REGC ) UNIV CALIFORNIA.
(X
)I   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
(X
)R   WPI; 2001-147178/15.
(X
```

```
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 683 BP; 198 A; 171 C; 142 G; 172 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.55e-20        Length:         683
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       4               Gaps:           0

US-10-821-670A-102 (1-187) x AAF26096 (1-683)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATACGGGCAGTGACTATT 627

RESULT 95
ADP88401
ID   ADP88401 standard; cDNA; 702 BP.
XX
AC   ADP88401;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human interleukin-12 alpha chain coding sequence.
XX
KW   antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW   antibacterial; protozoacide; gene therapy; expression vector;
KW   interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO2004052929-A2.
XX
PD   24-JUN-2004.
XX
PF   08-DEC-2003; 2003WO-IB006404.
XX
PR   06-DEC-2002; 2002GB-00028465.
XX
```

```
A   (UYBE-) UNIV QUEENS BELFAST.
X
I   Vandenbroeck K,  Alloza I;
X
R   WPI; 2004-487887/46.
X
T   New expression vector comprising DNA encoding a subunit of a dimeric form
T   of interleukin under transcriptional control of an ecdysone-inducible
T   promoter, useful in preparing a composition for treating e.g.,
T   inflammatory disease.
X
S   Disclosure; Page 85-86; 87pp; English.
X
C   The present invention relates to an expression vector comprising DNA
C   encoding a subunit of a dimeric form of interleukin under transcriptional
C   control of an ecdysone-inducible promoter. The expression vector is
C   useful in preparing a composition for treating a disease having a
C   pathogenesis which includes endogenous production of cytokine IL-12, IL-
C   23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
C   induced inflammation, epithelial airway inflammation such as asthma,
C   allergic disease, or autoimmune disease such as multiple sclerosis or
C   inflammatory bowel disease. The present sequence is the coding sequence
C   of the human interleukin-12 alpha chain used in the exemplification of
C   the invention.
X
Q   Sequence 702 BP; 199 A; 184 C; 147 G; 172 T; 0 U; 0 Other;

lignment Scores:
red. No.:              3.64e-20      Length:        702
core:                  29.00         Matches:       29
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            15.5%         Indels:        0
B:                     12            Gaps:          0

S-10-821-670A-102 (1-187) x ADP88401 (1-702)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       556 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 615

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b       616 GCTTTCAGAATTCGGGCAGTGACTATT 642

ESULT 96
AQ67880
D   AAQ67880 standard; DNA; 721 BP.
X
C   AAQ67880;
X
T   25-MAR-2003  (revised)
T   23-MAR-1995  (first entry)
X
E   EPV 42 kD promoter/Human IL-12 p35 subunit expression cassette.
X
W   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
W   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
W   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
W   polymerase chain reaction; poxvirus; pSD542; immunological response;
W   pathogen; human; interferon; IFN; ss.
X
S   Synthetic.
X
H   Key             Location/Qualifiers
T   promoter        1. .61
T                   /*tag=  a
T                   /note= "Vaccinia E3L promoter"
T   CDS             32. .1018
T                   /*tag=  b
T                   /product= "Human IL-12 p35"
X
N   WO9416716-A1.
XX
PD  04-AUG-1994.
XX
PF  21-JAN-1994;   94WO-US000888.
XX
PR  21-JAN-1993;   93US-00007115.
PR  19-JAN-1994;   94US-00184009.
XX
PA  (VIRO-) VIROGENETICS CORP.
XX
PI  Paoletti E,  Tartaglia J,  Cox WI;
XX
DR  WPI; 1994-263767/32.
XX
PT  Attenuated recombinant virus used for cancer therapy - comprises DNA
PT  encoding cytokine and/or tumour associated antigen.
XX
PS  Example 27; Fig 34; 232pp; English.
XX
CC  The sequences given in AAQ67879-80 are expression cassettes which contain
CC  the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC  control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC  promoter, respectively. These sequences were used in the construction of
CC  an ALVAC-based recombinant virus containing the genes for the two
CC  subunits of human IL-12. The p40 subunit was amplified using primers
CC  JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC  42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC  using primers JP186 and JP201 and placed under the control of the
CC  vaccinia E3L promoter using primers JP218 and JP220. The expression
CC  cassette was isolated and ligated with pBSSK+ generating plasmid
CC  PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC  assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC  cassettes are orientated head-to-head relative to each other. The
CC  combination casette containing the poxvirus promoted genes for both IL-12
CC  subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC  plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC  and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC  contains both the human IL-12 genes in the C6 locus. The resulting virus
CC  may be used in a composition for inducing an antigenic or immunological
CC  response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC  to correct PN field.)
XX
SQ  Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             3.74e-20      Length:        721
Score:                 29.00         Matches:       29
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           15.5%         Indels:        0
DB:                    2             Gaps:          0

US-10-821-670A-102 (1-187) x AAQ67880 (1-721)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
Db      662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 97
AAZ08515
ID  AAZ08515 standard; DNA; 721 BP.
XX
AC  AAZ08515;
XX
DT  19-OCT-1999  (first entry)
XX
DE  Vaccinia E3L/human IL-12 P35 expression cassette.
XX
KW  Attenuated recombinant virus; cytokine; tumour associated antigen;
```

KW NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Vaccinia virus.
XX
PN US5942235-A.
XX
PD 24-AUG-1999.
XX
PF 02-JUN-1995; 95US-00458356.
XX
PR 24-DEC-1981; 81US-00334456.
PR 08-DEC-1982; 82US-00446824.
PR 19-JUN-1984; 84US-00622135.
PR 27-AUG-1987; 87US-00090209.
PR 28-AUG-1987; 87US-00090711.
PR 20-OCT-1987; 87US-00110335.
PR 25-APR-1988; 88US-00186054.
PR 23-AUG-1988; 88US-00234390.
PR 14-JUN-1990; 90US-00537882.
PR 14-JUN-1990; 90US-00537890.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 04-MAY-1992; 92US-00881995.
PR 22-JUL-1992; 92US-00918278.
PR 20-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 14-APR-1994; 94US-00228926.
PR 13-SEP-1994; 94US-00306259.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Paoletti E;
XX
DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 27; Fig 34; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC Vaccinia E3L/human IL-12 P35 expression cassette used in the
CC exemplification of the present invention
XX
SQ Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.74e-20 Length: 721
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 15.5% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-102 (1-187) x AAZ08515 (1-721)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688
```

RESULT 98
ADR21891
ID ADR21891 standard; DNA; 721 BP.
XX
AC ADR21891;
XX
DT 04-NOV-2004 (first entry)
XX
DE Vaccinia E3L/human IL-12 expression cassette.
XX
KW Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW cancer therapy; ds; human; IL-12; interleukin-12; E3L;
KW expression cassette.
XX
OS Vaccinia virus.
OS Homo sapiens.
OS Synthetic.
XX
PN US6780407-B1.
XX
PD 24-AUG-2004.
XX
PF 15-SEP-2000; 2000US-00663667.
XX
PR 08-MAR-1989; 89US-00320471.
PR 14-FEB-1990; 90US-00478179.
PR 07-JAN-1991; 91US-00638080.
PR 07-MAR-1991; 91US-00666056.
PR 11-JUN-1991; 91US-00713967.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 21-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 30-AUG-1995; 95US-00521016.
XX
PA (AVET) AVENTIS PASTEUR.
XX
PI Paoletti E, Tartaglia J, Cox WI;
XX
DR WPI; 2004-601998/58.
XX
PT New recombinant poxvirus which is an attenuated avipox Virus that
PT expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
PS Example 27; SEQ ID NO 199; 181pp; English.
XX
CC The invention describes a recombinant poxvirus containing exogenous DNA
CC in a nonessential region of the poxvirus, where the poxvirus is an
CC attenuated avipox Virus that expresses an exogenous DNA encoding
CC carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC described are: a composition comprising a poxvirus above in admixture
CC with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC vivo comprising administering to a mammal the composition above.
CC Disclosed are: making recombinant poxvirus defined above; recombinant
CC poxvirus vaccine having an increased level of safety compared to known
CC recombinant poxvirus vaccines; and a modified vector for expressing a

```
C   gene product in a host. The recombinant poxvirus is useful for providing
C   a recombinant poxvirus vaccine having an increased level of safety
C   compared to known recombinant poxvirus vaccines. The recombinant poxvirus
C   is useful for cancer therapy. This sequence represents a human IL-12
C   expression cassette used in the creation of NYVAC rescue virus and
C   canarypox virus vector ALVAC comprising the human IL-12 gene.
X
Q   Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

lignment Scores:
red. No.:              3.74e-20       Length:        721
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     13             Gaps:          0

S-10-821-670A-102 (1-187) x ADR21891 (1-721)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b       662 GCTTTCAGAATTCGGGCAGTGACTATT 688

ESULT 99
DK98708
D   ADK98708 standard; DNA; 761 BP.
X
C   ADK98708;
X
T   06-MAY-2004  (first entry)
X
E   Human interleukin-12 (IL-12) P35 subunit DNA seqid 3.
X
W   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
X
S   Homo sapiens.
X
N   CN1408727-A.
X
D   09-APR-2003.
X
F   29-SEP-2001; 2001CN-00126923.
X
R   29-SEP-2001; 2001CN-00126923.
X
A   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
X
I   Wan G,  Li C;
X
R   WPI; 2003-664076/63.
X
T   Method for efficiently expressing recombinant human interleukin 12 in
T   eukaryotic cell.
X
S   Claim 6; SEQ ID NO 3; 14pp; Chinese.
X
C   The invention describes the process of producing human recombinant
C   interleukin-12 (IL-12) includes: providing a nucleotide sequence
C   corresponding to the P35 subunit with the first signal peptide and a
C   nucleotide sequence corresponding to the P40 subunit; inserting the
C   nucleotide sequences into an expression vector; converting the eukaryotic
C   cell with the expression vector; and culturing the transfected eukaryotic
C   cell in condition suitable for recombinant human IL-12 expression. The
C   process balances the expression amount of both P35 and P40 subunits and
C   thus raises the expression amount of IL-12 with bioactivity via raising
C   the expression strength of P35 subunit. This sequence represents the
C   human interleukin-12 (IL-12) P35 subunit polynucleotide.
X
Q   Sequence 761 BP; 205 A; 204 C; 164 G; 187 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:             3.94e-20       Length:        761
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    10             Gaps:          0

US-10-821-670A-102 (1-187) x ADK98708 (1-761)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      642 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 701

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
Db      702 GCTTTCAGAATTCGGGCAGTGACTATT 728

RESULT 100
ADK98706
ID   ADK98706 standard; DNA; 761 BP.
XX
AC   ADK98706;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin-12 (IL-12) P35 subunit DNA seqid 1.
XX
KW   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS   Homo sapiens.
XX
PN   CN1408727-A.
XX
PD   09-APR-2003.
XX
PF   29-SEP-2001; 2001CN-00126923.
XX
PR   29-SEP-2001; 2001CN-00126923.
XX
PA   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI   Wan G,  Li C;
XX
DR   WPI; 2003-664076/63.
XX
PT   Method for efficiently expressing recombinant human interleukin 12 in
PT   eukaryotic cell.
XX
PS   Claim 4; SEQ ID NO 1; 14pp; Chinese.
XX
CC   The invention describes the process of producing human recombinant
CC   interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC   corresponding to the P35 subunit with the first signal peptide and a
CC   nucleotide sequence corresponding to the P40 subunit; inserting the
CC   nucleotide sequences into an expression vector; converting the eukaryotic
CC   cell with the expression vector; and culturing the transfected eukaryotic
CC   cell in condition suitable for recombinant human IL-12 expression. The
CC   process balances the expression amount of both P35 and P40 subunits and
CC   thus raises the expression amount of IL-12 with bioactivity via raising
CC   the expression strength of P35 subunit. This sequence represents the
CC   human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ   Sequence 761 BP; 199 A; 209 C; 167 G; 185 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:             3.94e-20       Length:        761
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    10             Gaps:          0
```

US-10-821-670A-102 (1-187) x ADK98706 (1-761)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 701

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        702 GCTTTCAGAATTCGGGCAGTGACTATT 728
```

Search completed: June 10, 2006, 02:29:06
Job time : 470.088 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

)M protein - nucleic search, using frame_plus_p2n model

Run on: June 11, 2006, 22:10:55 ; Search time 903.079 Seconds
(without alignments)
3816.589 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 187
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size: 1

Total number of hits satisfying chosen parameters: 37767822

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110503_27781/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap
-SUFFIX=oligo.p2n.200scores.rnpbm -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10821670_@CGN_1_1_4932_@runat_07062006_110503_27781 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	187	100.0	561	3	US-09-917-265-101	Sequence 101, App
c	2	187	100.0	561	3	US-09-917-265-103	Sequence 103, App
	3	187	100.0	561	9	US-10-821-670-101	Sequence 101, App
c	4	187	100.0	561	9	US-10-821-670-103	Sequence 103, App
	5	187	100.0	591	3	US-09-917-265-35	Sequence 35, Appl
c	6	187	100.0	591	3	US-09-917-265-37	Sequence 37, Appl
	7	187	100.0	591	9	US-10-821-670-35	Sequence 35, Appl
c	8	187	100.0	591	9	US-10-821-670-37	Sequence 37, Appl
	9	187	100.0	666	3	US-09-917-265-32	Sequence 32, Appl
c	10	187	100.0	666	3	US-09-917-265-34	Sequence 34, Appl
	11	187	100.0	666	9	US-10-821-670-32	Sequence 32, Appl
c	12	187	100.0	666	9	US-10-821-670-34	Sequence 34, Appl
	13	187	100.0	1533	3	US-09-917-265-43	Sequence 43, Appl
c	14	187	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
	15	187	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
c	16	187	100.0	1533	9	US-10-821-670-45	Sequence 45, Appl
	17	187	100.0	1599	3	US-09-917-265-38	Sequence 38, Appl
c	18	187	100.0	1599	3	US-09-917-265-40	Sequence 40, Appl
	19	187	100.0	1599	9	US-10-821-670-38	Sequence 38, Appl
c	20	187	100.0	1599	9	US-10-821-670-40	Sequence 40, Appl
	21	185	98.9	591	6	US-10-079-616-9	Sequence 9, Appli
	22	185	98.9	689	6	US-10-079-616-26	Sequence 26, Appl
	23	185	98.9	1441	6	US-10-079-616-8	Sequence 8, Appli
	24	54	28.9	669	7	US-10-041-672C-2	Sequence 2, Appli
	25	52	27.8	591	3	US-09-917-265-49	Sequence 49, Appl
c	26	52	27.8	591	3	US-09-917-265-51	Sequence 51, Appl
	27	52	27.8	591	9	US-10-821-670-49	Sequence 49, Appl
c	28	52	27.8	591	9	US-10-821-670-51	Sequence 51, Appl
	29	52	27.8	666	3	US-09-917-265-46	Sequence 46, Appl
c	30	52	27.8	666	3	US-09-917-265-48	Sequence 48, Appl
	31	52	27.8	666	9	US-10-821-670-46	Sequence 46, Appl
c	32	52	27.8	666	9	US-10-821-670-48	Sequence 48, Appl
	33	52	27.8	1455	3	US-09-917-265-104	Sequence 104, App
c	34	52	27.8	1455	3	US-09-917-265-106	Sequence 106, App
	35	52	27.8	1455	9	US-10-821-670-104	Sequence 104, App
c	36	52	27.8	1455	9	US-10-821-670-106	Sequence 106, App
	37	52	27.8	1533	3	US-09-917-265-66	Sequence 66, Appl
c	38	52	27.8	1533	3	US-09-917-265-68	Sequence 68, Appl
	39	52	27.8	1533	9	US-10-821-670-66	Sequence 66, Appl
c	40	52	27.8	1533	9	US-10-821-670-68	Sequence 68, Appl
	41	52	27.8	1599	3	US-09-917-265-61	Sequence 61, Appl
c	42	52	27.8	1599	3	US-09-917-265-63	Sequence 63, Appl
	43	52	27.8	1599	9	US-10-821-670-61	Sequence 61, Appl
c	44	52	27.8	1599	9	US-10-821-670-63	Sequence 63, Appl
	45	29	15.5	201	8	US-10-741-601-946	Sequence 946, App
	46	29	15.5	201	8	US-10-741-601-947	Sequence 947, App
	47	29	15.5	201	8	US-10-741-601-951	Sequence 951, App
	48	29	15.5	201	8	US-10-741-601-955	Sequence 955, App
	49	29	15.5	201	8	US-10-741-601-957	Sequence 957, App
	50	29	15.5	201	8	US-10-741-601-960	Sequence 960, App
	51	29	15.5	201	8	US-10-741-601-7417	Sequence 7417, Ap
	52	29	15.5	201	8	US-10-741-601-7418	Sequence 7418, Ap
	53	29	15.5	201	8	US-10-741-601-7431	Sequence 7431, Ap
c	54	29	15.5	201	8	US-10-741-601-11370	Sequence 11370, A
c	55	29	15.5	201	8	US-10-741-601-11372	Sequence 11372, A
c	56	29	15.5	201	8	US-10-741-601-11417	Sequence 11417, A
	57	29	15.5	201	9	US-10-741-600-3487	Sequence 3487, Ap
	58	29	15.5	201	9	US-10-741-600-3488	Sequence 3488, Ap
	59	29	15.5	201	9	US-10-741-600-3492	Sequence 3492, Ap
	60	29	15.5	201	9	US-10-741-600-3496	Sequence 3496, Ap
	61	29	15.5	201	9	US-10-741-600-3498	Sequence 3498, Ap
	62	29	15.5	201	9	US-10-741-600-3501	Sequence 3501, Ap
	63	29	15.5	201	9	US-10-741-600-20963	Sequence 20963, A
	64	29	15.5	201	9	US-10-741-600-20964	Sequence 20964, A
	65	29	15.5	201	9	US-10-741-600-20992	Sequence 20992, A
c	66	29	15.5	201	9	US-10-741-600-28831	Sequence 28831, A
c	67	29	15.5	201	9	US-10-741-600-28833	Sequence 28833, A
c	68	29	15.5	201	9	US-10-741-600-28877	Sequence 28877, A
	69	29	15.5	201	10	US-10-995-561-1976	Sequence 1976, Ap
	70	29	15.5	201	10	US-10-995-561-1977	Sequence 1977, Ap
	71	29	15.5	201	10	US-10-995-561-1981	Sequence 1981, Ap
	72	29	15.5	201	10	US-10-995-561-1986	Sequence 1986, Ap
	73	29	15.5	201	10	US-10-995-561-1988	Sequence 1988, Ap
	74	29	15.5	201	10	US-10-995-561-1991	Sequence 1991, Ap

	75	29	15.5	201	10	US-10-995-561-18302 Sequence 18302, A
	76	29	15.5	201	10	US-10-995-561-18303 Sequence 18303, A
	77	29	15.5	201	10	US-10-995-561-18335 Sequence 18335, A
c	78	29	15.5	201	10	US-10-995-561-26362 Sequence 26362, A
c	79	29	15.5	201	10	US-10-995-561-26545 Sequence 26545, A
c	80	29	15.5	201	10	US-10-995-561-26548 Sequence 26548, A
c	81	29	15.5	201	10	US-10-995-561-73346 Sequence 73346, A
c	82	29	15.5	201	10	US-10-995-561-73349 Sequence 73349, A
c	83	29	15.5	201	10	US-10-995-561-73383 Sequence 73383, A
	84	29	15.5	660	3	US-09-754-014-6 Sequence 6, Appli
	85	29	15.5	660	3	US-09-754-014-7 Sequence 7, Appli
	86	29	15.5	660	3	US-09-754-014-8 Sequence 8, Appli
	87	29	15.5	660	3	US-09-836-866-4 Sequence 4, Appli
	88	29	15.5	721	7	US-10-267-384-199 Sequence 199, App
	89	29	15.5	762	3	US-09-826-025-21 Sequence 21, Appl
	90	29	15.5	762	9	US-10-785-577-21 Sequence 21, Appl
	91	29	15.5	762	9	US-10-688-845-57 Sequence 57, Appl
	92	29	15.5	811	7	US-10-373-456-19 Sequence 19, Appl
	93	29	15.5	856	7	US-10-349-507-4 Sequence 4, Appli
	94	29	15.5	856	7	US-10-267-565-4 Sequence 4, Appli
	95	29	15.5	868	7	US-10-373-456-17 Sequence 17, Appl
	96	29	15.5	1026	6	US-10-172-399-5 Sequence 5, Appli
	97	29	15.5	1026	8	US-10-641-643-1041 Sequence 1041, Ap
	98	29	15.5	1287	8	US-10-603-064-6 Sequence 6, Appli
	99	29	15.5	1316	9	US-10-476-960-3 Sequence 3, Appli
	100	29	15.5	1316	15	US-11-089-191-3 Sequence 3, Appli
	101	29	15.5	1395	3	US-09-924-703-5 Sequence 5, Appli
	102	29	15.5	1395	8	US-10-358-395-5 Sequence 5, Appli
	103	29	15.5	1444	7	US-10-429-802-43 Sequence 43, Appl
	104	29	15.5	1444	7	US-10-430-503-34 Sequence 34, Appl
	105	29	15.5	1494	8	US-10-322-696-131 Sequence 131, App
	106	29	15.5	1526	8	US-10-322-696-185 Sequence 185, App
	107	29	15.5	1532	8	US-10-741-601-29 Sequence 29, Appl
	108	29	15.5	1532	9	US-10-741-600-51 Sequence 51, Appl
	109	29	15.5	1532	10	US-10-995-561-38 Sequence 38, Appl
	110	29	15.5	1607	8	US-10-741-601-28 Sequence 28, Appl
	111	29	15.5	1607	9	US-10-741-600-50 Sequence 50, Appl
	112	29	15.5	1607	10	US-10-995-561-37 Sequence 37, Appl
	113	29	15.5	1645	6	US-10-228-811-2 Sequence 2, Appli
	114	29	15.5	1828	7	US-10-373-456-2 Sequence 2, Appli
	115	29	15.5	2390	10	US-10-528-644A-53 Sequence 53, Appl
	116	29	15.5	2466	7	US-10-373-456-1 Sequence 1, Appli
	117	29	15.5	5686	7	US-10-136-837-1 Sequence 1, Appli
	118	29	15.5	8578	3	US-09-828-825-1 Sequence 1, Appli
	119	29	15.5	8578	3	US-09-828-825-3 Sequence 3, Appli
	120	29	15.5	8608	3	US-09-828-825-7 Sequence 7, Appli
	121	29	15.5	8623	3	US-09-828-825-5 Sequence 5, Appli
	122	29	15.5	8629	3	US-09-828-825-15 Sequence 15, Appl
	123	29	15.5	8638	3	US-09-828-825-9 Sequence 9, Appli
	124	29	15.5	8644	3	US-09-828-825-13 Sequence 13, Appl
	125	29	15.5	8659	3	US-09-828-825-11 Sequence 11, Appl
	126	29	15.5	11453	10	US-10-511-237-3 Sequence 3, Appli
	127	29	15.5	11569	10	US-10-511-237-1 Sequence 1, Appli
	128	29	15.5	19277	8	US-10-741-601-5620 Sequence 5620, Ap
	129	29	15.5	19277	9	US-10-741-600-17576 Sequence 17576, A
	130	29	15.5	19277	10	US-10-995-561-13214 Sequence 13214, A
	131	29	15.5	27277	8	US-10-322-696-130 Sequence 130, App
c	132	29	15.5	29618	8	US-10-741-601-5750 Sequence 5750, Ap
c	133	29	15.5	29618	9	US-10-741-600-17908 Sequence 17908, A
c	134	29	15.5	29618	10	US-10-995-561-13444 Sequence 13444, A
c	135	29	15.5	61916	8	US-10-741-601-5631 Sequence 5631, Ap
c	136	29	15.5	61916	9	US-10-741-600-17621 Sequence 17621, A
c	137	29	15.5	305312	10	US-10-995-561-13236 Sequence 13236, A
	138	26	13.9	79	6	US-10-079-616-24 Sequence 24, Appl
	139	23	12.3	71	7	US-10-041-672C-8 Sequence 8, Appli
	140	20	10.7	201	8	US-10-741-601-943 Sequence 943, App
	141	20	10.7	201	8	US-10-741-601-952 Sequence 952, App
	142	20	10.7	201	8	US-10-741-601-7415 Sequence 7415, Ap
c	143	20	10.7	201	8	US-10-741-601-11410 Sequence 11410, A
	144	20	10.7	201	9	US-10-741-600-3484 Sequence 3484, Ap
	145	20	10.7	201	9	US-10-741-600-3493 Sequence 3493, Ap
	146	20	10.7	201	9	US-10-741-600-20983 Sequence 20983, A
c	147	20	10.7	201	9	US-10-741-600-28870 Sequence 28870, A
	148	20	10.7	201	10	US-10-995-561-1973 Sequence 1973, Ap
	149	20	10.7	201	10	US-10-995-561-1983 Sequence 1983, Ap
	150	20	10.7	201	10	US-10-995-561-18326 Sequence 18326, A
c	151	20	10.7	201	10	US-10-995-561-26586 Sequence 26586, A
c	152	20	10.7	201	10	US-10-995-561-73379 Sequence 73379, A
c	153	18	9.6	76	7	US-10-041-672C-6 Sequence 6, Appli
c	154	18	9.6	76	7	US-10-041-672C-9 Sequence 9, Appli
	155	13	7.0	60	3	US-09-908-975-12410 Sequence 12410, A
	156	13	7.0	201	10	US-10-995-561-1982 Sequence 1982, Ap
	157	13	7.0	201	10	US-10-995-561-18376 Sequence 18376, A
c	158	13	7.0	201	10	US-10-995-561-26316 Sequence 26316, A
c	159	13	7.0	201	10	US-10-995-561-73335 Sequence 73335, A
c	160	12	6.4	36	6	US-10-079-616-25 Sequence 25, Appl
	161	10	5.3	39	3	US-09-917-265-91 Sequence 91, Appl
	162	10	5.3	39	9	US-10-821-670-91 Sequence 91, Appl
	163	10	5.3	582	8	US-10-603-064-1 Sequence 1, Appli
	164	10	5.3	600	16	US-11-136-527-4750 Sequence 4750, Ap
	165	10	5.3	793	16	US-11-136-527-654 Sequence 654, App
	166	10	5.3	1231	8	US-10-322-696-128 Sequence 128, App
	167	10	5.3	1265	6	US-10-172-399-1 Sequence 1, Appli
	168	10	5.3	1278	8	US-10-603-064-5 Sequence 5, Appli
	169	10	5.3	1569	8	US-10-603-064-12 Sequence 12, Appl
	170	10	5.3	2013	8	US-10-603-064-11 Sequence 11, Appl
	171	10	5.3	2709	8	US-10-603-064-13 Sequence 13, Appl
	172	10	5.3	5966	7	US-10-136-837-3 Sequence 3, Appli
	173	10	5.3	11458	10	US-10-511-237-2 Sequence 2, Appli
	174	10	5.3	27125	8	US-10-322-696-127 Sequence 127, App
c	175	9	4.8	51	3	US-09-917-265-96 Sequence 96, Appl
c	176	9	4.8	51	9	US-10-821-670-96 Sequence 96, Appl
	177	9	4.8	201	8	US-10-741-601-7429 Sequence 7429, Ap
c	178	9	4.8	201	8	US-10-741-601-11308 Sequence 11308, A
	179	9	4.8	201	9	US-10-741-600-20990 Sequence 20990, A
c	180	9	4.8	201	9	US-10-741-600-28770 Sequence 28770, A
	181	9	4.8	201	10	US-10-995-561-18336 Sequence 18336, A
c	182	9	4.8	201	10	US-10-995-561-26272 Sequence 26272, A
c	183	9	4.8	201	10	US-10-995-561-73297 Sequence 73297, A
	184	9	4.8	282	3	US-09-864-408A-1829 Sequence 1829, Ap
	185	9	4.8	374849	6	US-10-087-192-1627 Sequence 1627, Ap
	186	8	4.3	25	10	US-10-809-189-121547 Sequence 121547,
	187	8	4.3	25	15	US-11-121-849-129988 Sequence 129988,
	188	8	4.3	25	16	US-11-136-527-32389 Sequence 32389, A
	189	8	4.3	25	16	US-11-136-527-32398 Sequence 32398, A
	190	8	4.3	25	16	US-11-136-527-32410 Sequence 32410, A
	191	8	4.3	25	16	US-11-136-527-224687 Sequence 224687,
c	192	8	4.3	27	3	US-09-917-265-90 Sequence 90, Appl
c	193	8	4.3	27	9	US-10-821-670-90 Sequence 90, Appl
c	194	8	4.3	41	3	US-09-917-265-92 Sequence 92, Appl
c	195	8	4.3	41	9	US-10-821-670-92 Sequence 92, Appl
	196	8	4.3	200	16	US-11-098-686-3366 Sequence 3366, Ap
	197	8	4.3	318	9	US-10-425-115-68596 Sequence 68596, A
	198	8	4.3	372	9	US-10-425-115-145066 Sequence 145066,
	199	8	4.3	379	10	US-10-779-543-11625 Sequence 11625, A
c	200	8	4.3	386	8	US-10-424-599-127878 Sequence 127878,

ALIGNMENTS

```
RESULT 1
US-09-917-265-101
; Sequence 101, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
```

LENGTH: 561
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(561)
OTHER INFORMATION:
US-09-917-265-101

Alignment Scores:

Pred. No.:	7.26e-186	Length:	561
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265-101 (1-561)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
```

RESULT 2
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-103

Alignment Scores:

Pred. No.:	7.26e-186	Length:	561
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265-103 (1-561)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 3
US-10-821-670-101
; Sequence 101, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2

```
  SEQ ID NO 101
    LENGTH: 561
    TYPE: DNA
    ORGANISM: Felis catus
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)..(561)
S-10-821-670-101

lignment Scores:
red. No.:              7.26e-186      Length:        561
core:                  187.00         Matches:       187
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-821-670-101 (1-561)

y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

y        181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
b        541 ATGAGCTATCTGAATGCTTCC 561

ESULT 4
S-10-821-670-103/c
 Sequence 103, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-103

Alignment Scores:
Pred. No.:              7.26e-186      Length:        561
Score:                  187.00         Matches:       187
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-821-670-103 (1-561)

Qy         1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy        21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy       101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy       121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy       141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy       161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy       181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
Db        21 ATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
```

```
SEQ ID NO 35
   LENGTH: 591
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(591)
   OTHER INFORMATION:
US-09-917-265-35

Alignment Scores:
Pred. No.:              7.62e-186      Length:         591
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-35 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591

RESULT 6
US-09-917-265-37/c
; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-37

Alignment Scores:
Pred. No.:              7.62e-186      Length:         591
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-37 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 7
US-10-821-670-35
; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
```

```
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 35
   LENGTH: 591
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(591)
S-10-821-670-35

lignment Scores:
red. No.:              7.62e-186      Length:        591
core:                  187.00         Matches:       187
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-821-670-35 (1-591)

y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

y          21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

y          41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

y          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

y          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

y        181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
b        571 ATGAGCTATCTGAATGCTTCC 591

ESULT 8
S-10-821-670-37/c
 Sequence 37, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-37

Alignment Scores:
Pred. No.:             7.62e-186      Length:        591
Score:                 187.00         Matches:       187
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           100.0%         Indels:        0
DB:                    9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-821-670-37 (1-591)

Qy         1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy        21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy       101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy       121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy       141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy       161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy       181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
Db        21 ATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
```

```
  SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
   LENGTH: 666
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(666)
   OTHER INFORMATION:
JS-09-917-265-32

Alignment Scores:
Pred. No.:              8.51e-186      Length:         666
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-32 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666

RESULT 10
JS-09-917-265-34/c
Sequence 34, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

Alignment Scores:
Pred. No.:              8.51e-186      Length:         666
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-34 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 11
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
```

```
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 32
   LENGTH: 666
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(666)
S-10-821-670-32

lignment Scores:
red. No.:              8.51e-186      Length:        666
core:                  187.00         Matches:       187
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-821-670-32 (1-666)

y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

y        181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
b        646 ATGAGCTATCTGAATGCTTCC 666

ESULT 12
S-10-821-670-34/c
 Sequence 34, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

Alignment Scores:
Pred. No.:             8.51e-186      Length:        666
Score:                 187.00         Matches:       187
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           100.0%         Indels:        0
DB:                    9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-821-670-34 (1-666)

Qy         1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy        21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy       101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy       121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy       141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy       161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy       181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
Db        21 ATGAGCTATCTGAATGCTTCC 1

RESULT 13
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE(
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
```

```
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 43
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1533)
   OTHER INFORMATION:
)S-09-917-265-43

\lignment Scores:
>red. No.:              1.85e-185      Length:          1533
;core:                  187.00         Matches:         187
>ercent Similarity:     100.0%         Conservative:    0
}est Local Similarity:  100.0%         Mismatches:      0
}uery Match:            100.0%         Indels:          0
)B:                     3              Gaps:            0

)S-10-821-670A-102 (1-187) x US-09-917-265-43 (1-1533)

}y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

}y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

}y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

}y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

}y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

}y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

}y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

}y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

}y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

}y        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
)b       1513 ATGAGCTATCTGAATGCTTCC 1533

!ESULT 14
)S-09-917-265-45/c
 Sequence 45, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

Alignment Scores:
Pred. No.:              1.85e-185      Length:          1533
Score:                  187.00         Matches:         187
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-917-265-45 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 15
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
```

```
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 43
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1533)
S-10-821-670-43

lignment Scores:
red. No.:              1.85e-185      Length:        1533
core:                  187.00         Matches:       187
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-821-670-43 (1-1533)

y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

y        181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||
b       1513 ATGAGCTATCTGAATGCTTCC 1533

ESULT 16
S-10-821-670-45/c
 Sequence 45, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:
Pred. No.:             1.85e-185      Length:        1533
Score:                 187.00         Matches:       187
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           100.0%         Indels:        0
DB:                    9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-821-670-45 (1-1533)

Qy         1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy        21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy       101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy       121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy       141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy       161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy       181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||
Db        21 ATGAGCTATCTGAATGCTTCC 1

RESULT 17
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
```

```
   PRIOR FILING DATE: 2000-08-04
   NUMBER OF SEQ ID NOS: 109
   SOFTWARE: PatentIn version 3.1
 SEQ ID NO 38
    LENGTH: 1599
    TYPE: DNA
    ORGANISM: Felis catus
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)..(1599)
    OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.:              1.92e-185      Length:         1599
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-38 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599

RESULT 18
US-09-917-265-40/c
 Sequence 40, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:
Pred. No.:              1.92e-185      Length:         1599
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-40 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        21 ATGAGCTATCTGAATGCTTCC 1

RESULT 19
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
```

```
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 38
   LENGTH: 1599
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1599)
S-10-821-670-38

lignment Scores:
red. No.:              1.92e-185      Length:         1599
core:                  187.00         Matches:        187
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            100.0%         Indels:         0
B:                     9              Gaps:           0

S-10-821-670A-102 (1-187) x US-10-821-670-38 (1-1599)

y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

y        181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
b       1579 ATGAGCTATCTGAATGCTTCC 1599

ESULT 20
S-10-821-670-40/c
 Sequence 40, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:
Pred. No.:             1.92e-185      Length:         1599
Score:                 187.00         Matches:        187
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           100.0%         Indels:         0
DB:                    9              Gaps:           0

US-10-821-670A-102 (1-187) x US-10-821-670-40 (1-1599)

Qy         1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy        21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy       101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy       121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy       141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy       161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy       181 MetSerTyrLeuAsnAlaSer 187
             |||||||||||||||||||||
Db        21 ATGAGCTATCTGAATGCTTCC 1

RESULT 21
US-10-079-616-9
; Sequence 9, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
```

```
        NUMBER OF SEQUENCES: 26
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: BROWDY AND NEIMARK
             STREET: 419 Seventh Street, N.W., Suite 300
             CITY: Washington
             STATE: D.C.
             COUNTRY: USA
             ZIP: 20004
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/10/079,616
             FILING DATE: 22-Feb-2002
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 09/011,143
             FILING DATE: 04-FEB-1998
             APPLICATION NUMBER: PCT/JP97/01824
             FILING DATE: 29-MAY-1997
             APPLICATION NUMBER: JP 165249/1996
             FILING DATE: 04-JUN-1996
        ATTORNEY/AGENT INFORMATION:
             NAME: BROWDY, Roger L.
             REGISTRATION NUMBER: 25,618
             REFERENCE/DOCKET NUMBER: IMAMURA=1
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: 202-628-5197
             TELEFAX: 202-737-3528
   INFORMATION FOR SEQ ID NO: 9:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 591 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
)S-10-079-616-9

\lignment Scores:
'red. No.:              9.57e-184       Length:         591
;core:                  185.00          Matches:        185
'ercent Similarity:     100.0%          Conservative:   0
}est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            98.9%           Indels:         0
)B:                     6               Gaps:           0

)S-10-821-670A-102 (1-187) x US-10-079-616-9 (1-591)

)y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

)y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

)y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

)y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

)y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

)y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

)b        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

)y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

)y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

)y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

)y        181 MetSerTyrLeuAsn 185
              ||||||||||||||||
)b        571 ATGAGCTACCTGAAT 585

RESULT 22
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

Alignment Scores:
Pred. No.:              1.1e-183        Length:         689
Score:                  185.00          Matches:        185
```

```
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            98.9%           Indels:        0
B:                     6               Gaps:          0

S-10-821-670A-102 (1-187) x US-10-079-616-26 (1-689)

y          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

y         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

y         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

y         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

y         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

y        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

y        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

y        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

y        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

y        181 MetSerTyrLeuAsn 185
             |||||||||||||||
b        652 ATGAGCTACCTGAAT 666

ESULT 23
S-10-079-616-8
 Sequence 8, Application US/10079616
 Publication No. US20020107366A1
   GENERAL INFORMATION:
        APPLICANT: IMAMURA, Takayuki
                   MAEDA, Hiroaki
                   FUJIYASU, Takeshi
                   IMAGAWA, Yoshitaka
                   TOKIYOSHI, Sachio
        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
        NUMBER OF SEQUENCES: 26
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: BROWDY AND NEIMARK
             STREET: 419 Seventh Street, N.W., Suite 300
             CITY: Washington
             STATE: D.C.
             COUNTRY: USA
             ZIP: 20004
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1441 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

Alignment Scores:
Pred. No.:             2.19e-183       Length:        1441
Score:                 185.00          Matches:       185
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           98.9%           Indels:        0
DB:                    6               Gaps:          0

US-10-821-670A-102 (1-187) x US-10-079-616-8 (1-1441)

Qy         1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy        21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy        41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       368 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 427

Qy        61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       428 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 487

Qy        81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       488 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 547

Qy       101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       548 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 607

Qy       121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       608 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 667

Qy       141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       668 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 727

Qy       161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       728 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 787

Qy       181 MetSerTyrLeuAsn 185
```

```
              ||||||||||||||||
Db        788 ATGAGCTACCTGAAT 802

RESULT 24
US-10-041-672C-2
  Sequence 2, Application US/10041672C
  Publication No. US20030157059A1
  GENERAL INFORMATION:
   APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
   APPLICANT:  Universitat Zurich
   TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
   FILE REFERENCE: NHL-NP-36
   CURRENT APPLICATION NUMBER: US/10/041,672C
   CURRENT FILING DATE:  2002-01-08
   NUMBER OF SEQ ID NOS: 11
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 2
    LENGTH: 669
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: feline IL-12 p35
US-10-041-672C-2

Alignment Scores:
Pred. No.:                3.32e-46        Length:         669
Score:                    54.00           Matches:        54
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              28.9%           Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-041-672C-2 (1-669)

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
               ||||||||||||||||||||||||||||||||||||||||||
Db         466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507

RESULT 25
US-09-917-265-49
  Sequence 49, Application US/09917265
  Patent No. US20020052030A1
  GENERAL INFORMATION:
   APPLICANT: Wonderling, Ramani S.
   APPLICANT:  Boroughs, Karen L.
   TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
   FILE REFERENCE: IM-5
   CURRENT APPLICATION NUMBER: US/09/917,265
   CURRENT FILING DATE:  2001-07-27
   PRIOR APPLICATION NUMBER: 60/223,016
   PRIOR FILING DATE: 2000-08-04
   NUMBER OF SEQ ID NOS: 109
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 49
    LENGTH: 591
    TYPE: DNA
    ORGANISM: Canis familiaris
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)..(591)
    OTHER INFORMATION:
US-09-917-265-49

Alignment Scores:
Pred. No.:                3.72e-44        Length:         591
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-49 (1-591)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 26
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

Alignment Scores:
Pred. No.:                3.72e-44        Length:         591
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-51 (1-591)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 27
US-10-821-670-49
; Sequence 49, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
```

```
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 49
   LENGTH: 591
   TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(591)
S-10-821-670-49

lignment Scores:
red. No.:              3.72e-44      Length:        591
core:                  52.00         Matches:       52
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            27.8%         Indels:        0
B:                     9             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-821-670-49 (1-591)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
b        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

ESULT 28
S-10-821-670-51/c
 Sequence 51, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 51
   LENGTH: 591
   TYPE: DNA
   ORGANISM: Canis familiaris
S-10-821-670-51

lignment Scores:
red. No.:              3.72e-44      Length:        591
core:                  52.00         Matches:       52
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            27.8%         Indels:        0
B:                     9             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-821-670-51 (1-591)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 29
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

Alignment Scores:
Pred. No.:             4.15e-44      Length:        666
Score:                 52.00         Matches:       52
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           27.8%         Indels:        0
DB:                    3             Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265-46 (1-666)

Qy        30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy        50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||||
Db       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 30
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
```

```
;   ORGANISM: Canis familiaris
)S-09-917-265-48

\lignment Scores:
?red. No.:                4.15e-44        Length:         666
;core:                    52.00           Matches:        52
?ercent Similarity:       100.0%          Conservative:   0
;est Local Similarity:    100.0%          Mismatches:     0
)uery Match:              27.8%           Indels:         0
)B:                       3               Gaps:           0

)S-10-821-670A-102 (1-187) x US-09-917-265-48 (1-666)

)y          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

)y          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

)y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
)b         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

?ESULT 31
)S-10-821-670-46
' Sequence 46, Application US/10821670
: Publication No. US20040248261A1
' GENERAL INFORMATION:
'  APPLICANT: Wonderling, Ramani S.
'  APPLICANT:  Boroughs, Karen L.
   TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
'  FILE REFERENCE: IM-5
:  CURRENT APPLICATION NUMBER: US/10/821,670
'  CURRENT FILING DATE:  2004-04-09
'  PRIOR APPLICATION NUMBER: 60/223,016
'  PRIOR FILING DATE: 2000-08-04
'  NUMBER OF SEQ ID NOS: 111
'  SOFTWARE: PatentIn version 3.2
' SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
:   ORGANISM: Canis familiaris
'   FEATURE:
    NAME/KEY: CDS
'   LOCATION: (1)..(666)
)S-10-821-670-46

\lignment Scores:
?red. No.:                4.15e-44        Length:         666
;core:                    52.00           Matches:        52
?ercent Similarity:       100.0%          Conservative:   0
;est Local Similarity:    100.0%          Mismatches:     0
)uery Match:              27.8%           Indels:         0
)B:                       9               Gaps:           0

)S-10-821-670A-102 (1-187) x US-10-821-670-46 (1-666)

)y          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

)y          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

)y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
)b         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

?ESULT 32
US-10-821-670-48/c
; Sequence 48, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-48

Alignment Scores:
Pred. No.:                4.15e-44        Length:         666
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              27.8%           Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-821-670-48 (1-666)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 33
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
;   OTHER INFORMATION:
US-09-917-265-104

Alignment Scores:
Pred. No.:                8.57e-44        Length:         1455
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
```

```
uery Match:            27.8%          Indels:        0
B:                     3              Gaps:          0

S-10-821-670A-102 (1-187) x US-09-917-265-104 (1-1455)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||
b        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

ESULT 34
S-09-917-265-106/c
 Sequence 106, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 106
   LENGTH: 1455
   TYPE: DNA
   ORGANISM: Canis familiaris
S-09-917-265-106

lignment Scores:
red. No.:              8.57e-44       Length:        1455
core:                  52.00          Matches:       52
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            27.8%          Indels:        0
B:                     3              Gaps:          0

S-10-821-670A-102 (1-187) x US-09-917-265-106 (1-1455)

y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
             |||||||||||||||||||||||||||||||||||
b        912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

ESULT 35
S-10-821-670-104
 Sequence 104, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-10-821-670-104

Alignment Scores:
Pred. No.:             8.57e-44       Length:        1455
Score:                 52.00          Matches:       52
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           27.8%          Indels:        0
DB:                    9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-821-670-104 (1-1455)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||
Db        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

RESULT 36
US-10-821-670-106/c
; Sequence 106, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-106

Alignment Scores:
Pred. No.:             8.57e-44       Length:        1455
Score:                 52.00          Matches:       52
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           27.8%          Indels:        0
DB:                    9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-821-670-106 (1-1455)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913
```

```
Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              ||||||||||||||||||||||||||||||||||||||
Db        912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

RESULT 37
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:
Pred. No.:                9e-44          Length:          1533
Score:                    52.00          Matches:         52
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              27.8%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-917-265-66 (1-1533)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              ||||||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 38
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

Alignment Scores:
Pred. No.:                9e-44          Length:          1533
Score:                    52.00          Matches:         52
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              27.8%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-102 (1-187) x US-09-917-265-68 (1-1533)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              ||||||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 39
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

Alignment Scores:
Pred. No.:                9e-44          Length:          1533
Score:                    52.00          Matches:         52
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              27.8%          Indels:          0
DB:                       9              Gaps:            0

US-10-821-670A-102 (1-187) x US-10-821-670-66 (1-1533)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              ||||||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 40
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
```

```
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 68
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Canis familiaris
S-10-821-670-68

lignment Scores:
red. No.:               9e-44          Length:        1533
core:                   52.00          Matches:       52
ercent Similarity:      100.0%         Conservative:  0
est Local Similarity:   100.0%         Mismatches:    0
uery Match:             27.8%          Indels:        0
B:                      9              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-821-670-68 (1-1533)

.y         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

.y         50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 b        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

.y         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
              |||||||||||||||||||||||||||||||||||||
 b        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

 ESULT 41
 S-09-917-265-61
  Sequence 61, Application US/09917265
  Patent No. US20020052030A1
  GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
   TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
   FILE REFERENCE: IM-5
   CURRENT APPLICATION NUMBER: US/09/917,265
   CURRENT FILING DATE:  2001-07-27
   PRIOR APPLICATION NUMBER: 60/223,016
   PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 61
    LENGTH: 1599
    TYPE: DNA
    ORGANISM: Canis familiaris
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)..(1599)
    OTHER INFORMATION:
 S-09-917-265-61

lignment Scores:
red. No.:               9.36e-44       Length:        1599
core:                   52.00          Matches:       52
ercent Similarity:      100.0%         Conservative:  0
est Local Similarity:   100.0%         Mismatches:    0
uery Match:             27.8%          Indels:        0
B:                      3              Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265-61 (1-1599)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db        1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 42
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

Alignment Scores:
Pred. No.:              9.36e-44       Length:        1599
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            27.8%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265-63 (1-1599)

Qy          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 43
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 61
   LENGTH: 1599
   TYPE: DNA
;  ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1599)
)S-10-821-670-61

\lignment Scores:
>red. No.:                9.36e-44        Length:         1599
;core:                    52.00           Matches:        52
>ercent Similarity:       100.0%          Conservative:   0
}est Local Similarity:    100.0%          Mismatches:     0
}uery Match:              27.8%           Indels:         0
)B:                       9               Gaps:           0

)S-10-821-670A-102 (1-187) x US-10-821-670-61 (1-1599)

}y          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

}y          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

}y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
)b        1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

{ESULT 44
)S-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
)S-10-821-670-63

\lignment Scores:
>red. No.:                9.36e-44        Length:         1599
;core:                    52.00           Matches:        52
>ercent Similarity:       100.0%          Conservative:   0
}est Local Similarity:    100.0%          Mismatches:     0
}uery Match:              27.8%           Indels:         0
)B:                       9               Gaps:           0

)S-10-821-670A-102 (1-187) x US-10-821-670-63 (1-1599)

}y          30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

}y          50 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

}y          70 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 81
               |||||||||||||||||||||||||||||||||||||
)b         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 45
US-10-741-601-946
; Sequence 946, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 946
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-946

Alignment Scores:
Pred. No.:                1.88e-20        Length:         201
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       8               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-741-601-946 (1-201)

Qy         149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy         169 AlaPheArgIleArgAlaValThrIle 177
               |||||||||||||||||||||||||
Db          64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 46
US-10-741-601-947
; Sequence 947, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 947
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-947

Alignment Scores:
Pred. No.:                1.88e-20        Length:         201
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       8               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-741-601-947 (1-201)

Qy         149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy         169 AlaPheArgIleArgAlaValThrIle 177
```

```
                ||||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

ESULT 47
S-10-741-601-951
 Sequence 951, Application US/10741601
 Publication No. US20040166519A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001500
  CURRENT APPLICATION NUMBER: US/10/741,601
  CURRENT FILING DATE:  2003-12-22
  NUMBER OF SEQ ID NOS: 26415
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 951
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
S-10-741-601-951

lignment Scores:
red. No.:              1.88e-20       Length:        201
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     8              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-741-601-951 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

ESULT 48
S-10-741-601-955
 Sequence 955, Application US/10741601
 Publication No. US20040166519A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001500
  CURRENT APPLICATION NUMBER: US/10/741,601
  CURRENT FILING DATE:  2003-12-22
  NUMBER OF SEQ ID NOS: 26415
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
S-10-741-601-955

lignment Scores:
red. No.:              1.88e-20       Length:        201
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     8              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-741-601-955 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 49
US-10-741-601-957
; Sequence 957, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 957
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-957

Alignment Scores:
Pred. No.:             1.88e-20       Length:        201
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    8              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-741-601-957 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 50
US-10-741-601-960
; Sequence 960, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 960
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-960

Alignment Scores:
Pred. No.:             1.88e-20       Length:        201
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    8              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-741-601-960 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172
```

```
)y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
)b        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

!ESULT 51
!S-10-741-601-7417
  Sequence 7417, Application US/10741601
  Publication No. US20040166519A1
  GENERAL INFORMATION:
   APPLICANT: CARGILL, Michele et al.
   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
   TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
   FILE REFERENCE: CL001500
   CURRENT APPLICATION NUMBER: US/10/741,601
   CURRENT FILING DATE:  2003-12-22
   NUMBER OF SEQ ID NOS: 26415
   SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 7417
    LENGTH: 201
    TYPE: DNA
    ORGANISM: Homo sapiens
!S-10-741-601-7417

!lignment Scores:
)red. No.:                1.88e-20       Length:         201
!core:                    29.00          Matches:        29
)ercent Similarity:       100.0%         Conservative:   0
!est Local Similarity:    100.0%         Mismatches:     0
!uery Match:              15.5%          Indels:         0
)B:                       8              Gaps:           0

!S-10-821-670A-102 (1-187) x US-10-741-601-7417 (1-201)

)y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

)y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
)b         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

!ESULT 52
!S-10-741-601-7418
  Sequence 7418, Application US/10741601
  Publication No. US20040166519A1
  GENERAL INFORMATION:
   APPLICANT: CARGILL, Michele et al.
   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
   TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
   FILE REFERENCE: CL001500
   CURRENT APPLICATION NUMBER: US/10/741,601
   CURRENT FILING DATE:  2003-12-22
   NUMBER OF SEQ ID NOS: 26415
   SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 7418
    LENGTH: 201
    TYPE: DNA
    ORGANISM: Homo sapiens
!S-10-741-601-7418

!lignment Scores:
)red. No.:                1.88e-20       Length:         201
!core:                    29.00          Matches:        29
)ercent Similarity:       100.0%         Conservative:   0
!est Local Similarity:    100.0%         Mismatches:     0
!uery Match:              15.5%          Indels:         0
)B:                       8              Gaps:           0

!S-10-821-670A-102 (1-187) x US-10-741-601-7418 (1-201)

)y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db          72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 53
US-10-741-601-7431
; Sequence 7431, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7431
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7431

Alignment Scores:
Pred. No.:                1.88e-20       Length:         201
Score:                    29.00          Matches:        29
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              15.5%          Indels:         0
DB:                       8              Gaps:           0

US-10-821-670A-102 (1-187) x US-10-741-601-7431 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 54
US-10-741-601-11370/c
; Sequence 11370, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11370
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11370

Alignment Scores:
Pred. No.:                1.88e-20       Length:         201
Score:                    29.00          Matches:        29
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              15.5%          Indels:         0
DB:                       8              Gaps:           0

US-10-821-670A-102 (1-187) x US-10-741-601-11370 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

y         169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
b         138 GCTTTCAGAATTCGGGCAGTGACTATT 112
```

ESULT 55
S-10-741-601-11372/c
Sequence 11372, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11372
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
S-10-741-601-11372

lignment Scores:

red. No.:	1.88e-20	Length:	201
core:	29.00	Matches:	29
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	15.5%	Indels:	0
B:	8	Gaps:	0

S-10-821-670A-102 (1-187) x US-10-741-601-11372 (1-201)

```
y         149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

y         169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
b         130 GCTTTCAGAATTCGGGCAGTGACTATT 104
```

ESULT 56
S-10-741-601-11417/c
Sequence 11417, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11417
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
S-10-741-601-11417

lignment Scores:

red. No.:	1.88e-20	Length:	201
core:	29.00	Matches:	29
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	15.5%	Indels:	0
B:	8	Gaps:	0

S-10-821-670A-102 (1-187) x US-10-741-601-11417 (1-201)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db         29 GCTTTCAGAATTCGGGCAGTGACTATT 3
```

RESULT 57
US-10-741-600-3487
; Sequence 3487, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3487
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-3487

Alignment Scores:

Pred. No.:	1.88e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-741-600-3487 (1-201)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90
```

RESULT 58
US-10-741-600-3488
; Sequence 3488, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3488
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-3488

Alignment Scores:

Pred. No.:	1.88e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-741-600-3488 (1-201)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 59
US-10-741-600-3492
; Sequence 3492, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3492
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3492

Alignment Scores:
Pred. No.:                1.88e-20      Length:          201
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       9             Gaps:            0

US-10-821-670A-102 (1-187) x US-10-741-600-3492 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 60
US-10-741-600-3496
; Sequence 3496, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3496
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3496

Alignment Scores:
Pred. No.:                1.88e-20      Length:          201
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       9             Gaps:            0

US-10-821-670A-102 (1-187) x US-10-741-600-3496 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 61
US-10-741-600-3498
; Sequence 3498, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3498
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3498

Alignment Scores:
Pred. No.:                1.88e-20      Length:          201
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       9             Gaps:            0

US-10-821-670A-102 (1-187) x US-10-741-600-3498 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 62
US-10-741-600-3501
; Sequence 3501, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3501
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3501

Alignment Scores:
Pred. No.:                1.88e-20      Length:          201
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       9             Gaps:            0
```

```
S-10-821-670A-102 (1-187) x US-10-741-600-3501 (1-201)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
b        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

ESULT 63
S-10-741-600-20963
 Sequence 20963, Application US/10741600
 Publication No. US20050026169A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001499
  CURRENT APPLICATION NUMBER: US/10/741,600
  CURRENT FILING DATE:  2003-12-22
  NUMBER OF SEQ ID NOS: 73997
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 20963
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
S-10-741-600-20963

lignment Scores:
red. No.:              1.88e-20       Length:         201
core:                  29.00          Matches:        29
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            15.5%          Indels:         0
B:                     9              Gaps:           0

S-10-821-670A-102 (1-187) x US-10-741-600-20963 (1-201)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
b         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

ESULT 64
S-10-741-600-20964
 Sequence 20964, Application US/10741600
 Publication No. US20050026169A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001499
  CURRENT APPLICATION NUMBER: US/10/741,600
  CURRENT FILING DATE:  2003-12-22
  NUMBER OF SEQ ID NOS: 73997
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 20964
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
S-10-741-600-20964

lignment Scores:
red. No.:              1.88e-20       Length:         201
core:                  29.00          Matches:        29
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            15.5%          Indels:         0
DB:                    9              Gaps:           0

US-10-821-670A-102 (1-187) x US-10-741-600-20964 (1-201)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
Db        72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 65
US-10-741-600-20992
; Sequence 20992, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20992
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20992

Alignment Scores:
Pred. No.:             1.88e-20       Length:         201
Score:                 29.00          Matches:        29
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           15.5%          Indels:         0
DB:                    9              Gaps:           0

US-10-821-670A-102 (1-187) x US-10-741-600-20992 (1-201)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
Db       173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 66
US-10-741-600-28831/c
; Sequence 28831, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28831
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28831

Alignment Scores:
Pred. No.:             1.88e-20       Length:         201
Score:                 29.00          Matches:        29
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
```

```
)uery Match:            15.5%          Indels:        0
)B:                     9              Gaps:          0

)S-10-821-670A-102 (1-187) x US-10-741-600-28831 (1-201)

)y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

)y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
)b        138 GCTTTCAGAATTCGGGCAGTGACTATT 112

(ESULT 67
)S-10-741-600-28833/c
· Sequence 28833, Application US/10741600
· Publication No. US20050026169A1
· GENERAL INFORMATION:
·  APPLICANT: CARGILL, Michele et al.
·  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
·  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
·  FILE REFERENCE: CL001499
·  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
·  NUMBER OF SEQ ID NOS: 73997
·  SOFTWARE: FastSEQ for Windows Version 4.0
· SEQ ID NO 28833
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
)S-10-741-600-28833

\lignment Scores:
'red. No.:              1.88e-20       Length:        201
;core:                  29.00          Matches:       29
'ercent Similarity:     100.0%         Conservative:  0
;est Local Similarity:  100.0%         Mismatches:    0
)uery Match:            15.5%          Indels:        0
)B:                     9              Gaps:          0

)S-10-821-670A-102 (1-187) x US-10-741-600-28833 (1-201)

)y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

)y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
)b        130 GCTTTCAGAATTCGGGCAGTGACTATT 104

(ESULT 68
)S-10-741-600-28877/c
· Sequence 28877, Application US/10741600
· Publication No. US20050026169A1
; GENERAL INFORMATION:
·  APPLICANT: CARGILL, Michele et al.
·  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
·  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
·  FILE REFERENCE: CL001499
·  CURRENT APPLICATION NUMBER: US/10/741,600
·  CURRENT FILING DATE:  2003-12-22
·  NUMBER OF SEQ ID NOS: 73997
·  SOFTWARE: FastSEQ for Windows Version 4.0
· SEQ ID NO 28877
;   LENGTH: 201
·   TYPE: DNA
;   ORGANISM: Homo sapiens
)S-10-741-600-28877

\lignment Scores:
'red. No.:              1.88e-20       Length:        201
;core:                  29.00          Matches:       29
'ercent Similarity:     100.0%         Conservative:  0
```

```
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-741-600-28877 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         29 GCTTTCAGAATTCGGGCAGTGACTATT 3

RESULT 69
US-10-995-561-1976
; Sequence 1976, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1976
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1976

Alignment Scores:
Pred. No.:              1.88e-20       Length:        201
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     10             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-995-561-1976 (1-201)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 70
US-10-995-561-1977
; Sequence 1977, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1977
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1977

Alignment Scores:
```

```
red. No.:              1.88e-20        Length:         201
core:                  29.00           Matches:        29
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            15.5%           Indels:         0
B:                     10              Gaps:           0

S-10-821-670A-102 (1-187) x US-10-995-561-1977 (1-201)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
b         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

ESULT 71
S-10-995-561-1981
 Sequence 1981, Application US/10995561
 Publication No. US20050272054A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
  TITLE OF INVENTION:  DETECTION AND USES THEREOF
  FILE REFERENCE: CL001559
  CURRENT APPLICATION NUMBER: US/10/995,561
  CURRENT FILING DATE:  2004-11-24
  NUMBER OF SEQ ID NOS: 85702
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1981
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
S-10-995-561-1981

lignment Scores:
red. No.:              1.88e-20        Length:         201
core:                  29.00           Matches:        29
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            15.5%           Indels:         0
B:                     10              Gaps:           0

S-10-821-670A-102 (1-187) x US-10-995-561-1981 (1-201)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
b        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

ESULT 72
S-10-995-561-1986
 Sequence 1986, Application US/10995561
 Publication No. US20050272054A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
  TITLE OF INVENTION:  DETECTION AND USES THEREOF
  FILE REFERENCE: CL001559
  CURRENT APPLICATION NUMBER: US/10/995,561
  CURRENT FILING DATE:  2004-11-24
  NUMBER OF SEQ ID NOS: 85702
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1986
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
US-10-995-561-1986

Alignment Scores:
Pred. No.:             1.88e-20        Length:         201
Score:                 29.00           Matches:        29
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           15.5%           Indels:         0
DB:                    10              Gaps:           0

US-10-821-670A-102 (1-187) x US-10-995-561-1986 (1-201)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
Db        64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 73
US-10-995-561-1988
; Sequence 1988, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1988
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1988

Alignment Scores:
Pred. No.:             1.88e-20        Length:         201
Score:                 29.00           Matches:        29
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           15.5%           Indels:         0
DB:                    10              Gaps:           0

US-10-821-670A-102 (1-187) x US-10-995-561-1988 (1-201)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
Db        72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 74
US-10-995-561-1991
; Sequence 1991, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1991
```

; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-1991

Alignment Scores:

Pred. No.:	1.88e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	10	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-995-561-1991 (1-201)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199
```

RESULT 75
US-10-995-561-18302
; Sequence 18302, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18302
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-18302

Alignment Scores:

Pred. No.:	1.88e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	10	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-995-561-18302 (1-201)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90
```

RESULT 76
US-10-995-561-18303
; Sequence 18303, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18303
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-18303

Alignment Scores:

Pred. No.:	1.88e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	10	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-995-561-18303 (1-201)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98
```

RESULT 77
US-10-995-561-18335
; Sequence 18335, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18335
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-18335

Alignment Scores:

Pred. No.:	1.88e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	10	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-995-561-18335 (1-201)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199
```

RESULT 78
US-10-995-561-26362/c
; Sequence 26362, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

```
  FILE REFERENCE: CL001559
  CURRENT APPLICATION NUMBER: US/10/995,561
  CURRENT FILING DATE:  2004-11-24
  NUMBER OF SEQ ID NOS: 85702
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26362
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
S-10-995-561-26362

lignment Scores:
red. No.:              1.88e-20       Length:        201
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     10             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-995-561-26362 (1-201)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b        29 GCTTTCAGAATTCGGGCAGTGACTATT 3

ESULT 79
S-10-995-561-26545/c
 Sequence 26545, Application US/10995561
 Publication No. US20050272054A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
  TITLE OF INVENTION:  DETECTION AND USES THEREOF
  FILE REFERENCE: CL001559
  CURRENT APPLICATION NUMBER: US/10/995,561
  CURRENT FILING DATE:  2004-11-24
  NUMBER OF SEQ ID NOS: 85702
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26545
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
S-10-995-561-26545

lignment Scores:
red. No.:              1.88e-20       Length:        201
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     10             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-995-561-26545 (1-201)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b       138 GCTTTCAGAATTCGGGCAGTGACTATT 112

ESULT 80
S-10-995-561-26548/c
 Sequence 26548, Application US/10995561
 Publication No. US20050272054A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26548
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26548

Alignment Scores:
Pred. No.:             1.88e-20       Length:        201
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    10             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-995-561-26548 (1-201)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
Db      130 GCTTTCAGAATTCGGGCAGTGACTATT 104

RESULT 81
US-10-995-561-73346/c
; Sequence 73346, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73346
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73346

Alignment Scores:
Pred. No.:             1.88e-20       Length:        201
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    10             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-995-561-73346 (1-201)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
Db      138 GCTTTCAGAATTCGGGCAGTGACTATT 112

RESULT 82
US-10-995-561-73349/c
; Sequence 73349, Application US/10995561
```

```
  Publication No. US20050272054A1
 GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele et al.
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
  TITLE OF INVENTION:  DETECTION AND USES THEREOF
  FILE REFERENCE: CL001559
  CURRENT APPLICATION NUMBER: US/10/995,561
  CURRENT FILING DATE:  2004-11-24
  NUMBER OF SEQ ID NOS: 85702
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 73349
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
JS-10-995-561-73349

\lignment Scores:
>red. No.:                1.88e-20        Length:         201
}core:                    29.00           Matches:        29
>ercent Similarity:       100.0%          Conservative:   0
}est Local Similarity:    100.0%          Mismatches:     0
}uery Match:              15.5%           Indels:         0
}B:                       10              Gaps:           0

JS-10-821-670A-102 (1-187) x US-10-995-561-73349 (1-201)

}y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
}b        190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

}y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
}b        130 GCTTTCAGAATTCGGGCAGTGACTATT 104

!ESULT 83
JS-10-995-561-73383/c
 Sequence 73383, Application US/10995561
  Publication No. US20050272054A1
 GENERAL INFORMATION:
   APPLICANT: CARGILL, Michele et al.
   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
   TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
   TITLE OF INVENTION:  DETECTION AND USES THEREOF
   FILE REFERENCE: CL001559
   CURRENT APPLICATION NUMBER: US/10/995,561
   CURRENT FILING DATE:  2004-11-24
   NUMBER OF SEQ ID NOS: 85702
   SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 73383
   LENGTH: 201
   TYPE: DNA
   ORGANISM: Homo sapiens
JS-10-995-561-73383

\lignment Scores:
>red. No.:                1.88e-20        Length:         201
}core:                    29.00           Matches:        29
>ercent Similarity:       100.0%          Conservative:   0
}est Local Similarity:    100.0%          Mismatches:     0
}uery Match:              15.5%           Indels:         0
}B:                       10              Gaps:           0

JS-10-821-670A-102 (1-187) x US-10-995-561-73383 (1-201)

}y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
}b         89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

}y        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
}b         29 GCTTTCAGAATTCGGGCAGTGACTATT 3
```

```
RESULT 84
US-09-754-014-6
; Sequence 6, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 660 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-754-014-6

Alignment Scores:
Pred. No.:                5.68e-20        Length:         660
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              15.5%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-754-014-6 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 85
US-09-754-014-7
; Sequence 7, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
```

```
                  Bruce Freimark
                  Deepa Deshpande
        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                            AND USES
        NUMBER OF SEQUENCES: 12
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: Lyon & Lyon
             STREET: 633 West Fifth Street
                     Suite 4700
             CITY: Los Angeles
             STATE: California
             COUNTRY: U.S.A.
             ZIP: 90071-2066
        COMPUTER READABLE FORM:
             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                          storage
             COMPUTER: IBM Compatible
             OPERATING SYSTEM: IBM P.C. DOS 5.0
             SOFTWARE: FastSEQ for Windows 2.0
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/754,014
             FILING DATE: 03-Jan-2001
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 08/948,958
             FILING DATE: <Unknown>
        ATTORNEY/AGENT INFORMATION:
             NAME: Berkman, Charles S.
             REGISTRATION NUMBER: 38,077
             REFERENCE/DOCKET NUMBER: 226/284
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (213) 489-1600
             TELEFAX: (213) 955-0440
             TELEX: 67-3510
   INFORMATION FOR SEQ ID NO: 7:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 660 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
S-09-754-014-7

lignment Scores:
red. No.:               5.68e-20        Length:         660
core:                   29.00           Matches:        29
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             15.5%           Indels:         0
B:                      3               Gaps:           0

S-10-821-670A-102 (1-187) x US-09-754-014-7 (1-660)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
b        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

ESULT 86
S-09-754-014-8
 Sequence 8, Application US/09754014
 Patent No. US20020119940A1
   GENERAL INFORMATION:
        APPLICANT: Jeff No. US20020119940A1dstrom
                   Bruce Freimark
                   Deepa Deshpande
        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                            AND USES
        NUMBER OF SEQUENCES: 12
        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lyon & Lyon
;            STREET: 633 West Fifth Street
;                    Suite 4700
;            CITY: Los Angeles
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 90071-2066
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                         storage
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: IBM P.C. DOS 5.0
;            SOFTWARE: FastSEQ for Windows 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/754,014
;            FILING DATE: 03-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/948,958
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Berkman, Charles S.
;            REGISTRATION NUMBER: 38,077
;            REFERENCE/DOCKET NUMBER: 226/284
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (213) 489-1600
;            TELEFAX: (213) 955-0440
;            TELEX: 67-3510
;  INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 660 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-754-014-8

Alignment Scores:
Pred. No.:              5.68e-20        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.5%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-754-014-8 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGGGCCGTGACCATC 627

RESULT 87
US-09-836-866-4
; Sequence 4, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;       APPLICANT: No. US20020123473A1dstrom, Jeff
;                  Freimark, Bruce
;                  Deshpande, Deepa
;       TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                           DELIVERY SYTEMS AND USES
;       NUMBER OF SEQUENCES: 8
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lyon & Lyon
;            STREET: 633 West Fifth Street
;                    Suite 4700
;            CITY: Los Angeles
;            STATE: California
;            COUNTRY: U.S.A.
```

```
          ZIP: 90071-2066
       COMPUTER READABLE FORM:
          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                       storage
          COMPUTER: IBM Compatible
          OPERATING SYSTEM: IBM P.C. DOS 5.0
          SOFTWARE: FastSEQ for Windows 2.0
       CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/836,866
          FILING DATE: 16-Apr-2001
          CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 08/949,160
          FILING DATE: <Unknown>
       ATTORNEY/AGENT INFORMATION:
          NAME: Warburg, Richard J.
          REGISTRATION NUMBER: 32,327
          REFERENCE/DOCKET NUMBER: 226/285
       TELECOMMUNICATION INFORMATION:
          TELEPHONE: (213) 489-1600
          TELEFAX: (213) 955-0440
          TELEX: 67-3510
    INFORMATION FOR SEQ ID NO: 4:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 660 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-836-866-4

Alignment Scores:
Pred. No.:                5.68e-20      Length:          660
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-102 (1-187) x US-09-836-866-4 (1-660)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 88
US-10-267-384-199
; Sequence 199, Application US/10267384
; Publication No. US20030198623A1
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/267,384
;             FILING DATE: 09-Oct-2002
;             CLASSIFICATION: 435
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-10-267-384-199

Alignment Scores:
Pred. No.:                6.16e-20      Length:          721
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       7             Gaps:            0

US-10-821-670A-102 (1-187) x US-10-267-384-199 (1-721)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 89
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
```

```
        SEQUENCE CHARACTERISTICS:
             LENGTH: 762 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: double
             TOPOLOGY: linear
        MOLECULE TYPE: other nucleic acid
             DESCRIPTION: /desc = "DNA"
        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
S-09-826-025-21

lignment Scores:
red. No.:              6.49e-20       Length:        762
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     3              Gaps:          0

S-10-821-670A-102 (1-187) x US-09-826-025-21 (1-762)

y        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

y        169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
b        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

ESULT 90
S-10-785-577-21
; Sequence 21, Application US/10785577
. Publication No. US20040237129A1
   GENERAL INFORMATION:
        APPLICANT: Chang, Lung-Ji
        TITLE OF INVENTION: Combination Immunogene Therapy
        NUMBER OF SEQUENCES: 25
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: Medlen & Carroll, LLP
             STREET: 220 Montgomery Street, Suite 2200
             CITY: San Francisco
             STATE: California
             COUNTRY: United States of America
             ZIP: 94104
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/10/785,577
             FILING DATE: 23-Feb-2004
             CLASSIFICATION: 424
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: US/08/838,702
             FILING DATE: 9-Apr-1997
        ATTORNEY/AGENT INFORMATION:
             NAME: Ingolia, Diane E.
             REGISTRATION NUMBER: 40,027
             REFERENCE/DOCKET NUMBER: CHANG-02687
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (415) 705-8410
             TELEFAX: (415) 397-8338
   INFORMATION FOR SEQ ID NO: 21:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 762 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: double
             TOPOLOGY: linear
        MOLECULE TYPE: other nucleic acid
             DESCRIPTION: /desc = "DNA"
        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
S-10-785-577-21
```

```
Alignment Scores:
Pred. No.:              6.49e-20       Length:        762
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-785-577-21 (1-762)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
Db       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 91
US-10-688-845-57
; Sequence 57, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
;  APPLICANT: Lotze, Michael T
;  APPLICANT:  Tahara, Hideaki
;  TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
;  FILE REFERENCE: UPT-004
;  CURRENT APPLICATION NUMBER: US/10/688,845
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,865
;  PRIOR FILING DATE: 2002-10-15
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-688-845-57

Alignment Scores:
Pred. No.:              6.49e-20       Length:        762
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            15.5%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-688-845-57 (1-762)

Qy       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy       169 AlaPheArgIleArgAlaValThrIle 177
             |||||||||||||||||||||||||||
Db       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 92
US-10-373-456-19
; Sequence 19, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 811
```

TYPE: DNA
ORGANISM: Homo sapiens
US-10-373-456-19

Alignment Scores:

Pred. No.:	6.87e-20	Length:	811
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-373-456-19 (1-811)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 548

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        549 GCTTTCAGAATTCGGGCAGTGACTATT 575
```

RESULT 93
US-10-349-507-4
; Sequence 4, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
; APPLICANT: Hekimi , Siegfried
; APPLICANT: Jiang , Ning
; APPLICANT: Benard, Claire
; APPLICANT: Kebir , Hania
; APPLICANT: McCright, Brenton
; APPLICANT: Lakowski , Bernard
; TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: 11202-006-999
; CURRENT APPLICATION NUMBER: US/10/349,507
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 10/312,187
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/CA01/00913
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/213,174
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/254,932
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)...(826)
US-10-349-507-4

Alignment Scores:

Pred. No.:	7.22e-20	Length:	856
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-349-507-4 (1-856)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796
```

RESULT 94
US-10-267-565-4
; Sequence 4, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
; APPLICANT: Gately, Maurice
; APPLICANT: Gubler, Ulrich
; APPLICANT: Hulmes, Jeffery
; APPLICANT: Podlaski, Frank
; APPLICANT: Stern, Alvin
; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
; TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THERETO
; FILE REFERENCE: 11126-005
; CURRENT APPLICATION NUMBER: US/10/267,565
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 09/401,839
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/459,151
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 08/205,011
; PRIOR FILING DATE: 1994-03-02
; PRIOR APPLICATION NUMBER: 07/857,023
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/572,284
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: 07/520,935
; PRIOR FILING DATE: 1990-05-09
; PRIOR APPLICATION NUMBER: 07/455,708
; PRIOR FILING DATE: 1989-12-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)...(826)
US-10-267-565-4

Alignment Scores:

Pred. No.:	7.22e-20	Length:	856
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	15.5%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-267-565-4 (1-856)

```
Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796
```

RESULT 95
US-10-373-456-17
; Sequence 17, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
; APPLICANT: Podhajcer, Osvaldo
; TITLE OF INVENTION: Anti-Tumor Vaccine and Method
; FILE REFERENCE: 1423P-US/101141-14
; CURRENT APPLICATION NUMBER: US/10/373,456
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,836
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 20

```
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 17
   LENGTH: 868
   TYPE: DNA
   ORGANISM: Homo sapiens
S-10-373-456-17

lignment Scores:
red. No.:              7.32e-20       Length:        868
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     7              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-373-456-17 (1-868)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       552 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 611

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b       612 GCTTTCAGAATTCGGGCAGTGACTATT 638

ESULT 96
S-10-172-399-5
 Sequence 5, Application US/10172399
  Publication No. US20030045495A1
  GENERAL INFORMATION:
   APPLICANT: Li, Chuan-Yuan
   APPLICANT:  Dewhirst, Mark
   APPLICANT:  Huang, Qian
   TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
   FILE REFERENCE: 180-129
   CURRENT APPLICATION NUMBER: US/10/172,399
   CURRENT FILING DATE:  2002-06-14
   NUMBER OF SEQ ID NOS: 13
   SOFTWARE: PatentIn version 3.0
  SEQ ID NO 5
   LENGTH: 1026
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (170)..(829)
S-10-172-399-5

lignment Scores:
red. No.:              8.55e-20       Length:        1026
core:                  29.00          Matches:       29
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            15.5%          Indels:        0
B:                     6              Gaps:          0

S-10-821-670A-102 (1-187) x US-10-172-399-5 (1-1026)

y       149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

y       169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
b       770 GCTTTCAGAATTCGGGCAGTGACTATT 796

ESULT 97
S-10-641-643-1041
 Sequence 1041, Application US/10641643
 Publication No. US20040077003A1
   GENERAL INFORMATION:
        APPLICANT: Cocks, Benjamin G.
                   Susan G. Stuart
                   Jeffrey J. Seilhamer
        TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                            GENE EXPRESSION
        NUMBER OF SEQUENCES: 1508
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
             STREET: 3174 PORTER DRIVE
             CITY: PALO ALTO
             STATE: CALIFORNIA
             COUNTRY: USA
             ZIP: 94304
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/10/641,643
             FILING DATE: 14-Aug-2003
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: <Unknown>
             FILING DATE: <Unknown>
        ATTORNEY/AGENT INFORMATION:
             NAME: Zeller, Karen J.
             REGISTRATION NUMBER: 37,071
             REFERENCE/DOCKET NUMBER: PA-0001 US
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (650) 855-0555
             TELEFAX: (650) 845-4166
   INFORMATION FOR SEQ ID NO: 1041:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 1026 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        IMMEDIATE SOURCE:
             LIBRARY: GENBANK
             CLONE: g180623
        SEQUENCE DESCRIPTION: SEQ ID NO: 1041 :
US-10-641-643-1041

Alignment Scores:
Pred. No.:             8.55e-20       Length:        1026
Score:                 29.00          Matches:       29
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           15.5%          Indels:        0
DB:                    8              Gaps:          0

US-10-821-670A-102 (1-187) x US-10-641-643-1041 (1-1026)

Qy      149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy      169 AlaPheArgIleArgAlaValThrIle 177
            |||||||||||||||||||||||||
Db      770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 98
US-10-603-064-6
; Sequence 6, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
```

```
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-10-603-064-6

Alignment Scores:
Pred. No.:                1.05e-19      Length:          1287
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       8             Gaps:            0

US-10-821-670A-102 (1-187) x US-10-603-064-6 (1-1287)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254

RESULT 99
US-10-476-960-3
; Sequence 3, Application US/10476960
; Publication No. US20040248828A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTSP-0392
;  CURRENT APPLICATION NUMBER: US/10/476,960
;  CURRENT FILING DATE:  2003-11-05
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-10-476-960-3

Alignment Scores:
Pred. No.:                1.08e-19      Length:          1316
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       9             Gaps:            0

US-10-821-670A-102 (1-187) x US-10-476-960-3 (1-1316)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        804 GCTTTCAGAATTCGGGCAGTGACTATT 830

RESULT 100
US-11-089-191-3
; Sequence 3, Application US/11089191
; Publication No. US20050261228A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Susan Gregory
;  APPLICANT:  Ronnie C. Hanecak
;  APPLICANT:  Kevin P. Anderson
;  APPLICANT:  Ming-Yi Chiang
;  APPLICANT:  Vickie Brown-Driver
;  APPLICANT:  David J. Ecker
;  APPLICANT:  Timothy Vickers
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Eric G. Marcusson
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Sanjay Bhanot
;  APPLICANT:  Elizabeth J. Ackermann
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: BNDL-0021US.P1
;  CURRENT APPLICATION NUMBER: US/11/089,191
;  CURRENT FILING DATE:  2005-03-23
;  PRIOR APPLICATION NUMBER: 10/476,960
;  PRIOR FILING DATE: 2003-11-07
;  PRIOR APPLICATION NUMBER: PCT/US02/13871
;  PRIOR FILING DATE: 2002-05-01
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  PRIOR APPLICATION NUMBER: 10/67,236
;  PRIOR FILING DATE: 2003-09-17
;  PRIOR APPLICATION NUMBER: 10/038,335
;  PRIOR FILING DATE: 2002-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
;  PRIOR APPLICATION NUMBER: 10/515,546
;  PRIOR FILING DATE: 2004-11-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-11-089-191-3

Alignment Scores:
Pred. No.:                1.08e-19      Length:          1316
Score:                    29.00         Matches:         29
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              15.5%         Indels:          0
DB:                       15            Gaps:            0

US-10-821-670A-102 (1-187) x US-11-089-191-3 (1-1316)

Qy        149 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

Qy        169 AlaPheArgIleArgAlaValThrIle 177
              |||||||||||||||||||||||||
Db        804 GCTTTCAGAATTCGGGCAGTGACTATT 830
```

earch completed: June 12, 2006, 17:16:32
ob time : 908.079 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

)M protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 02:09:37 ; Search time 12.7446 Seconds
(without alignments)
2793.504 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 187
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 253354 seqs, 63461778 residues

Word size: 1

Total number of hits satisfying chosen parameters: 506227

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110508_27905/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap
-SUFFIX=oligo.p2n.200scores.rnpbn -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10821670_@CGN_1_1_62_@runat_07062006_110508_27905 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	8	4.3	528	6	US-10-322-836-19	Sequence 19, Appl
	2	8	4.3	879	6	US-10-322-836-17	Sequence 17, Appl
	3	8	4.3	1017	6	US-10-322-836-15	Sequence 15, Appl
	4	8	4.3	1248	6	US-10-322-836-27	Sequence 27, Appl
	5	8	4.3	1293	6	US-10-322-836-5	Sequence 5, Appli
	6	8	4.3	1317	6	US-10-322-836-41	Sequence 41, Appl
	7	8	4.3	1455	6	US-10-322-836-39	Sequence 39, Appl
	8	8	4.3	1599	6	US-10-322-836-25	Sequence 25, Appl
	9	8	4.3	1644	6	US-10-322-836-3	Sequence 3, Appli
	10	8	4.3	1737	6	US-10-322-836-23	Sequence 23, Appl
	11	8	4.3	1782	6	US-10-322-836-1	Sequence 1, Appli
	12	8	4.3	2021	6	US-10-953-349-4560	Sequence 4560, Ap
	13	8	4.3	2037	6	US-10-322-836-45	Sequence 45, Appl
	14	8	4.3	2082	6	US-10-322-836-33	Sequence 33, Appl
	15	8	4.3	2175	6	US-10-322-836-43	Sequence 43, Appl
	16	8	4.3	2220	6	US-10-322-836-31	Sequence 31, Appl
	17	8	4.3	3791	6	US-10-530-792A-1	Sequence 1, Appli
	18	8	4.3	6663	7	US-11-217-529-3234	Sequence 3234, Ap
	19	7	3.7	331	6	US-10-488-619-837	Sequence 837, App
C	20	7	3.7	582	6	US-10-953-349-25251	Sequence 25251, A
	21	7	3.7	660	7	US-11-217-529-81369	Sequence 81369, A
C	22	7	3.7	704	6	US-10-488-619-2648	Sequence 2648, Ap
	23	7	3.7	906	6	US-10-953-349-4834	Sequence 4834, Ap
	24	7	3.7	921	7	US-11-217-529-5460	Sequence 5460, Ap
	25	7	3.7	953	7	US-11-311-754-5	Sequence 5, Appli
C	26	7	3.7	994	6	US-10-953-349-28356	Sequence 28356, A
C	27	7	3.7	997	6	US-10-560-723-79	Sequence 79, Appl
	28	7	3.7	1062	6	US-10-953-349-39566	Sequence 39566, A
C	29	7	3.7	1202	6	US-10-953-349-17414	Sequence 17414, A
C	30	7	3.7	1313	6	US-10-953-349-24555	Sequence 24555, A
C	31	7	3.7	1454	6	US-10-953-349-35965	Sequence 35965, A
	32	7	3.7	1483	6	US-10-953-349-36433	Sequence 36433, A
C	33	7	3.7	1538	6	US-10-953-349-17700	Sequence 17700, A
C	34	7	3.7	1660	6	US-10-953-349-24275	Sequence 24275, A
C	35	7	3.7	1761	7	US-11-217-529-174380	Sequence 174380,
C	36	7	3.7	1804	7	US-11-251-465-7	Sequence 7, Appli
	37	7	3.7	1831	7	US-11-311-754-27	Sequence 27, Appl
	38	7	3.7	1868	6	US-10-505-928-693	Sequence 693, App
C	39	7	3.7	1914	6	US-10-953-349-11252	Sequence 11252, A
C	40	7	3.7	2036	7	US-11-293-697-1094	Sequence 1094, Ap
C	41	7	3.7	2037	7	US-11-217-529-77609	Sequence 77609, A
	42	7	3.7	2241	7	US-11-217-529-2489	Sequence 2489, Ap
	43	7	3.7	2275	7	US-11-293-697-507	Sequence 507, App
C	44	7	3.7	2315	6	US-10-511-937-649	Sequence 649, App
	45	7	3.7	2662	7	US-11-293-697-753	Sequence 753, App
	46	7	3.7	2805	7	US-11-217-529-82539	Sequence 82539, A
C	47	7	3.7	2905	7	US-11-293-697-74	Sequence 74, Appl
	48	7	3.7	3294	7	US-11-293-697-1397	Sequence 1397, Ap
C	49	7	3.7	3558	6	US-10-505-928-814	Sequence 814, App
C	50	7	3.7	7422	7	US-11-217-529-1506	Sequence 1506, Ap
	51	6	3.2	22	7	US-11-266-409-9	Sequence 9, Appli
	52	6	3.2	25	7	US-11-217-529-36402	Sequence 36402, A
	53	6	3.2	25	7	US-11-217-529-87245	Sequence 87245, A
C	54	6	3.2	25	7	US-11-217-529-88955	Sequence 88955, A
	55	6	3.2	25	7	US-11-217-529-109690	Sequence 109690,
	56	6	3.2	25	7	US-11-217-529-148883	Sequence 148883,
	57	6	3.2	25	7	US-11-217-529-162336	Sequence 162336,
	58	6	3.2	25	7	US-11-217-529-162342	Sequence 162342,
C	59	6	3.2	25	7	US-11-217-529-184372	Sequence 184372,
C	60	6	3.2	51	7	US-11-143-642-246	Sequence 246, App
C	61	6	3.2	69	7	US-11-296-092-22	Sequence 22, Appl
C	62	6	3.2	84	6	US-10-525-817-154	Sequence 154, App
C	63	6	3.2	84	6	US-10-525-817-155	Sequence 155, App
C	64	6	3.2	84	6	US-10-525-817-156	Sequence 156, App
C	65	6	3.2	84	6	US-10-525-817-157	Sequence 157, App
C	66	6	3.2	93	7	US-11-217-529-6033	Sequence 6033, Ap
	67	6	3.2	114	6	US-10-471-571A-5635	Sequence 5635, Ap
	68	6	3.2	162	7	US-11-217-529-81244	Sequence 81244, A
C	69	6	3.2	213	6	US-10-471-571A-4689	Sequence 4689, Ap
C	70	6	3.2	231	7	US-11-217-529-174474	Sequence 174474,
	71	6	3.2	276	7	US-11-217-529-166542	Sequence 166542,
C	72	6	3.2	303	7	US-11-217-529-174171	Sequence 174171,
C	73	6	3.2	310	7	US-11-301-554-610	Sequence 610, App
	74	6	3.2	327	7	US-11-217-529-4461	Sequence 4461, Ap
C	75	6	3.2	336	7	US-11-254-679-18	Sequence 18, Appl
	76	6	3.2	345	6	US-10-511-937-623	Sequence 623, App
	77	6	3.2	351	7	US-11-254-679-20	Sequence 20, Appl
C	78	6	3.2	362	7	US-11-301-554-1167	Sequence 1167, Ap
C	79	6	3.2	389	6	US-10-953-349-18005	Sequence 18005, A
	80	6	3.2	389	7	US-11-301-554-900	Sequence 900, App
C	81	6	3.2	390	6	US-10-488-619-2081	Sequence 2081, Ap
C	82	6	3.2	400	6	US-10-488-619-2364	Sequence 2364, Ap

c 83	6	3.2	421	6	US-10-488-619-316	Sequence 316, App
84	6	3.2	423	7	US-11-301-554-573	Sequence 573, App
c 85	6	3.2	437	6	US-10-560-723-109	Sequence 109, App
86	6	3.2	438	6	US-10-488-619-826	Sequence 826, App
87	6	3.2	438	6	US-10-488-619-2365	Sequence 2365, Ap
88	6	3.2	443	6	US-10-953-349-13876	Sequence 13876, A
89	6	3.2	470	6	US-10-488-619-338	Sequence 338, App
90	6	3.2	480	7	US-11-301-554-1170	Sequence 1170, Ap
c 91	6	3.2	480	7	US-11-297-957-5	Sequence 5, Appli
c 92	6	3.2	508	7	US-11-296-092-18	Sequence 18, Appl
c 93	6	3.2	508	7	US-11-296-092-19	Sequence 19, Appl
94	6	3.2	511	6	US-10-511-937-2900	Sequence 2900, Ap
95	6	3.2	517	6	US-10-473-173-459	Sequence 459, App
c 96	6	3.2	522	6	US-10-488-619-1461	Sequence 1461, Ap
c 97	6	3.2	534	7	US-11-217-529-78894	Sequence 78894, A
c 98	6	3.2	536	6	US-10-953-349-10529	Sequence 10529, A
99	6	3.2	536	6	US-10-953-349-13039	Sequence 13039, A
c 100	6	3.2	540	7	US-11-301-554-14	Sequence 14, Appl
c 101	6	3.2	540	7	US-11-217-529-76012	Sequence 76012, A
c 102	6	3.2	552	7	US-11-217-529-4706	Sequence 4706, Ap
c 103	6	3.2	557	6	US-10-953-349-5665	Sequence 5665, Ap
c 104	6	3.2	558	7	US-11-217-529-82089	Sequence 82089, A
105	6	3.2	561	7	US-11-301-554-72	Sequence 72, Appl
c 106	6	3.2	564	7	US-11-301-554-729	Sequence 729, App
c 107	6	3.2	564	7	US-11-217-529-174198	Sequence 174198,
c 108	6	3.2	565	6	US-10-953-349-9446	Sequence 9446, Ap
c 109	6	3.2	579	6	US-10-560-723-169	Sequence 169, App
c 110	6	3.2	594	7	US-11-217-529-342	Sequence 342, App
c 111	6	3.2	599	7	US-11-301-554-1892	Sequence 1892, Ap
c 112	6	3.2	603	7	US-11-217-529-81147	Sequence 81147, A
c 113	6	3.2	609	6	US-10-953-349-17062	Sequence 17062, A
114	6	3.2	611	6	US-10-511-937-3111	Sequence 3111, Ap
115	6	3.2	612	6	US-10-471-571A-3357	Sequence 3357, Ap
116	6	3.2	615	6	US-10-953-349-18285	Sequence 18285, A
117	6	3.2	616	6	US-10-953-349-38776	Sequence 38776, A
118	6	3.2	626	6	US-10-953-349-38454	Sequence 38454, A
119	6	3.2	631	6	US-10-953-349-27089	Sequence 27089, A
120	6	3.2	640	6	US-10-953-349-35681	Sequence 35681, A
121	6	3.2	642	7	US-11-217-529-78002	Sequence 78002, A
c 122	6	3.2	669	7	US-11-257-062-37	Sequence 37, Appl
c 123	6	3.2	669	7	US-11-217-529-174016	Sequence 174016,
124	6	3.2	677	7	US-11-136-524-20	Sequence 20, Appl
125	6	3.2	684	7	US-11-217-529-77983	Sequence 77983, A
126	6	3.2	696	6	US-10-953-349-5986	Sequence 5986, Ap
127	6	3.2	699	6	US-10-471-571A-4419	Sequence 4419, Ap
128	6	3.2	701	6	US-10-953-349-36866	Sequence 36866, A
c 129	6	3.2	702	6	US-10-953-349-40119	Sequence 40119, A
130	6	3.2	705	6	US-10-953-349-25288	Sequence 25288, A
c 131	6	3.2	718	6	US-10-953-349-4712	Sequence 4712, Ap
c 132	6	3.2	728	6	US-10-953-349-7939	Sequence 7939, Ap
c 133	6	3.2	732	6	US-10-471-571A-1157	Sequence 1157, Ap
134	6	3.2	735	7	US-11-217-529-77210	Sequence 77210, A
135	6	3.2	735	7	US-11-217-529-80568	Sequence 80568, A
136	6	3.2	738	7	US-11-217-529-3017	Sequence 3017, Ap
c 137	6	3.2	747	6	US-10-953-349-4053	Sequence 4053, Ap
c 138	6	3.2	766	6	US-10-953-349-9488	Sequence 9488, Ap
c 139	6	3.2	766	6	US-10-953-349-16518	Sequence 16518, A
c 140	6	3.2	776	6	US-10-953-349-10625	Sequence 10625, A
141	6	3.2	789	6	US-10-471-571A-2447	Sequence 2447, Ap
142	6	3.2	789	7	US-11-217-529-76157	Sequence 76157, A
c 143	6	3.2	798	7	US-11-217-529-1769	Sequence 1769, Ap
c 144	6	3.2	806	6	US-10-953-349-19195	Sequence 19195, A
145	6	3.2	810	7	US-11-217-529-3877	Sequence 3877, Ap
146	6	3.2	822	6	US-10-953-349-37373	Sequence 37373, A
147	6	3.2	824	6	US-10-488-619-1821	Sequence 1821, Ap
c 148	6	3.2	829	6	US-10-953-349-37645	Sequence 37645, A
c 149	6	3.2	831	6	US-10-471-571A-789	Sequence 789, App
150	6	3.2	835	6	US-10-953-349-13657	Sequence 13657, A
151	6	3.2	849	7	US-11-217-529-80730	Sequence 80730, A
c 152	6	3.2	861	6	US-10-471-571A-4551	Sequence 4551, Ap
153	6	3.2	874	6	US-10-505-928-248	Sequence 248, App
154	6	3.2	878	6	US-10-953-349-6367	Sequence 6367, Ap
c 155	6	3.2	879	6	US-10-471-571A-1881	Sequence 1881, Ap
c 156	6	3.2	888	6	US-10-953-349-29674	Sequence 29674, A
157	6	3.2	888	7	US-11-122-986-274	Sequence 274, App
158	6	3.2	888	7	US-11-122-986-276	Sequence 276, App
c 159	6	3.2	897	6	US-10-953-349-3055	Sequence 3055, Ap
160	6	3.2	900	6	US-10-471-571A-4209	Sequence 4209, Ap
c 161	6	3.2	932	6	US-10-953-349-9647	Sequence 9647, Ap
162	6	3.2	941	6	US-10-473-173-42	Sequence 42, Appl
163	6	3.2	943	6	US-10-953-349-7027	Sequence 7027, Ap
c 164	6	3.2	950	6	US-10-953-349-28095	Sequence 28095, A
165	6	3.2	952	6	US-10-505-928-768	Sequence 768, App
c 166	6	3.2	956	6	US-10-953-349-3171	Sequence 3171, Ap
c 167	6	3.2	960	7	US-11-258-392-1	Sequence 1, Appli
c 168	6	3.2	1001	7	US-11-190-942-2	Sequence 2, Appli
169	6	3.2	1003	7	US-11-226-605-64	Sequence 64, Appl
170	6	3.2	1006	6	US-10-953-349-4371	Sequence 4371, Ap
171	6	3.2	1011	6	US-10-953-349-38632	Sequence 38632, A
172	6	3.2	1012	6	US-10-953-349-24147	Sequence 24147, A
c 173	6	3.2	1032	6	US-10-973-274-1	Sequence 1, Appli
174	6	3.2	1032	7	US-11-217-529-81929	Sequence 81929, A
c 175	6	3.2	1032	7	US-11-217-529-195605	Sequence 195605,
c 176	6	3.2	1032	7	US-11-217-529-195606	Sequence 195606,
c 177	6	3.2	1032	7	US-11-217-529-195650	Sequence 195650,
c 178	6	3.2	1032	7	US-11-217-529-195651	Sequence 195651,
179	6	3.2	1041	6	US-10-471-571A-1463	Sequence 1463, Ap
180	6	3.2	1048	6	US-10-953-349-36989	Sequence 36989, A
181	6	3.2	1050	7	US-11-217-529-2868	Sequence 2868, Ap
c 182	6	3.2	1056	6	US-10-471-571A-1151	Sequence 1151, Ap
183	6	3.2	1059	7	US-11-217-529-2297	Sequence 2297, Ap
184	6	3.2	1064	6	US-10-953-349-16601	Sequence 16601, A
185	6	3.2	1068	7	US-11-217-529-3134	Sequence 3134, Ap
186	6	3.2	1068	7	US-11-217-529-77750	Sequence 77750, A
c 187	6	3.2	1068	7	US-11-217-529-82320	Sequence 82320, A
188	6	3.2	1071	7	US-11-217-529-1718	Sequence 1718, Ap
c 189	6	3.2	1074	7	US-11-217-529-81112	Sequence 81112, A
c 190	6	3.2	1083	7	US-11-217-529-77116	Sequence 77116, A
c 191	6	3.2	1083	7	US-11-217-529-78870	Sequence 78870, A
192	6	3.2	1106	6	US-10-953-349-37010	Sequence 37010, A
c 193	6	3.2	1107	6	US-10-953-349-31177	Sequence 31177, A
c 194	6	3.2	1107	6	US-10-471-571A-1935	Sequence 1935, Ap
195	6	3.2	1110	7	US-11-217-529-80913	Sequence 80913, A
196	6	3.2	1113	7	US-11-217-529-82444	Sequence 82444, A
197	6	3.2	1122	7	US-11-217-529-77176	Sequence 77176, A
c 198	6	3.2	1128	7	US-11-217-529-1068	Sequence 1068, Ap
c 199	6	3.2	1129	6	US-10-953-349-36589	Sequence 36589, A
c 200	6	3.2	1130	6	US-10-953-349-4332	Sequence 4332, Ap

ALIGNMENTS

```
RESULT 1
US-10-322-836-19
; Sequence 19, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 528
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
```

; NAME/KEY: CDS
; LOCATION: (1)...(525)
JS-10-322-836-19

Alignment Scores:
Pred. No.: 7.2 Length: 528
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.3% Indels: 0
DB: 6 Gaps: 0

JS-10-821-670A-102 (1-187) x US-10-322-836-19 (1-528)

Qy 21 GlnLysAlaArgGlnThrLeuGlu 28
||||||||||||||||||||||||||
Db 61 CAAAAAGCCAGGCAGACCCTGGAG 84

RESULT 2
JS-10-322-836-17
; Sequence 17, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(876)
JS-10-322-836-17

Alignment Scores:
Pred. No.: 11.6 Length: 879
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.3% Indels: 0
DB: 6 Gaps: 0

JS-10-821-670A-102 (1-187) x US-10-322-836-17 (1-879)

Qy 21 GlnLysAlaArgGlnThrLeuGlu 28
||||||||||||||||||||||||||
Db 61 CAAAAAGCCAGGCAGACCCTGGAG 84

RESULT 3
JS-10-322-836-15
; Sequence 15, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1014)
US-10-322-836-15

Alignment Scores:
Pred. No.: 13.3 Length: 1017
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.3% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-102 (1-187) x US-10-322-836-15 (1-1017)

Qy 21 GlnLysAlaArgGlnThrLeuGlu 28
||||||||||||||||||||||||||
Db 61 CAAAAAGCCAGGCAGACCCTGGAG 84

RESULT 4
US-10-322-836-27
; Sequence 27, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1245)
US-10-322-836-27

Alignment Scores:
Pred. No.: 16.1 Length: 1248
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.3% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-102 (1-187) x US-10-322-836-27 (1-1248)

Qy 21 GlnLysAlaArgGlnThrLeuGlu 28
||||||||||||||||||||||||||
Db 781 CAAAAAGCCAGGCAGACCCTGGAG 804

RESULT 5
US-10-322-836-5

Sequence 5, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 1293
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1290)
S-10-322-836-5

lignment Scores:

red. No.:	16.7	Length:	1293
core:	8.00	Matches:	8
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	4.3%	Indels:	0
B:	6	Gaps:	0

S-10-821-670A-102 (1-187) x US-10-322-836-5 (1-1293)

```
y         21 GlnLysAlaArgGlnThrLeuGlu 28
             |||||||||||||||||||||||||
b        826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

ESULT 6
S-10-322-836-41
Sequence 41, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 41
LENGTH: 1317
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1314)
S-10-322-836-41

lignment Scores:

red. No.:	17	Length:	1317
core:	8.00	Matches:	8
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-322-836-41 (1-1317)

```
Qy         21 GlnLysAlaArgGlnThrLeuGlu 28
              |||||||||||||||||||||||||
Db         61 CAAAAAGCCAGGCAGACCCTGGAG 84
```

RESULT 7
US-10-322-836-39
; Sequence 39, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1452)
US-10-322-836-39

Alignment Scores:

Pred. No.:	18.6	Length:	1455
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-322-836-39 (1-1455)

```
Qy         21 GlnLysAlaArgGlnThrLeuGlu 28
              |||||||||||||||||||||||||
Db         61 CAAAAAGCCAGGCAGACCCTGGAG 84
```

RESULT 8
US-10-322-836-25
; Sequence 25, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 1599
; TYPE: DNA

```
   ORGANISM: Homo sapien
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)...(1596)
IS-10-322-836-25

Alignment Scores:
Pred. No.:                20.3          Length:        1599
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              4.3%          Indels:        0
DB:                       6             Gaps:          0

IS-10-821-670A-102 (1-187) x US-10-322-836-25 (1-1599)

Qy          21 GlnLysAlaArgGlnThrLeuGlu 28
               ||||||||||||||||||||||||
Db         781 CAAAAAGCCAGGCAGACCCTGGAG 804

RESULT 9
IS-10-322-836-3
; Sequence 3, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 1644
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1641)
IS-10-322-836-3

Alignment Scores:
Pred. No.:                20.9          Length:        1644
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              4.3%          Indels:        0
DB:                       6             Gaps:          0

IS-10-821-670A-102 (1-187) x US-10-322-836-3 (1-1644)

Qy          21 GlnLysAlaArgGlnThrLeuGlu 28
               ||||||||||||||||||||||||
Db         826 CAAAAAGCCAGGCAGACCCTGGAG 849

RESULT 10
IS-10-322-836-23
; Sequence 23, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 1737
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1734)
US-10-322-836-23

Alignment Scores:
Pred. No.:                22            Length:        1737
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              4.3%          Indels:        0
DB:                       6             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-322-836-23 (1-1737)

Qy          21 GlnLysAlaArgGlnThrLeuGlu 28
               ||||||||||||||||||||||||
Db         781 CAAAAAGCCAGGCAGACCCTGGAG 804

RESULT 11
US-10-322-836-1
; Sequence 1, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1782
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1779)
US-10-322-836-1

Alignment Scores:
Pred. No.:                22.5          Length:        1782
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              4.3%          Indels:        0
DB:                       6             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-322-836-1 (1-1782)

Qy          21 GlnLysAlaArgGlnThrLeuGlu 28
               ||||||||||||||||||||||||
Db         826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

```
ESULT 12
S-10-953-349-4560
 Sequence 4560, Application US/10953349
 Publication No. US20060107345A1
 GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION:  ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE:  2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 4560
   LENGTH: 2021
   TYPE: DNA
   ORGANISM: Arabidopsis thaliana
S-10-953-349-4560

lignment Scores:
red. No.:               25.3          Length:        2021
core:                   8.00          Matches:       8
ercent Similarity:      100.0%        Conservative:  0
est Local Similarity:   100.0%        Mismatches:    0
uery Match:             4.3%          Indels:        0
B:                      6             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-953-349-4560 (1-2021)

y          89 ThrLeuCysLeuSerSerIleTyr 96
              |||||||||||||||||||||||||
b        1004 ACCTTGTGTTTGTCTTCTATCTAT 1027

ESULT 13
S-10-322-836-45
 Sequence 45, Application US/10322836
 Publication No. US20060090212A1
 GENERAL INFORMATION:
  APPLICANT: Turner, Alexander C., Jr.
  APPLICANT:  Zambrowicz, Brian
  APPLICANT:  Nehls, Michael
  APPLICANT:  Freidrich, Glenn A.
  APPLICANT:  Sands, Arthur T.
  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
  TITLE OF INVENTION:  ENCODED THEREBY
  FILE REFERENCE: 8535-0037-999
  CURRENT APPLICATION NUMBER: US/10/322,836
  CURRENT FILING DATE:  2002-12-18
  PRIOR APPLICATION NUMBER: US/09/579,114
  PRIOR FILING DATE: 2000-05-25
  NUMBER OF SEQ ID NOS: 50
  SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 45
   LENGTH: 2037
   TYPE: DNA
   ORGANISM: Homo sapien
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)...(2034)
S-10-322-836-45

lignment Scores:
red. No.:               25.5          Length:        2037
core:                   8.00          Matches:       8
ercent Similarity:      100.0%        Conservative:  0
est Local Similarity:   100.0%        Mismatches:    0
uery Match:             4.3%          Indels:        0
B:                      6             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-322-836-45 (1-2037)

y          21 GlnLysAlaArgGlnThrLeuGlu 28
              ||||||||||||||||||||||||||
Db        781 CAAAAAGCCAGGCAGACCCTGGAG 804

RESULT 14
US-10-322-836-33
; Sequence 33, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
;   LENGTH: 2082
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(2079)
US-10-322-836-33

Alignment Scores:
Pred. No.:              26            Length:        2082
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.3%          Indels:        0
DB:                     6             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-322-836-33 (1-2082)

Qy         21 GlnLysAlaArgGlnThrLeuGlu 28
              ||||||||||||||||||||||||||
Db        826 CAAAAAGCCAGGCAGACCCTGGAG 849

RESULT 15
US-10-322-836-43
; Sequence 43, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 43
;   LENGTH: 2175
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(2172)
US-10-322-836-43

Alignment Scores:
```

Pred. No.:	27.1	Length:	2175
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-322-836-43 (1-2175)

```
Qy         21 GlnLysAlaArgGlnThrLeuGlu 28
              ||||||||||||||||||||||||
Db        781 CAAAAAGCCAGGCAGACCCTGGAG 804
```

RESULT 16
US-10-322-836-31
; Sequence 31, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2217)
US-10-322-836-31

Alignment Scores:			
Pred. No.:	27.6	Length:	2220
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-322-836-31 (1-2220)

```
Qy         21 GlnLysAlaArgGlnThrLeuGlu 28
              ||||||||||||||||||||||||
Db        826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

RESULT 17
US-10-530-792A-1
; Sequence 1, Application US/10530792A
; Publication No. US20060105340A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-008
; CURRENT APPLICATION NUMBER: US/10/530,792A
; CURRENT FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-530-792A-1

Alignment Scores:			
Pred. No.:	45.6	Length:	3791
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-530-792A-1 (1-3791)

```
Qy         76 GlySerCysLeuAlaSerArgLys 83
              |||||||||||||||||||||||
Db        231 GGGTCATGCCTGGCCAGCAGAAAG 254
```

RESULT 18
US-11-217-529-3234
; Sequence 3234, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3234
; LENGTH: 6663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3234

Alignment Scores:			
Pred. No.:	77.4	Length:	6663
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.3%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-3234 (1-6663)

```
Qy        129 ThrAlaIleAspGluLeuLeuGln 136
              ||||||||||||||||||||||||
Db       1729 ACTGCCATTGATGAACTATTACAA 1752
```

RESULT 19
US-10-488-619-837
; Sequence 837, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 837

LENGTH: 331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(331)
OTHER INFORMATION: n is g, c, a or t
S-10-488-619-837

lignment Scores:

red. No.:	51.6	Length:	331
core:	7.00	Matches:	7
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.7%	Indels:	0
B:	6	Gaps:	0

S-10-821-670A-102 (1-187) x US-10-488-619-837 (1-331)

```
y         76 GlySerCysLeuAlaSerArg 82
             ||||||||||||||||||||
b        108 GGCTCCTGCCTGGCCTCTAGG 128
```

ESULT 20
S-10-953-349-25251/c
Sequence 25251, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 25251
LENGTH: 582
TYPE: DNA
ORGANISM: Triticum aestivum
S-10-953-349-25251

lignment Scores:

red. No.:	87.5	Length:	582
core:	7.00	Matches:	7
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.7%	Indels:	0
B:	6	Gaps:	0

S-10-821-670A-102 (1-187) x US-10-953-349-25251 (1-582)

```
y        129 ThrAlaIleAspGluLeuLeu 135
             ||||||||||||||||||||
b         88 ACGGCCATAGATGAGTTGCTG 68
```

ESULT 21
S-11-217-529-81369
Sequence 81369, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 81369
LENGTH: 660
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-81369

Alignment Scores:

Pred. No.:	98.4	Length:	660
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-81369 (1-660)

```
Qy         96 TyrGluAspLeuLysMetTyr 102
              ||||||||||||||||||||
Db        124 TATGAAGACCTGAAGATGTAT 144
```

RESULT 22
US-10-488-619-2648/c
Sequence 2648, Application US/10488619
Publication No. US20060099578A1
GENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
FILE REFERENCE: 98-01 WO
CURRENT APPLICATION NUMBER: US/10/488,619
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2648
LENGTH: 704
TYPE: DNA
ORGANISM: Mus musculus
US-10-488-619-2648

Alignment Scores:

Pred. No.:	105	Length:	704
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-488-619-2648 (1-704)

```
Qy        134 LeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||
Db        154 CTTCTCCAAGCTCTGAATGTC 134
```

RESULT 23
US-10-953-349-4834
Sequence 4834, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4834
LENGTH: 906
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-953-349-4834

```
Alignment Scores:
Pred. No.:                132             Length:         906
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.7%            Indels:         0
DB:                       6               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-953-349-4834 (1-906)

Qy         65 LeuAlaSerArgGluIleSer 71
              |||||||||||||||||||||
Db        681 TTGGCTAGCAGAGAAATCAGT 701

RESULT 24
US-11-217-529-5460
; Sequence 5460, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5460
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-5460

Alignment Scores:
Pred. No.:                134             Length:         921
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.7%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x US-11-217-529-5460 (1-921)

Qy         170 PheArgIleArgAlaValThr 176
               |||||||||||||||||||||
Db         867 TTTCGAATTCGAGCGGTTACC 887

RESULT 25
US-11-311-754-5
; Sequence 5, Application US/11311754
; Publication No. US20060099635A1
; GENERAL INFORMATION:
;  APPLICANT: Vincent Ling
;  APPLICANT:  Kyriaki Dunussi-Joannopoulos
;  TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: GNN-007
;  CURRENT APPLICATION NUMBER: US/11/311,754
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: US/09/667,135
;  PRIOR FILING DATE: 2000-09-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 953
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (24)..(950)
US-11-311-754-5

Alignment Scores:
Pred. No.:                139             Length:         953
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.7%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x US-11-311-754-5 (1-953)

Qy         146 ProGlnAsnSerSerLeuGlu 152
               |||||||||||||||||||||
Db         225 CCACAGAACAGCTCCTTGGAA 245

RESULT 26
US-10-953-349-28356/c
; Sequence 28356, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28356
;   LENGTH: 994
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-28356

Alignment Scores:
Pred. No.:                144             Length:         994
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.7%            Indels:         0
DB:                       6               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-953-349-28356 (1-994)

Qy          82 ArgLysThrSerPheMetThr 88
               |||||||||||||||||||||
Db         340 AGGAAGACCAGCTTCATGACG 320

RESULT 27
US-10-560-723-79/c
; Sequence 79, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
;  APPLICANT: EXONHIT THERAPEUTICALS
;  TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
;  TITLE OF INVENTION:  CANCER THERAPY AND DIAGNOSIS
;  FILE REFERENCE: B0213WO
;  CURRENT APPLICATION NUMBER: US/10/560,723
;  CURRENT FILING DATE:  2005-12-15
;  NUMBER OF SEQ ID NOS: 185
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
;   LENGTH: 997
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-560-723-79

Alignment Scores:
Pred. No.:                145             Length:         997
```

```
core:                  7.00          Matches:       7
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            3.7%          Indels:        0
B:                     6             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-560-723-79 (1-997)

y         76 GlySerCysLeuAlaSerArg 82
             ||||||||||||||||||||
b        839 GGCTCCTGCCTGGCCTCTAGG 819

ESULT 28
S-10-953-349-39566
 Sequence 39566, Application US/10953349
 Publication No. US20060107345A1
 GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION:  ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE:  2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 39566
   LENGTH: 1062
   TYPE: DNA
   ORGANISM: Zea mays subsp. mays
S-10-953-349-39566

lignment Scores:
red. No.:              154           Length:        1062
core:                  7.00          Matches:       7
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            3.7%          Indels:        0
B:                     6             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-953-349-39566 (1-1062)

y         88 ThrThrLeuCysLeuSerSer 94
             ||||||||||||||||||||
b        188 ACTACGTTGTGTCTGAGTTCA 208

ESULT 29
S-10-953-349-17414/c
 Sequence 17414, Application US/10953349
 Publication No. US20060107345A1
 GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION:  ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE:  2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 17414
   LENGTH: 1202
   TYPE: DNA
   ORGANISM: Glycine max
S-10-953-349-17414

lignment Scores:
red. No.:              173           Length:        1202
core:                  7.00          Matches:       7
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            3.7%          Indels:        0
B:                     6             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-953-349-17414 (1-1202)

Qy        161 IleLysLeuCysIleLeuLeu 167
             |||||||||||||||||||||
Db        882 ATTAAACTCTGTATTTTACTT 862

RESULT 30
US-10-953-349-24555/c
; Sequence 24555, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24555
;   LENGTH: 1313
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-24555

Alignment Scores:
Pred. No.:             187           Length:        1313
Score:                 7.00          Matches:       7
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           3.7%          Indels:        0
DB:                    6             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-953-349-24555 (1-1313)

Qy        142 SerValThrValProGlnAsn 148
             ||||||||||||||||||||
Db        199 AGTGTTACTGTTCCCCAAAAC 179

RESULT 31
US-10-953-349-35965/c
; Sequence 35965, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35965
;   LENGTH: 1454
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-35965

Alignment Scores:
Pred. No.:             206           Length:        1454
Score:                 7.00          Matches:       7
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           3.7%          Indels:        0
DB:                    6             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-953-349-35965 (1-1454)

Qy        162 LysLeuCysIleLeuLeuHis 168
             ||||||||||||||||||||
Db        575 AAGCTCTGTATTCTGCTACAT 555

RESULT 32
US-10-953-349-36433
```

; Sequence 36433, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36433
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-36433

Alignment Scores:

Pred. No.:	210	Length:	1483
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-953-349-36433 (1-1483)

Qy 11 ThrLeuLeuArgAlaIleSer 17
||||||||||||||||||||
Db 1092 ACACTCTTGCGAGCCATCTCT 1112

RESULT 33
US-10-953-349-17700/c
; Sequence 17700, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17700
; LENGTH: 1538
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17700

Alignment Scores:

Pred. No.:	217	Length:	1538
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-953-349-17700 (1-1538)

Qy 149 SerSerLeuGluGluProAsp 155
||||||||||||||||||||
Db 368 TCTTCACTTGAAGAACCCGAT 348

RESULT 34
US-10-953-349-24275/c
; Sequence 24275, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24275
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-24275

Alignment Scores:

Pred. No.:	233	Length:	1660
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-953-349-24275 (1-1660)

Qy 162 LysLeuCysIleLeuLeuHis 168
||||||||||||||||||||
Db 965 AAGTTGTGTATTCTGTTGCAC 945

RESULT 35
US-11-217-529-174380/c
; Sequence 174380, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174380
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174380

Alignment Scores:

Pred. No.:	247	Length:	1761
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-174380 (1-1761)

Qy 12 LeuLeuArgAlaIleSerAsn 18
||||||||||||||||||||
Db 307 TTATTACGGGCGATATCAAAT 287

RESULT 36
US-11-251-465-7/c
; Sequence 7, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The

```
  TITLE OF INVENTION:  Same, Useful In The Treatment Of Joint Degenerative And
  TITLE OF INVENTION:  Inflammatory Diseases
  FILE REFERENCE: P30,172-A USA
  CURRENT APPLICATION NUMBER: US/11/251,465
  CURRENT FILING DATE:  2005-10-14
  PRIOR APPLICATION NUMBER: 60/619,384
  PRIOR FILING DATE: 2004-10-15
  NUMBER OF SEQ ID NOS: 880
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 7
   LENGTH: 1804
   TYPE: DNA
   ORGANISM: Homo sapiens
S-11-251-465-7

lignment Scores:
red. No.:               252           Length:        1804
core:                   7.00          Matches:       7
ercent Similarity:      100.0%        Conservative:  0
est Local Similarity:   100.0%        Mismatches:    0
uery Match:             3.7%          Indels:        0
B:                      7             Gaps:          0

S-10-821-670A-102 (1-187) x US-11-251-465-7 (1-1804)

y        134 LeuLeuGlnAlaLeuAsnVal 140
             |||||||||||||||||||
b       1109 CTCCTGCAGGCTCTCAACGTG 1089

ESULT 37
S-11-311-754-27
 Sequence 27, Application US/11311754
 Publication No. US20060099635A1
 GENERAL INFORMATION:
  APPLICANT: Vincent Ling
  APPLICANT:  Kyriaki Dunussi-Joannopoulos
  TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
  FILE REFERENCE: GNN-007
  CURRENT APPLICATION NUMBER: US/11/311,754
  CURRENT FILING DATE:  2005-12-19
  PRIOR APPLICATION NUMBER: US/09/667,135
  PRIOR FILING DATE: 2000-09-21
  NUMBER OF SEQ ID NOS: 38
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 27
   LENGTH: 1831
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: hGL50-mIgG2am nucleotide sequence
S-11-311-754-27

lignment Scores:
red. No.:               256           Length:        1831
core:                   7.00          Matches:       7
ercent Similarity:      100.0%        Conservative:  0
est Local Similarity:   100.0%        Mismatches:    0
uery Match:             3.7%          Indels:        0
B:                      7             Gaps:          0

S-10-821-670A-102 (1-187) x US-11-311-754-27 (1-1831)

y        146 ProGlnAsnSerSerLeuGlu 152
             |||||||||||||||||||
b        237 CCACAGAACAGCTCCTTGGAA 257

ESULT 38
S-10-505-928-693
 Sequence 693, Application US/10505928
 Publication No. US20060088532A1
 GENERAL INFORMATION:
  APPLICANT: Ludwig Institute for Cancer Research et al.
  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 693
;   LENGTH: 1868
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-693

Alignment Scores:
Pred. No.:              261           Length:        1868
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            3.7%          Indels:        0
DB:                     6             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-505-928-693 (1-1868)

Qy         44 LysAspLysThrSerThrVal 50
              |||||||||||||||||||
Db        708 AAAGACAAAACTTCAACAGTG 728

RESULT 39
US-10-953-349-11252/c
; Sequence 11252, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11252
;   LENGTH: 1914
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-11252

Alignment Scores:
Pred. No.:              267           Length:        1914
Score:                  7.00          Matches:       7
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            3.7%          Indels:        0
DB:                     6             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-953-349-11252 (1-1914)

Qy         51 GluAlaCysLeuProLeuGlu 57
              |||||||||||||||||||
Db        932 GAAGCCTGTCTTCCTCTGGAA 912

RESULT 40
US-11-293-697-1094/c
; Sequence 1094, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
```

```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1094
;   LENGTH: 2036
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1094

Alignment Scores:
Pred. No.:                283             Length:         2036
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.7%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x US-11-293-697-1094 (1-2036)

Qy          50 ValGluAlaCysLeuProLeu 56
               |||||||||||||||||||||
Db         582 GTTGAAGCTTGTCTCCCACTT 562

RESULT 41
US-11-217-529-77609/c
; Sequence 77609, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77609
;   LENGTH: 2037
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77609

Alignment Scores:
Pred. No.:                283             Length:         2037
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.7%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x US-11-217-529-77609 (1-2037)

Qy          81 SerArgLysThrSerPheMet 87
               |||||||||||||||||||||
Db         314 TCTCGCAAAACTAGCTTTATG 294

RESULT 42
US-11-217-529-2489
; Sequence 2489, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2489
;   LENGTH: 2241
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-2489

Alignment Scores:
Pred. No.:                309             Length:         2241
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.7%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x US-11-217-529-2489 (1-2241)

Qy          96 TyrGluAspLeuLysMetTyr 102
               |||||||||||||||||||
Db        1705 TATGAAGACTTGAAGATGTAC 1725

RESULT 43
US-11-293-697-507
; Sequence 507, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 507
;   LENGTH: 2275
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-507

Alignment Scores:
Pred. No.:                314             Length:         2275
Score:                    7.00            Matches:        7
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.7%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x US-11-293-697-507 (1-2275)

Qy          62 GluSerCysLeuAlaSerArg 68
               |||||||||||||||||||||
Db        1307 GAGAGCTGCTTGGCTTCAAGG 1327

RESULT 44
US-10-511-937-649/c
; Sequence 649, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
```

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 649
LENGTH: 2315
TYPE: DNA
ORGANISM: Homo sapiens
S-10-511-937-649

lignment Scores:

red. No.:	319	Length:	2315
core:	7.00	Matches:	7
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.7%	Indels:	0
B:	6	Gaps:	0

S-10-821-670A-102 (1-187) x US-10-511-937-649 (1-2315)

```
y        147 GlnAsnSerSerLeuGluGlu 153
             ||||||||||||||||||||
b       1460 CAGAATTCTTCATTAGAGGAA 1440
```

ESULT 45
S-11-293-697-753
Sequence 753, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 753
LENGTH: 2662
TYPE: DNA
ORGANISM: Homo sapiens
S-11-293-697-753

lignment Scores:

red. No.:	363	Length:	2662
core:	7.00	Matches:	7
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.7%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-102 (1-187) x US-11-293-697-753 (1-2662)

```
y        139 AsnValAsnSerValThrVal 145
             ||||||||||||||||||||
b       1505 AATGTGAATTCAGTAACTGTG 1525
```

ESULT 46
S-11-217-529-82539
Sequence 82539, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82539
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82539

Alignment Scores:

Pred. No.:	382	Length:	2805
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-82539 (1-2805)

```
Qy        130 AlaIleAspGluLeuLeuGln 136
              ||||||||||||||||||||
Db       1738 GCCATTGATGAATTATTACAA 1758
```

RESULT 47
US-11-293-697-74/c
; Sequence 74, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-74

Alignment Scores:

Pred. No.:	394	Length:	2905
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-293-697-74 (1-2905)

```
Qy        146 ProGlnAsnSerSerLeuGlu 152
              ||||||||||||||||||||
Db        246 CCGCAAAACTCTTCGCTGGAG 226
```

RESULT 48
US-11-293-697-1397
; Sequence 1397, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1397
; LENGTH: 3294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1397

Alignment Scores:

Pred. No.:	444	Length:	3294
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-293-697-1397 (1-3294)

```
Qy         63 SerCysLeuAlaSerArgGlu 69
              |||||||||||||||||||||
Db       1271 AGTTGCTTAGCAAGCAGGGAA 1291
```

RESULT 49
US-10-505-928-814/c
; Sequence 814, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 814
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-814

Alignment Scores:

Pred. No.:	477	Length:	3558
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-505-928-814 (1-3558)

```
Qy         79 LeuAlaSerArgLysThrSer 85
              |||||||||||||||||||||
Db        460 CTTGCAAGCCGTAAAACTTCT 440
```

RESULT 50
US-11-217-529-1506/c
; Sequence 1506, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1506
; LENGTH: 7422
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1506

Alignment Scores:

Pred. No.:	949	Length:	7422
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.7%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-1506 (1-7422)

```
Qy         53 CysLeuProLeuGluLeuThr 59
              |||||||||||||||||||||
Db        685 TGTCTGCCGTTAGAGTTAACC 665
```

RESULT 51
US-11-266-409-9
; Sequence 9, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
; APPLICANT: SUZUMURA, AKIO
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: 279847US40
; CURRENT APPLICATION NUMBER: US/11/266,409
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: US 60/624,851
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-266-409-9

Alignment Scores:

Pred. No.:	45.1	Length:	22
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-266-409-9 (1-22)

```
Qy         98 AspLeuLysMetTyrGln 103
              ||||||||||||||||||
Db          1 GACTTGAAGATGTACCAG 18
```

RESULT 52
US-11-217-529-36402
; Sequence 36402, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO

```
  APPLICANT:  FUJIMURA, TOMOKO
; APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 36402
   LENGTH: 25
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-36402

lignment Scores:
red. No.:               50.9          Length:        25
core:                   6.00          Matches:       6
ercent Similarity:      100.0%        Conservative:  0
est Local Similarity:   100.0%        Mismatches:    0
uery Match:             3.2%          Indels:        0
B:                      7             Gaps:          0

S-10-821-670A-102 (1-187) x US-11-217-529-36402 (1-25)

y         46 LysThrSerThrValGlu 51
             |||||||||||||||||
b          3 AAAACCTCCACCGTAGAG 20

ESULT 53
S-11-217-529-87245
 Sequence 87245, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 87245
   LENGTH: 25
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-87245

lignment Scores:
red. No.:               50.9          Length:        25
core:                   6.00          Matches:       6
ercent Similarity:      100.0%        Conservative:  0
est Local Similarity:   100.0%        Mismatches:    0
uery Match:             3.2%          Indels:        0
B:                      7             Gaps:          0

S-10-821-670A-102 (1-187) x US-11-217-529-87245 (1-25)

y         47 ThrSerThrValGluAla 52
             |||||||||||||||||
b          3 ACCTCTACTGTGGAGGCA 20

ESULT 54
S-11-217-529-88955/c
 Sequence 88955, Application US/11217529
 Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88955
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-88955

Alignment Scores:
Pred. No.:              50.9          Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            3.2%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-102 (1-187) x US-11-217-529-88955 (1-25)

Qy         80 AlaSerArgLysThrSer 85
              |||||||||||||||||
Db         23 GCTTCAAGAAAGACATCC 6

RESULT 55
US-11-217-529-109690
; Sequence 109690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 109690
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-109690

Alignment Scores:
Pred. No.:              50.9          Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            3.2%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-102 (1-187) x US-11-217-529-109690 (1-25)

Qy        151 LeuGluGluProAspPhe 156
              |||||||||||||||||
Db          5 CTTGAGGAACCCGATTTT 22
```

RESULT 56
US-11-217-529-148883
; Sequence 148883, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-148883

Alignment Scores:

Pred. No.:	50.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-148883 (1-25)

```
Qy          91 CysLeuSerSerIleTyr 96
               |||||||||||||||||
Db           4 TGCCTTTCCTCTATTTAT 21
```

RESULT 57
US-11-217-529-162336
; Sequence 162336, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162336
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-162336

Alignment Scores:

Pred. No.:	50.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-162336 (1-25)

```
Qy          87 MetThrThrLeuCysLeu 92
               |||||||||||||||||
Db           4 ATGACCACCCTTTGCCTC 21
```

RESULT 58
US-11-217-529-162342
; Sequence 162342, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162342
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-162342

Alignment Scores:

Pred. No.:	50.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-162342 (1-25)

```
Qy          87 MetThrThrLeuCysLeu 92
               |||||||||||||||||
Db           3 ATGACCACCCTTTGCCTC 20
```

RESULT 59
US-11-217-529-184372/c
; Sequence 184372, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 184372
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-184372

Alignment Scores:

Pred. No.:	50.9	Length:	25
Score:	6.00	Matches:	6

```
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            3.2%            Indels:        0
B:                     7               Gaps:          0

S-10-821-670A-102 (1-187) x US-11-217-529-184372 (1-25)

y         10 GlnThrLeuLeuArgAla 15
             |||||||||||||||||
b         21 CAGACTCTTCTGAGAGCC 4

ESULT 60
S-11-143-642-246/c
 Sequence 246, Application US/11143642
 Publication No. US20060099610A1
 GENERAL INFORMATION:
  APPLICANT: Jukka T. SALONEN et al.
  TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF ACUTE MYOCARDIAL INFARCTIC
  FILE REFERENCE: 0933-0245PUS1
  CURRENT APPLICATION NUMBER: US/11/143,642
  CURRENT FILING DATE:  2005-06-03
  NUMBER OF SEQ ID NOS: 2039
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 246
   LENGTH: 51
   TYPE: DNA
   ORGANISM: Homo sapiens
S-11-143-642-246

lignment Scores:
red. No.:              99.2            Length:        51
core:                  6.00            Matches:       6
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            3.2%            Indels:        0
B:                     7               Gaps:          0

S-10-821-670A-102 (1-187) x US-11-143-642-246 (1-51)

y         79 LeuAlaSerArgLysThr 84
             ||||||||||||||||||
b         49 TTAGCAAGCAGGAAAACT 32

ESULT 61
S-11-296-092-22/c
 Sequence 22, Application US/11296092
 Publication No. US20060105427A1
 GENERAL INFORMATION:
  APPLICANT: Baker, Kevin
  APPLICANT:  Botstein,David
  APPLICANT:  Eaton,Dan
  APPLICANT:  Ferrara,Napoleone
  APPLICANT:  Filvaroff,Ellen
  APPLICANT:  Gerritsen,Mary
  APPLICANT:  Goddard,Audrey
  APPLICANT:  Godowski,Paul
  APPLICANT:  Grimaldi,Christopher
  APPLICANT:  Gurney,Austin
  APPLICANT:  Hillan,Kenneth
  APPLICANT:  Kljavin,Ivar
  APPLICANT:  Napier,Mary
  APPLICANT:  Roy,Margaret
  APPLICANT:  Tumas,Daniel
  APPLICANT:  Wood,William
  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
  FILE REFERENCE: P2548P1C1
  CURRENT APPLICATION NUMBER: US/11/296,092
  CURRENT FILING DATE:  2005-12-07
  PRIOR APPLICATION NUMBER: US/09/866,028
  PRIOR FILING DATE: 2001-05-25
  PRIOR APPLICATION NUMBER: 60/067,411
  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 22
;   LENGTH: 69
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-11-296-092-22

Alignment Scores:
Pred. No.:             132             Length:        69
Score:                 6.00            Matches:       6
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           3.2%            Indels:        0
DB:                    7               Gaps:          0

US-10-821-670A-102 (1-187) x US-11-296-092-22 (1-69)

Qy         92 LeuSerSerIleTyrGlu 97
              |||||||||||||||||
Db         27 CTTTCGTCCATCTATGAG 10

RESULT 62
US-10-525-817-154/c
; Sequence 154, Application US/10525817
; Publication No. US20060099592A1
; GENERAL INFORMATION:
;  APPLICANT: Nuevolution A/S
;  TITLE OF INVENTION: Enzymatic encoding
;  FILE REFERENCE: P912PC00
;  CURRENT APPLICATION NUMBER: US/10/525,817
;  CURRENT FILING DATE:  2005-02-25
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
;   LENGTH: 84
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially produced
US-10-525-817-154

Alignment Scores:
Pred. No.:             158             Length:        84
Score:                 6.00            Matches:       6
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           3.2%            Indels:        0
DB:                    6               Gaps:          0

US-10-821-670A-102 (1-187) x US-10-525-817-154 (1-84)

Qy         80 AlaSerArgLysThrSer 85
              |||||||||||||||||
Db         35 GCTTCTAGGAAGACTTCC 18
```

```
RESULT 63
US-10-525-817-155/c
; Sequence 155, Application US/10525817
; Publication No. US20060099592A1
; GENERAL INFORMATION:
;  APPLICANT: Nuevolution A/S
;  TITLE OF INVENTION: Enzymatic encoding
;  FILE REFERENCE: P912PC00
;  CURRENT APPLICATION NUMBER: US/10/525,817
;  CURRENT FILING DATE:  2005-02-25
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
;   LENGTH: 84
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially produced
US-10-525-817-155

Alignment Scores:
Pred. No.:                158             Length:         84
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.2%            Indels:         0
DB:                       6               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-525-817-155 (1-84)

Qy          80 AlaSerArgLysThrSer 85
               |||||||||||||||||
Db          35 GCTTCTAGGAAGACTTCC 18

RESULT 64
US-10-525-817-156/c
; Sequence 156, Application US/10525817
; Publication No. US20060099592A1
; GENERAL INFORMATION:
;  APPLICANT: Nuevolution A/S
;  TITLE OF INVENTION: Enzymatic encoding
;  FILE REFERENCE: P912PC00
;  CURRENT APPLICATION NUMBER: US/10/525,817
;  CURRENT FILING DATE:  2005-02-25
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
;   LENGTH: 84
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially produced
US-10-525-817-156

Alignment Scores:
Pred. No.:                158             Length:         84
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.2%            Indels:         0
DB:                       6               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-525-817-156 (1-84)

Qy          80 AlaSerArgLysThrSer 85
               |||||||||||||||||
Db          35 GCTTCTAGGAAGACTTCC 18

RESULT 65
US-10-525-817-157/c
; Sequence 157, Application US/10525817
; Publication No. US20060099592A1
; GENERAL INFORMATION:
;  APPLICANT: Nuevolution A/S
;  TITLE OF INVENTION: Enzymatic encoding
;  FILE REFERENCE: P912PC00
;  CURRENT APPLICATION NUMBER: US/10/525,817
;  CURRENT FILING DATE:  2005-02-25
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
;   LENGTH: 84
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially produced
US-10-525-817-157

Alignment Scores:
Pred. No.:                158             Length:         84
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.2%            Indels:         0
DB:                       6               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-525-817-157 (1-84)

Qy          80 AlaSerArgLysThrSer 85
               |||||||||||||||||
Db          35 GCTTCTAGGAAGACTTCC 18

RESULT 66
US-11-217-529-6033/c
; Sequence 6033, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6033
;   LENGTH: 93
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-6033

Alignment Scores:
Pred. No.:                174             Length:         93
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.2%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-102 (1-187) x US-11-217-529-6033 (1-93)

Qy         142 SerValThrValProGln 147
               |||||||||||||||||
Db          45 TCTGTGACCGTCCCCCAA 28

RESULT 67
US-10-471-571A-5635
; Sequence 5635, Application US/10471571A
; Publication No. US20060115490A1
```

```
 GENERAL INFORMATION:
  APPLICANT: CHIRON SpA
  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
  FILE REFERENCE: P026927WO
  CURRENT APPLICATION NUMBER: US/10/471,571A
  CURRENT FILING DATE:  2003-09-12
  PRIOR APPLICATION NUMBER: GB-0107661.1
  PRIOR FILING DATE: 2001-03-27
  NUMBER OF SEQ ID NOS: 5642
  SOFTWARE: SeqWin99, version 1.03
 SEQ ID NO 5635
   LENGTH: 114
   TYPE: DNA
   ORGANISM: Staphylococcus aureus
S-10-471-571A-5635

lignment Scores:
red. No.:              211           Length:        114
core:                  6.00          Matches:       6
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            3.2%          Indels:        0
B:                     6             Gaps:          0

S-10-821-670A-102 (1-187) x US-10-471-571A-5635 (1-114)

y         60 MetAsnGluSerCysLeu 65
             |||||||||||||||||
b         79 ATGAATGAAAGTTGCCTT 96

ESULT 68
S-11-217-529-81244
 Sequence 81244, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 81244
   LENGTH: 162
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-81244

lignment Scores:
red. No.:              293           Length:        162
core:                  6.00          Matches:       6
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            3.2%          Indels:        0
B:                     7             Gaps:          0

S-10-821-670A-102 (1-187) x US-11-217-529-81244 (1-162)

y         91 CysLeuSerSerIleTyr 96
             |||||||||||||||||
b         78 TGCCTTTCCTCTATTTAT 95

ESULT 69
S-10-471-571A-4689/c
 Sequence 4689, Application US/10471571A
 Publication No. US20060115490A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4689
;   LENGTH: 213
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-4689

Alignment Scores:
Pred. No.:             378           Length:        213
Score:                 6.00          Matches:       6
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           3.2%          Indels:        0
DB:                    6             Gaps:          0

US-10-821-670A-102 (1-187) x US-10-471-571A-4689 (1-213)

Qy        120 GlnIlePheLeuAspGln 125
              ||||||||||||||||||
Db         31 CAAATTTTTCTGGATCAA 14

RESULT 70
US-11-217-529-174474/c
; Sequence 174474, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174474
;   LENGTH: 231
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174474

Alignment Scores:
Pred. No.:             408           Length:        231
Score:                 6.00          Matches:       6
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           3.2%          Indels:        0
DB:                    7             Gaps:          0

US-10-821-670A-102 (1-187) x US-11-217-529-174474 (1-231)

Qy         69 GluIleSerLeuIleThr 74
              ||||||||||||||||||
Db        141 GAGATTTCCCTCATCACC 124

RESULT 71
US-11-217-529-166542
; Sequence 166542, Application US/11217529
; Publication No. US20060099612A1
```

; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166542
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166542

Alignment Scores:

Pred. No.:	482	Length:	276
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-166542 (1-276)

```
Qy         27 LeuGluPheTyrSerCys 32
              ||||||||||||||||||
Db         11 TTGGAGTTTTATAGTTGT 28
```

RESULT 72
US-11-217-529-174171/c
; Sequence 174171, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174171
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174171

Alignment Scores:

Pred. No.:	526	Length:	303
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-174171 (1-303)

```
Qy         91 CysLeuSerSerIleTyr 96
              ||||||||||||||||||
Db        234 TGTCTGAGCAGTATTTAT 217
```

RESULT 73
US-11-301-554-610/c
; Sequence 610, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 610
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-610

Alignment Scores:

Pred. No.:	538	Length:	310
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-301-554-610 (1-310)

```
Qy         25 GlnThrLeuGluPheTyr 30
              ||||||||||||||||||
Db        106 CAAACTCTGGAGTTCTAT 89
```

RESULT 74
US-11-217-529-4461
; Sequence 4461, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4461
LENGTH: 327
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
S-11-217-529-4461

lignment Scores:

red. No.:	565	Length:	327
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.2%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-102 (1-187) x US-11-217-529-4461 (1-327)

```
y         74 ThrAsnGlySerCysLeu 79
             |||||||||||||||||
b         93 ACTAATGGAAGTTGTTTA 110
```

ESULT 75
S-11-254-679-18/c
Sequence 18, Application US/11254679
Publication No. US20060099207A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Allan, Christian
APPLICANT: Gao, Changshou
APPLICANT: An, Ling-Ling
APPLICANT: Kiener, Peter
APPLICANT: Mao, Su-Yau
APPLICANT: Coyle, Anthony
TITLE OF INVENTION: High Affinity Antibodies Against HMGB1 and Method of Use Thereof
FILE REFERENCE: HB601US
CURRENT APPLICATION NUMBER: US/11/254,679
CURRENT FILING DATE: 2005-10-21
PRIOR APPLICATION NUMBER: 60/620,726
PRIOR FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: 60/651,512
PRIOR FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/658,572
PRIOR FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/662,944
PRIOR FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/713,712
PRIOR FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18
LENGTH: 336
TYPE: DNA
ORGANISM: Homo sapiens
S-11-254-679-18

lignment Scores:

red. No.:	580	Length:	336
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-254-679-18 (1-336)

```
Qy         47 ThrSerThrValGluAla 52
              |||||||||||||||||
Db        307 ACGTCCACTGTGGAGGCC 290
```

RESULT 76
US-10-511-937-623
; Sequence 623, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 623
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-623

Alignment Scores:

Pred. No.:	594	Length:	345
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-511-937-623 (1-345)

```
Qy         26 ThrLeuGluPheTyrSer 31
              |||||||||||||||||
Db        124 ACTCTTGAGTTCTATTCT 141
```

RESULT 77
US-11-254-679-20
; Sequence 20, Application US/11254679
; Publication No. US20060099207A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Kiener, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyle, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMGB1 and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512

; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
JS-11-254-679-20

Alignment Scores:

Pred. No.:	604	Length:	351
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

JS-10-821-670A-102 (1-187) x US-11-254-679-20 (1-351)

```
Qy        144 ThrValProGlnAsnSer 149
              |||||||||||||||||
Db        284 ACTGTACCACAGAATTCT 301
```

RESULT 78
JS-11-301-554-1167/c
; Sequence 1167, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1167
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1167

Alignment Scores:

Pred. No.:	622	Length:	362
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-301-554-1167 (1-362)

```
Qy         19 ThrLeuGlnLysAlaArg 24
              |||||||||||||||||
Db        219 ACTCTGCAGAAAGCCAGA 202
```

RESULT 79
US-10-953-349-18005/c
; Sequence 18005, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18005
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-18005

Alignment Scores:

Pred. No.:	665	Length:	389
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-953-349-18005 (1-389)

```
Qy         74 ThrAsnGlySerCysLeu 79
              |||||||||||||||||
Db        267 ACCAATGGCTCTTGTCTT 250
```

RESULT 80
US-11-301-554-900
; Sequence 900, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C21
CURRENT APPLICATION NUMBER: US/11/301,554
CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US 10/113,872
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 10/017,754
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/849,626
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 09/736,457
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 09/702,705
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US 09/677,419
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 09/671,325
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/658,824
PRIOR FILING DATE: 2000-09-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 900
LENGTH: 389
TYPE: DNA
ORGANISM: Homo sapiens
S-11-301-554-900

lignment Scores:

red. No.:	665	Length:	389
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.2%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-102 (1-187) x US-11-301-554-900 (1-389)

```
y         65 LeuAlaSerArgGluIle 70
             ||||||||||||||||||
b         30 CTTGCTTCAAGGGAAATT 47
```

ESULT 81
S-10-488-619-2081/c
Sequence 2081, Application US/10488619
Publication No. US20060099578A1
GENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
FILE REFERENCE: 98-01 WO
CURRENT APPLICATION NUMBER: US/10/488,619
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2081
LENGTH: 390
TYPE: DNA
ORGANISM: Mus musculus
S-10-488-619-2081

lignment Scores:

red. No.:	667	Length:	390
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-488-619-2081 (1-390)

```
Qy         65 LeuAlaSerArgGluIle 70
              ||||||||||||||||||
Db        337 CTGGCCAGCAGGGAGATT 320
```

RESULT 82
US-10-488-619-2364/c
; Sequence 2364, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2364
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2364

Alignment Scores:

Pred. No.:	683	Length:	400
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-488-619-2364 (1-400)

```
Qy        139 AsnValAsnSerValThr 144
              ||||||||||||||||||
Db        284 AATGTCAACAGTGTAACT 267
```

RESULT 83
US-10-488-619-316/c
; Sequence 316, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 316
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-316

Alignment Scores:

Pred. No.:	716	Length:	421
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-488-619-316 (1-421)

```
Qy         76 GlySerCysLeuAlaSer 81
              ||||||||||||||||||
Db        259 GGTTCCTGTCTAGCTTCC 242
```

RESULT 84
US-11-301-554-573
; Sequence 573, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 573
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-573

Alignment Scores:

Pred. No.:	719	Length:	423
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-301-554-573 (1-423)

```
Qy        162 LysLeuCysIleLeuLeu 167
              |||||||||||||||||
Db        389 AAACTTTGTATCTTGCTG 406
```

RESULT 85
US-10-560-723-109/c
; Sequence 109, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
; APPLICANT: EXONHIT THERAPEUTICALS
; TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: B0213WO
; CURRENT APPLICATION NUMBER: US/10/560,723
; CURRENT FILING DATE: 2005-12-15
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-560-723-109

Alignment Scores:

Pred. No.:	742	Length:	437
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-560-723-109 (1-437)

```
Qy         66 AlaSerArgGluIleSer 71
              |||||||||||||||||
Db        311 GCCAGCAGAGAAATCTCT 294
```

RESULT 86
US-10-488-619-826
; Sequence 826, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 826
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-826

Alignment Scores:

Pred. No.:	743	Length:	438
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-488-619-826 (1-438)

```
Qy         69 GluIleSerLeuIleThr 74
              |||||||||||||||||
Db        390 GAAATATCATTGATCACA 407
```

RESULT 87
US-10-488-619-2365
; Sequence 2365, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1

```
  SEQ ID NO 2365
    LENGTH: 438
    TYPE: DNA
;   ORGANISM: Mus musculus
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: (1)..(438)
    OTHER INFORMATION: n is g, c, a or t
JS-10-488-619-2365

Alignment Scores:
Pred. No.:                743             Length:         438
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.2%            Indels:         0
DB:                       6               Gaps:           0

'S-10-821-670A-102 (1-187) x US-10-488-619-2365 (1-438)

Qy        139 AsnValAsnSerValThr 144
              ||||||||||||||||||
Db        106 AATGTCAACAGTGTAACT 123

'ESULT 88
'S-10-953-349-13876
  Sequence 13876, Application US/10953349
  Publication No. US20060107345A1
  GENERAL INFORMATION:
    APPLICANT: ALEXANDROV, Nickolai et al.
    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
    TITLE OF INVENTION:  ENCONDED THERBY
    FILE REFERENCE: 2750-1579PUS2
    CURRENT APPLICATION NUMBER: US/10/953,349
    CURRENT FILING DATE:  2004-09-30
    NUMBER OF SEQ ID NOS: 40252
    SOFTWARE: PatentIn version 3.3
  SEQ ID NO 13876
    LENGTH: 443
    TYPE: DNA
    ORGANISM: Glycine max
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: (98)..(98)
    OTHER INFORMATION: n is a, c, g, or t
'S-10-953-349-13876

Alignment Scores:
Pred. No.:                751             Length:         443
'core:                    6.00            Matches:        6
'ercent Similarity:       100.0%          Conservative:   0
'est Local Similarity:    100.0%          Mismatches:     0
)uery Match:              3.2%            Indels:         0
'B:                       6               Gaps:           0

'S-10-821-670A-102 (1-187) x US-10-953-349-13876 (1-443)

'y        72 LeuIleThrAsnGlySer 77
             |||||||||||||||||
'b        56 TTAATCACCAATGGCTCG 73

ESULT 89
'S-10-488-619-338
  Sequence 338, Application US/10488619
  Publication No. US20060099578A1
  GENERAL INFORMATION:
    APPLICANT: Greenlee, Winner and Sullivan, P.C.
    TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
    TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
    FILE REFERENCE: 98-01 WO
    CURRENT APPLICATION NUMBER: US/10/488,619
    CURRENT FILING DATE:  2004-03-01
    NUMBER OF SEQ ID NOS: 3040
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 338
;   LENGTH: 470
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-488-619-338

Alignment Scores:
Pred. No.:                794             Length:         470
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.2%            Indels:         0
DB:                       6               Gaps:           0

US-10-821-670A-102 (1-187) x US-10-488-619-338 (1-470)

Qy         67 SerArgGluIleSerLeu 72
              |||||||||||||||||
Db        306 TCCAGAGAAATCTCATTA 323

RESULT 90
US-11-301-554-1170
; Sequence 1170, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Durham, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C21
;  CURRENT APPLICATION NUMBER: US/11/301,554
;  CURRENT FILING DATE:  2005-12-13
;  PRIOR APPLICATION NUMBER: US 10/283,017
;  PRIOR FILING DATE: 2002-10-28
;  PRIOR APPLICATION NUMBER: US 10/113,872
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 10/017,754
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: US 09/902,941
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 09/849,626
;  PRIOR FILING DATE: 2001-05-03
;  PRIOR APPLICATION NUMBER: US 09/736,457
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 09/702,705
;  PRIOR FILING DATE: 2000-10-30
;  PRIOR APPLICATION NUMBER: US 09/677,419
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: US 09/671,325
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US 09/658,824
;  PRIOR FILING DATE: 2000-09-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2157
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1170
;   LENGTH: 480
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-301-554-1170
```

Alignment Scores:

Pred. No.:	810	Length:	480
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-301-554-1170 (1-480)

```
Qy         19 ThrLeuGlnLysAlaArg 24
              ||||||||||||||||||
Db        263 ACTCTGCAGAAAGCCAGA 280
```

RESULT 91
US-11-297-957-5/c
; Sequence 5, Application US/11297957
; Publication No. US20060110386A1
; GENERAL INFORMATION:
; APPLICANT: Reche-Gallardo, Pedro A.
; APPLICANT: Soumelis, Vassili
; APPLICANT: Liu, Yong-Jun
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Bazan, Jose F.
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS;
; TITLE OF INVENTION: RELATED REAGENTS AND METHODS
; FILE REFERENCE: dx01341
; CURRENT APPLICATION NUMBER: US/11/297,957
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US/10/008,566
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/298268
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/247218
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(477)
; OTHER INFORMATION:
US-11-297-957-5

Alignment Scores:

Pred. No.:	810	Length:	480
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-297-957-5 (1-480)

```
Qy         91 CysLeuSerSerIleTyr 96
              ||||||||||||||||||
Db        369 TGCCTGAGTAGCATTTAT 352
```

RESULT 92
US-11-296-092-18/c
; Sequence 18, Application US/11296092
; Publication No. US20060105427A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,092
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 18
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-296-092-18

Alignment Scores:

Pred. No.:	854	Length:	508
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-296-092-18 (1-508)

```
Qy         92 LeuSerSerIleTyrGlu 97
              |||||||||||||||||||
Db         57 CTTTCGTCCATCTATGAG 40
```

RESULT 93
US-11-296-092-19/c
; Sequence 19, Application US/11296092
; Publication No. US20060105427A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth

APPLICANT: Kljavin,Ivar
APPLICANT: Napier,Mary
APPLICANT: Roy,Margaret
APPLICANT: Tumas,Daniel
APPLICANT: Wood,William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/11/296,092
CURRENT FILING DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 19
LENGTH: 508
TYPE: DNA
ORGANISM: Homo Sapien
S-11-296-92-19

lignment Scores:

red. No.:	854	Length:	508
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.2%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-102 (1-187) x US-11-296-092-19 (1-508)

```
y         92 LeuSerSerIleTyrGlu 97
             |||||||||||||||||
b         57 CTTTCGTCCATCTATGAG 40
```

ESULT 94
S-10-511-937-2900
Sequence 2900, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2900
LENGTH: 511
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (500)..(500)
OTHER INFORMATION: n is a, c, g, t or u
US-10-511-937-2900

Alignment Scores:

Pred. No.:	859	Length:	511
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-511-937-2900 (1-511)

```
Qy        112 LysLeuLeuMetAspPro 117
              ||||||||||||||||||
Db        375 AAACTGTTGATGGATCCA 392
```

RESULT 95
US-10-473-173-459
Sequence 459, Application US/10473173
Publication No. US20060088823A1
GENERAL INFORMATION:
APPLICANT: VAN ANDEL INSTITUTE
TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
FILE REFERENCE: 38345-170094
CURRENT APPLICATION NUMBER: US/10/473,173
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US 60/279,411
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 498
SOFTWARE: PatentIn version 3.2
SEQ ID NO 459
LENGTH: 517
TYPE: DNA
ORGANISM: Homo sapiens
US-10-473-173-459

Alignment Scores:

Pred. No.:	868	Length:	517
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-473-173-459 (1-517)

```
Qy        175 ValThrIleAsnArgMet 180
              ||||||||||||||||||
Db         34 GTCACAATAAATAGAATG 51
```

RESULT 96
US-10-488-619-1461/c
Sequence 1461, Application US/10488619
Publication No. US20060099578A1
GENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
FILE REFERENCE: 98-01 WO

; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1461
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1461

Alignment Scores:

Pred. No.:	876	Length:	522
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-488-619-1461 (1-522)

```
Qy         64 CysLeuAlaSerArgGlu 69
              |||||||||||||||||
Db        305 TGTTTGGCTAGTAGGGAA 288
```

RESULT 97
US-11-217-529-78894/c
; Sequence 78894, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78894
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78894

Alignment Scores:

Pred. No.:	895	Length:	534
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-102 (1-187) x US-11-217-529-78894 (1-534)

```
Qy        147 GlnAsnSerSerLeuGlu 152
              |||||||||||||||||
Db         22 CAAAACTCATCACTGGAG 5
```

RESULT 98
US-10-953-349-10529/c
; Sequence 10529, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10529
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10529

Alignment Scores:

Pred. No.:	898	Length:	536
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-953-349-10529 (1-536)

```
Qy        159 ThrLysIleLysLeuCys 164
              ||||||||||||||||||
Db        499 ACAAAGATAAAACTTTGC 482
```

RESULT 99
US-10-953-349-13039
; Sequence 13039, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13039
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-13039

Alignment Scores:

Pred. No.:	898	Length:	536
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-953-349-13039 (1-536)

```
Qy        134 LeuLeuGlnAlaLeuAsn 139
              ||||||||||||||||||
Db        293 CTGTTGCAGGCACTGAAT 310
```

RESULT 100
US-11-301-554-14/c
; Sequence 14, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.

APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C21
CURRENT APPLICATION NUMBER: US/11/301,554
CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US 10/113,872
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 10/017,754
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/849,626
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 09/736,457
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 09/702,705
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US 09/677,419
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 09/671,325
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/658,824
PRIOR FILING DATE: 2000-09-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 540
TYPE: DNA
ORGANISM: Homo sapiens
S-11-301-554-14

lignment Scores:

red. No.:	904	Length:	540
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	3.2%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-102 (1-187) x US-11-301-554-14 (1-540)

```
y         88 ThrThrLeuCysLeuSer 93
             |||||||||||||||||
b        402 ACTACACTTTGTCTATCA 385
```

earch completed: June 10, 2006, 02:17:32
ob time : 31.7446 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

on: June 10, 2006, 01:33:29 ; Search time 7472.55 Seconds
(without alignments)
4210.361 Million cell updates/sec

le: US-10-821-670A-56
fect score: 328
uence: 1 MHPQQLVIAWFSLVLLAPPL.....VQARDRYYSSSWSNWASVSC 328

ring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

rched: 6366136 seqs, 31973710525 residues

d size: 1

al number of hits satisfying chosen parameters: 12722146

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Listing first 200 summaries

mand line parameters:
DEL=frame+_p2n.model -DEV=xlh
/abss/ABSSWEB_spool/US10821670/runat_07062006_110449_27523/app_query.fasta_1
=GenEmbl -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rge -MINMATCH=0.1
OPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
ANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
IGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
XLEN=2000000000 -HOST=abss08
ER=US10821670_@CGN_1_1_6646_@runat_07062006_110449_27523 -NCPU=6 -ICPU=3
MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
RN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
APOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

abase : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt No.	Score	% Query Match	Length	DB	ID	Description
1	328	100.0	985	2	AR595967	AR595967 Sequence
2	328	100.0	985	2	AR595968	AR595968 Sequence
3	328	100.0	987	2	AR595950	AR595950 Sequence
c 4	328	100.0	987	2	AR595951	AR595951 Sequence
5	328	100.0	990	2	AX076200	AX076200 Sequence
6	328	100.0	990	2	AX076482	AX076482 Sequence
7	328	100.0	4522	2	AX076209	AX076209 Sequence
8	328	100.0	4522	2	AX076476	AX076476 Sequence
9	316	96.3	2193	2	AR242435	AR242435 Sequence
10	316	96.3	2193	2	AR280203	AR280203 Sequence
11	316	96.3	2193	2	AR322418	AR322418 Sequence
12	306	93.3	921	2	AR242436	AR242436 Sequence
13	306	93.3	921	2	AR242437	AR242437 Sequence
14	306	93.3	921	2	AR280204	AR280204 Sequence
15	306	93.3	921	2	AR280205	AR280205 Sequence
16	306	93.3	921	2	AR322419	AR322419 Sequence
17	306	93.3	921	2	AR322420	AR322420 Sequence
18	277	84.5	990	14	FCU83184	U83184 Felis catus
19	216	65.9	1006	14	FCIL12P40	Y07762 Felis catus
20	216	65.9	1599	2	AR595956	AR595956 Sequence
c 21	216	65.9	1599	2	AR595957	AR595957 Sequence
22	205	62.5	921	2	AR595948	AR595948 Sequence
c 23	205	62.5	921	2	AR595949	AR595949 Sequence
24	205	62.5	1533	2	AR595959	AR595959 Sequence
c 25	205	62.5	1533	2	AR595960	AR595960 Sequence
26	126	38.4	431	14	AF054607	AF054607 Felis cat
27	52	15.9	990	2	AX154603	AX154603 Sequence
28	49	14.9	984	2	AX154600	AX154600 Sequence
29	42	12.8	984	2	AX154599	AX154599 Sequence
30	41	12.5	972	8	AY191829	AY191829 Synthetic
31	41	12.5	975	2	AX154597	AX154597 Sequence
32	39	11.9	993	14	AB107654	AB107654 Lama glam
33	39	11.9	1005	5	AY234218	AY234218 Papio anu
34	39	11.9	1005	5	CTU19834	U19834 Cercocebus
35	39	11.9	1080	5	MMU19841	U19841 Macaca mula
36	37	11.3	921	2	AR595965	AR595965 Sequence
c 37	37	11.3	921	2	AR595966	AR595966 Sequence
38	37	11.3	924	2	BD171282	BD171282 Novel can
39	37	11.3	987	2	AR595969	AR595969 Sequence
c 40	37	11.3	987	2	AR595970	AR595970 Sequence
41	37	11.3	990	2	AR151061	AR151061 Sequence
42	37	11.3	990	2	AR151071	AR151071 Sequence
43	37	11.3	990	2	BD014653	BD014653 Process f
44	37	11.3	990	2	BD014663	BD014663 Process f
45	37	11.3	990	2	E15017	E15017 Canine mRNA
46	37	11.3	990	2	AR316460	AR316460 Sequence
47	37	11.3	990	2	AR316470	AR316470 Sequence
48	37	11.3	1015	14	CFU49100	U49100 Canis famil
49	37	11.3	1533	2	AR595973	AR595973 Sequence
c 50	37	11.3	1533	2	AR595974	AR595974 Sequence
51	37	11.3	1599	2	AR595971	AR595971 Sequence
c 52	37	11.3	1599	2	AR595972	AR595972 Sequence
53	37	11.3	2154	2	BD171281	BD171281 Novel can
54	37	11.3	2267	2	AR596011	AR596011 Sequence
c 55	37	11.3	2267	2	AR596012	AR596012 Sequence
56	36	11.0	446	14	AF091134	AF091134 Canis fam
57	36	11.0	452	14	AF333121	AF333121 Canis fam
58	36	11.0	588	14	AF349536	AF349536 Canis fam
59	35	10.7	906	2	BD021808	BD021808 Natural k
60	35	10.7	906	2	BD021809	BD021809 Natural k
61	35	10.7	975	2	AX154602	AX154602 Sequence
62	35	10.7	987	2	AR008950	AR008950 Sequence
63	35	10.7	987	2	BD007070	BD007070 IL-12 gen
64	35	10.7	987	2	BD007076	BD007076 Gene expr
65	35	10.7	987	2	BD007077	BD007077 Gene expr
66	35	10.7	987	2	BD007078	BD007078 Gene expr
67	35	10.7	987	2	BD136034	BD136034 Interfero
68	35	10.7	987	2	BD136035	BD136035 Interfero
69	35	10.7	987	2	BD136036	BD136036 Interfero
70	35	10.7	987	2	CQ803342	CQ803342 Sequence
71	35	10.7	987	2	CS131491	CS131491 Sequence
72	35	10.7	987	2	I28591	I28591 Sequence 1
73	35	10.7	987	2	AX154633	AX154633 Sequence
74	35	10.7	1007	5	AF180563	AF180563 Homo sapi
75	35	10.7	1008	14	AB246353	AB246353 Bubalus b

76	35	10.7	1012	14	AY198121	AY198121 Bubalus b
77	35	10.7	1018	2	AR052857	AR052857 Sequence
78	35	10.7	1018	2	AR288169	AR288169 Sequence
79	35	10.7	1018	2	AR567156	AR567156 Sequence
80	35	10.7	1029	2	CQ829448	CQ829448 Sequence
81	35	10.7	1046	5	BC074723	BC074723 Homo sapi
82	35	10.7	1073	5	BC067498	BC067498 Homo sapi
83	35	10.7	1073	5	BC067499	BC067499 Homo sapi
84	35	10.7	1073	5	BC067500	BC067500 Homo sapi
85	35	10.7	1073	5	BC067501	BC067501 Homo sapi
86	35	10.7	1073	5	BC067502	BC067502 Homo sapi
87	35	10.7	1389	2	AR393788	AR393788 Sequence
88	35	10.7	1389	2	AX084106	AX084106 Sequence
89	35	10.7	1397	2	BD165800	BD165800 Antibody
90	35	10.7	1399	2	AR091391	AR091391 Sequence
91	35	10.7	1399	5	HUMCLMF40	M65272 Human cytot
92	35	10.7	1560	2	AR091395	AR091395 Sequence
93	35	10.7	1623	2	AR091394	AR091394 Sequence
94	35	10.7	2307	2	CQ715179	CQ715179 Sequence
95	35	10.7	2362	2	AR082684	AR082684 Sequence
96	35	10.7	2362	2	AR122960	AR122960 Sequence
97	35	10.7	2362	2	I28325	I28325 Sequence 1
98	35	10.7	2362	2	AR309636	AR309636 Sequence
99	35	10.7	2362	2	I89770	I89770 Sequence 1
100	35	10.7	5686	2	BD136048	BD136048 Interfero
101	35	10.7	6139	2	AR091393	AR091393 Sequence
102	33	10.1	681	7	BV440664	BV440664 S237P6324
103	30	9.1	621	7	BV242752	BV242752 S234P6134
104	28	8.5	224	14	DQ152965	DQ152965 Ovis arie
105	28	8.5	525	14	CEU10160	U10160 Cervus elap
106	28	8.5	969	2	AX154601	AX154601 Sequence
107	28	8.5	984	2	AX154598	AX154598 Sequence
108	28	8.5	984	14	AF004024	AF004024 Ovis arie
109	28	8.5	984	14	AF209435	AF209435 Ovis arie
110	28	8.5	993	14	AY603406	AY603406 Capra hir
111	28	8.5	993	14	CEU57752	U57752 Cervus elap
112	28	8.5	1008	14	AB246273	AB246273 Bubalus c
113	28	8.5	1008	14	AB246358	AB246358 Bubalus b
114	28	8.5	1012	14	AF007576	AF007576 Capra hir
115	28	8.5	1012	14	BTU11815	U11815 Bos taurus
116	28	8.5	1019	2	E35794	E35794 Process for
117	28	8.5	2090	14	SSU08317	U08317 Sus scrofa
118	27	8.2	932	14	AY686641S1	AY686641 Equus cab
119	27	8.2	1058	14	ECIL12P40	Y11129 Equus cabal
120	27	8.2	1626	8	AF401989	AF401989 Synthetic
121	23	7.0	987	2	BD105974	BD105974 Animal mo
122	23	7.0	987	2	AR533404	AR533404 Sequence
123	23	7.0	1870	2	A92079	A92079 Sequence 3
124	23	7.0	1870	2	AR230691	AR230691 Sequence
125	23	7.0	2318	2	AR228993	AR228993 Sequence
126	23	7.0	2318	5	HUMNKSFP40	M65290 Human natur
127	22	6.7	200	5	AY591921	AY591921 Macaca fa
128	22	6.7	999	6	AB025724	AB025724 Cavia por
129	22	6.7	15648	5	AF512686	AF512686 Homo sapi
130	22	6.7	18340	5	AY008847	AY008847 Homo sapi
131	22	6.7	108511	5	AC011418	AC011418 Homo sapi
132	21	6.4	528	6	AF082494	AF082494 Marmota m
133	21	6.4	984	6	AF288519	AF288519 Marmota m
134	21	6.4	984	6	MMIL12P40	X97019 M.monax mRN
135	21	6.4	1425	6	AF421395	AF421395 Sigmodon
136	20	6.1	399	2	CS211342	CS211342 Sequence
137	20	6.1	399	2	CS214984	CS214984 Sequence
138	20	6.1	399	6	AF046211	AF046211 Mesocrice
139	20	6.1	2276	6	AB085792	AB085792 Mesocrice
140	19	5.8	928	11	MGA564203	AJ564203 Meleagris
141	19	5.8	948	2	CQ760887	CQ760887 Sequence
142	19	5.8	948	2	CQ760890	CQ760890 Sequence
143	19	5.8	948	2	CQ760892	CQ760892 Sequence
144	19	5.8	948	11	DQ202328	DQ202328 Gallus ga
145	19	5.8	948	11	AY262752	AY262752 Gallus ga
146	17	5.2	73	2	AR439759	AR439759 Sequence
147	17	5.2	73	2	AX268996	AX268996 Sequence
148	17	5.2	508	6	AF097507	AF097507 Cavia por
149	17	5.2	600	2	E26663	E26663 Improved me
150	17	5.2	821	6	RNU16674	U16674 Rattus norv
151	17	5.2	1008	6	AF133197	AF133197 Rattus no
152	17	5.2	1061	2	AR069654	AR069654 Sequence
153	17	5.2	1143	6	AF128214	AF128214 Mus muscu
154	17	5.2	1143	6	AF128215	AF128215 Mus muscu
155	17	5.2	1381	6	BC103608	BC103608 Mus muscu
156	17	5.2	1381	6	BC103609	BC103609 Mus muscu
157	17	5.2	1381	6	BC103610	BC103610 Mus muscu
158	17	5.2	1381	6	BC103614	BC103614 Mus muscu
159	17	5.2	1409	2	AR393787	AR393787 Sequence
160	17	5.2	1409	2	AX084105	AX084105 Sequence
161	17	5.2	1472	2	AR393786	AR393786 Sequence
162	17	5.2	1472	2	AX084104	AX084104 Sequence
163	17	5.2	1569	2	AR393796	AR393796 Sequence
164	17	5.2	1569	2	AX084114	AX084114 Sequence
165	17	5.2	1582	14	AY686641S2	AY686644 Equus cab
166	17	5.2	1669	8	AF411293	AF411293 Synthetic
167	17	5.2	1840	6	MUSIL40A	M86671 Mus musculu
168	17	5.2	2013	2	AR393795	AR393795 Sequence
169	17	5.2	2013	2	AX084113	AX084113 Sequence
170	17	5.2	2438	2	CQ812173	CQ812173 Sequence
171	17	5.2	2709	2	AR393797	AR393797 Sequence
172	17	5.2	2709	2	AX084115	AX084115 Sequence
173	17	5.2	5252	2	CQ803341	CQ803341 Sequence
174	17	5.2	5966	2	BD136050	BD136050 Interfero
175	17	5.2	9049	2	CQ803350	CQ803350 Sequence
176	17	5.2	10633	2	CQ803349	CQ803349 Sequence
177	17	5.2	11746	2	CQ803348	CQ803348 Sequence
178	17	5.2	38246	2	CQ803351	CQ803351 Sequence
179	16	4.9	1062	6	AF288612	AF288612 Meriones
180	13	4.0	987	2	BD136055	BD136055 Interfero
181	13	4.0	1000	6	S82420S3	S82422 interleukin
182	13	4.0	76047	6	AL669944	AL669944 Mouse DNA
183	13	4.0	110000	12	AC073744_2	Continuation (3 of
184	13	4.0	110000	12	AC073744_3	Continuation (4 of
185	13	4.0	189236	6	AL607030	AL607030 Mouse DNA
c 186	13	4.0	268294	12	AC020885	AC020885 Mus muscu
187	13	4.0	287927	12	AC079530	AC079530 Mus muscu
188	12	3.7	38	2	AR242440	AR242440 Sequence
189	12	3.7	38	2	AR280208	AR280208 Sequence
190	12	3.7	38	2	AR322423	AR322423 Sequence
191	12	3.7	1897	11	GGA564201	AJ564201 Gallus ga
192	12	3.7	285389	12	AC096348	AC096348 Rattus no
193	11	3.4	9821	11	GGA564202	AJ564202 Gallus ga
c 194	10	3.0	30	2	AX027245	AX027245 Sequence
195	10	3.0	500	6	S82420S5	S82424 interleukin
c 196	10	3.0	2553	10	AF394057	AF394057 Porcine c
c 197	10	3.0	5668	10	AF268041	AF268041 Porcine c
c 198	10	3.0	6249	10	AF268039	AF268039 Porcine c
199	10	3.0	21925	2	AX647863	AX647863 Sequence
200	10	3.0	26184	2	AX647497	AX647497 Sequence

ALIGNMENTS

```
RESULT 1
AR595967
LOCUS       AR595967                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 55 from patent US 6818444.
ACCESSION   AR595967
VERSION     AR595967.1  GI:56646948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 55 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
```

```
                /organism="unknown"
                /mol_type="genomic DNA"
GIN

gnment Scores:
i. No.:              0              Length:        985
re:                  328.00         Matches:       328
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            100.0%         Indels:        0
                     2              Gaps:          0

10-821-670A-56 (1-328) x AR595967 (1-985)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 2
AR595968/c
LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:        985
Score:                  328.00         Matches:       328
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x AR595968 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
```

```
505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
 85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

321 SerAsnTrpAlaSerValSerCys 328
 25 AGCAACTGGGCATCCGTGTCCTGC 2

ULT 3
95950
US      AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
INITION  Sequence 29 from patent US 6818444.
ESSION   AR595950
SION     AR595950.1  GI:56646931
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 987)
UTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL   Patent: US 6818444-A 29 16-NOV-2004;
         Heska Corporation; Fort Collins, CO
TURES             Location/Qualifiers
  source          1. .987
                  /organism="unknown"
                  /mol_type="genomic DNA"
IN

nment Scores:
i. No.:              0              Length:        987
e:                   328.00         Matches:       328
 ent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
y Match:             100.0%         Indels:        0
                     2              Gaps:          0

10-821-670A-56 (1-328) x AR595950 (1-987)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
Db       121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db       181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
Db       241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
Db       301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db       361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
Db       421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy       161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
Db       481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db       601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
Db       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
Db       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
Db       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
Db       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
Db       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy       321 SerAsnTrpAlaSerValSerCys 328
Db       961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 4
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
```

```
:ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
:OURNAL   Patent: US 6818444-A 31 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
:TURES              Location/Qualifiers
   source           1. .987
                    /organism="unknown"
                    /mol_type="genomic DNA"
:GIN

.gnment Scores:
:d. No.:              0              Length:         987
:re:                  328.00         Matches:        328
:cent Similarity:     100.0%         Conservative:   0
:t Local Similarity:  100.0%         Mismatches:     0
:ry Match:            100.0%         Indels:         0
                      2              Gaps:           0

10-821-670A-56 (1-328) x AR595951 (1-987)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||
Db       27 AGCAACTGGGCATCCGTGTCCTGC 4

RESULT 5
AX076200
LOCUS       AX076200                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES              Location/Qualifiers
     source           1. .990
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="feline IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:         990
Score:                  328.00         Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AX076200 (1-990)

Qy        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy       21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy       41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy       61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy       81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy      101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
```

```
121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

321 SerAsnTrpAlaSerValSerCys 328
961 AGCAACTGGGCATCCGTGTCCTGC 984
```

```
ULT 6
76482
:S        AX076482                 990 bp    DNA     linear   PAT 06-FEB-2001
INITION   Sequence 8 from Patent WO0104280.
ESSION    AX076482
SION      AX076482.1  GI:12711034
'ORDS     .
:CE       synthetic construct
-GANISM   synthetic construct
          other sequences; artificial sequences.
:RENCE    1
UTHORS    Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
ITLE      Vaccine against lentiviral infections, such as the feline immune
          deficiency virus of the cat
OURNAL    Patent: WO 0104280-A 8 18-JAN-2001;
          Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
          Universitaet Zuerich (CH)
TURES             Location/Qualifiers
  source          1. .990
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
GIN

gnment Scores:
d. No.:             0             Length:        990
re:                 328.00        Matches:       328
cent Similarity:    100.0%        Conservative:  0
```

```
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            100.0%        Indels:        0
DB:                     2             Gaps:          0

US-10-821-670A-56 (1-328) x AX076482 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984
```

```
ULT 7
076209
US       AX076209                4522 bp    DNA     linear   PAT 06-FEB-2001
INITION  Sequence 10 from Patent WO0104155.
ESSION   AX076209
SION     AX076209.1  GI:12710834
WORDS    .
RCE      synthetic construct
RGANISM  synthetic construct
         other sequences; artificial sequences.
ERENCE   1
UTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
ITLE     Feline interleukin-12 as an immune stimulant
OURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
         Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
         Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
         CALIFORNIA (US)
TURES             Location/Qualifiers
   source         1. .4522
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="Plasmid pMol-fil12p40"
IGIN

gnment Scores:
d. No.:              0             Length:         4522
re:                  328.00        Matches:        328
cent Similarity:     100.0%        Conservative:   0
t Local Similarity:  100.0%        Mismatches:     0
ry Match:            100.0%        Indels:         0
                     2             Gaps:           0

10-821-670A-56 (1-328) x AX076209 (1-4522)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||
Db     4007 AGCAACTGGGCATCCGTGTCCTGC 4030

RESULT 8
AX076476
LOCUS       AX076476                4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
ORIGIN

Alignment Scores:
Pred. No.:              0             Length:         4522
Score:                  328.00        Matches:        328
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            100.0%        Indels:         0
DB:                     2             Gaps:           0

US-10-821-670A-56 (1-328) x AX076476 (1-4522)

Qy        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy       21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166
```

```
  41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

  61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

  81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

 101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

 121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

 141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

 161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

 181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

 201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

 221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

 241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

 261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

 281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

 301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

 321 SerAsnTrpAlaSerValSerCys 328
     |||||||||||||||||||||||
4007 AGCAACTGGGCATCCGTGTCCTGC 4030

LT 9
2435
S       AR242435              2193 bp    mRNA    linear   PAT 20-DEC-2002
NITION  Sequence 5 from patent US 6472509.
SSION   AR242435
ION     AR242435.1  GI:27288852
ORDS    .
CE      Unknown.
RGANISM Unknown.
        Unclassified.
ERENCE  1  (bases 1 to 2193)
UTHORS  Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          2193
Score:                    316.00         Matches:         316
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              96.3%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-56 (1-328) x AR242435 (1-2193)

Qy          13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

Qy          33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy          53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy          73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

Qy          93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

Qy         113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

Qy         133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

Qy         153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

Qy         173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

Qy         193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

Qy         213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy         233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy         253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879
```

```
       273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

       293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

       313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||
      1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 1047

ULT 10
80203
US       AR280203                2193 bp    mRNA    linear   PAT 10-APR-2003
INITION  Sequence 5 from patent US 6518045.
ESSION   AR280203
SION     AR280203.1  GI:29715593
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 2193)
UTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE     Feline cytokine protein
OURNAL   Patent: US 6518045-A 5 11-FEB-2003;
         Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
         Kumamoto-ken;
         EPX;
TURES             Location/Qualifiers
   source         1. .2193
                  /organism="unknown"
                  /mol_type="mRNA"
GIN

gnment Scores:
d. No.:              0              Length:        2193
re:                  316.00         Matches:       316
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            96.3%          Indels:        0
                     2              Gaps:          0

10-821-670A-56 (1-328) x AR280203 (1-2193)

        13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

        33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

        53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

        73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

        93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

       113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

       133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

Qy       153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

Qy       173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

Qy       193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

Qy       213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy       233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy       253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

Qy       273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

Qy       293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

Qy       313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 11
AR322418
LOCUS       AR322418                2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:        2193
Score:                  316.00         Matches:       316
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            96.3%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x AR322418 (1-2193)

Qy        13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159
```

```
 33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

 53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

 73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

 93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
    ||||||||||||||||||||||||||||||||||||||||||||||||
1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 1047
```

```
ULT 12
42436
US       AR242436                 921 bp    mRNA    linear   PAT 20-DEC-2002
INITION  Sequence 6 from patent US 6472509.
ESSION   AR242436
SION     AR242436.1  GI:27288853
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 921)
UTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 6 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          921
Score:                    306.00         Matches:         306
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              93.3%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-56 (1-328) x AR242436 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
```

```
          781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

          303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

          323 TrpAlaSerValSerCys 328
              ||||||||||||||||||
          901 TGGGCATCCGTGTCCTGC 918

:ULT 13
:42437
:US       AR242437                 921 bp    mRNA    linear   PAT 20-DEC-2002
'INITION  Sequence 7 from patent US 6472509.
:ESSION   AR242437
:SION     AR242437.1  GI:27288854
'WORDS    .
(URCE     Unknown.
)RGANISM  Unknown.
          Unclassified.
'ERENCE   1  (bases 1 to 921)
AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
'ITLE     Feline cytokine protein
JOURNAL   Patent: US 6472509-A 7 29-OCT-2002;
          Juridical Foundation: The Chemo-Seso-Therapeutic Research
          Institute; Kumamoto;
          EPX;
ATURES              Location/Qualifiers
   source           1. .921
                    /organism="unknown"
                    /mol_type="mRNA"
:GIN

gnment Scores:
d. No.:             0              Length:         921
re:                 306.00         Matches:        306
cent Similarity:    100.0%         Conservative:   0
t Local Similarity: 100.0%         Mismatches:     0
ry Match:           93.3%          Indels:         0
                    2              Gaps:           0

10-821-670A-56 (1-328) x AR242437 (1-921)

           23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

           43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

           63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

           83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

          103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

          123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

          143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

          163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCys 328
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGC 918

RESULT 14
AR280204
LOCUS       AR280204                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6518045.
ACCESSION   AR280204
VERSION     AR280204.1  GI:29715594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 6 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES              Location/Qualifiers
     source           1. .921
                      /organism="unknown"
                      /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:         921
Score:                  306.00         Matches:        306
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            93.3%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AR280204 (1-921)

Qy          23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy          43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
901 TGGGCATCCGTGTCCTGC 918

ULT 15
80205
US       AR280205                 921 bp    mRNA    linear   PAT 10-APR-2003
INITION  Sequence 7 from patent US 6518045.
ESSION   AR280205
SION     AR280205.1  GI:29715595
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 921)
UTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE     Feline cytokine protein
OURNAL   Patent: US 6518045-A 7 11-FEB-2003;
         Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
         Kumamoto-ken;
         EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0                Length:          921
Score:                    306.00           Matches:         306
Percent Similarity:       100.0%           Conservative:    0
Best Local Similarity:    100.0%           Mismatches:      0
Query Match:              93.3%            Indels:          0
DB:                       2                Gaps:            0

US-10-821-670A-56 (1-328) x AR280205 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

        323 TrpAlaSerValSerCys 328
            |||||||||||||||||
        901 TGGGCATCCGTGTCCTGC 918

ULT 16
22419
US        AR322419                  921 bp    mRNA    linear   PAT 17-AUG-2003
INITION   Sequence 6 from patent US 6566097.
ESSION    AR322419
SION      AR322419.1  GI:33708172
WORDS     .
RCE       Unknown.
RGANISM   Unknown.
          Unclassified.
ERENCE    1  (bases 1 to 921)
UTHORS    Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE      Feline cytokine protein
OURNAL    Patent: US 6566097-A 6 20-MAY-2003;
          Juridical Foundation The Chemo-Sero-Therapeutic Research
          Institute;;
          EPX;
TURES               Location/Qualifiers
   source           1. .921
                    /organism="unknown"
                    /mol_type="mRNA"
IGIN

gnment Scores:
d. No.:                0              Length:         921
re:                    306.00         Matches:        306
cent Similarity:       100.0%         Conservative:   0
t Local Similarity:    100.0%         Mismatches:     0
ry Match:              93.3%          Indels:         0
                       2              Gaps:           0

10-821-670A-56 (1-328) x AR322419 (1-921)

         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy      243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy      323 TrpAlaSerValSerCys 328
            |||||||||||||||||
Db      901 TGGGCATCCGTGTCCTGC 918

RESULT 17
AR322420
LOCUS       AR322420                  921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 7 from patent US 6566097.
ACCESSION   AR322420
VERSION     AR322420.1  GI:33708173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 7 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES              Location/Qualifiers
     source           1. .921
                      /organism="unknown"
                      /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:         921
Score:                    306.00         Matches:        306
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              93.3%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-56 (1-328) x AR322420 (1-921)

Qy          23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy          43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
 61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
901 TGGGCATCCGTGTCCTGC 918

ULT 18
83184
US       FCU83184                 990 bp    mRNA    linear   MAM 16-JUL-1999
INITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ESSION   U83184
SION     U83184.1  GI:2735050
WORDS    .
RCE      Felis catus (cat)
RGANISM  Felis catus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
         Felinae; Felis.
ERENCE   1  (bases 1 to 990)
UTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
         Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCDTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:                0                Length:          990
Score:                    277.00           Matches:         277
Percent Similarity:       100.0%           Conservative:    0
Best Local Similarity:    100.0%           Mismatches:      0
Query Match:              84.5%            Indels:          0
DB:                       14               Gaps:            0

US-10-821-670A-56 (1-328) x FCU83184 (1-990)

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACGCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGA 513

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

      232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

      252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

      272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

      292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

      312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 984

ULT 19
L12P40
US       FCIL12P40                 1006 bp    mRNA    linear   MAM 18-APR-2005
INITION  Felis catus mRNA for interleukin-12 p40 chain.
ESSION   Y07762
SION     Y07762.1  GI:2102664
WORDS    interleukin-12 p40.
RCE      Felis catus (cat)
RGANISM  Felis catus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
         Felinae; Felis.
ERENCE   1
UTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
ITLE     Molecular cloning of cat interleukin-12
OURNAL   Immunogenetics 45 (6), 462-463 (1997)
 PUBMED  9089110
ERENCE   2  (bases 1 to 1006)
UTHORS   Schijns,V.E.C.J.
ITLE     Direct Submission
OURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
         Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
         Utrecht, NETHERLANDS
TURES             Location/Qualifiers
   source         1. .1006
                  /organism="Felis catus"
                  /mol_type="mRNA"
                  /db_xref="taxon:9685"
                  /cell_type="lymphocyte"
                  /tissue_type="peripheral blood"
   gene           1. .1006
                  /gene="IL-12.p40"
   CDS            1. .990
                  /gene="IL-12.p40"
                  /note="heterodimer with IL-12 p35 chain"
                  /codon_start=1
                  /product="interleukin-12 p40 chain"
                  /protein_id="CAA69068.1"
                  /db_xref="GI:2102665"
                  /db_xref="GOA:O02744"
                  /db_xref="InterPro:IPR002996"
                  /db_xref="InterPro:IPR003530"
                  /db_xref="InterPro:IPR003961"
                  /db_xref="InterPro:IPR007110"
                  /db_xref="InterPro:IPR008957"
                  /db_xref="UniProtKB/Swiss-Prot:O02744"
                  /translation="MHPQQLVIAWLSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                  MVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                  LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                  GSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                  LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                  QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:              1.2e-256        Length:         1006
Score:                  216.00          Matches:        316
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            65.9%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-56 (1-328) x FCIL12P40 (1-1006)

Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933
```

```
       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 984

ULT 20
95956
US       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
INITION  Sequence 38 from patent US 6818444.
ESSION   AR595956
SION     AR595956.1  GI:56646937
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 1599)
UTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL   Patent: US 6818444-A 38 16-NOV-2004;
         Heska Corporation; Fort Collins, CO
TURES             Location/Qualifiers
  source          1. .1599
                  /organism="unknown"
                  /mol_type="genomic DNA"
GIN

gnment Scores:
d. No.:              1.94e-256      Length:         1599
re:                  216.00         Matches:        316
cent Similarity:     99.7%          Conservative:   0
t Local Similarity:  99.7%          Mismatches:     1
ry Match:            65.9%          Indels:         0
                     2              Gaps:           0

10-821-670A-56 (1-328) x AR595956 (1-1599)

        12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

        32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

        72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

        92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

       112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

       132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

       152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

       172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

       192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy     212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy     232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy     252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy     272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy     292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

Qy     312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 984

RESULT 21
AR595957/c
LOCUS       AR595957                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.94e-256      Length:         1599
Score:                  216.00         Matches:        316
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            65.9%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AR595957 (1-1599)

Qy      12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

Qy      32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

Qy      52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

Qy      72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327
```

```
        92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

       112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

       132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

       152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

       172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

       192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

       212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

       232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

       252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

       272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
       666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 616
```

ULT 22
95948
US AR595948 921 bp DNA linear PAT 15-DEC-2004
INITION Sequence 26 from patent US 6818444.
ESSION AR595948
SION AR595948.1 GI:56646929
WORDS .
RCE Unknown.
RGANISM Unknown.
Unclassified.
ERENCE 1 (bases 1 to 921)
UTHORS Wonderling,R.S. and Boroughs,K.L.
ITLE Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL Patent: US 6818444-A 26 16-NOV-2004;
Heska Corporation; Fort Collins, CO
TURES Location/Qualifiers
source 1. .921
/organism="unknown"
/mol_type="genomic DNA"
GIN

gnment Scores:
d. No.: 4.73e-243 Length: 921
re: 205.00 Matches: 305

```
Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            62.5%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x AR595948 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCys 328
              |||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGC 918

RESULT 23
AR595949/c
```

```
US       AR595949                 921 bp    DNA     linear   PAT 15-DEC-2004
INITION  Sequence 28 from patent US 6818444.
ESSION   AR595949
SION     AR595949.1  GI:56646930
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 921)
UTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL   Patent: US 6818444-A 28 16-NOV-2004;
         Heska Corporation; Fort Collins, CO
URES             Location/Qualifiers
  source         1. .921
                 /organism="unknown"
                 /mol_type="genomic DNA"
GIN

gnment Scores:
d. No.:              4.73e-243      Length:         921
re:                  205.00         Matches:        305
cent Similarity:     99.7%          Conservative:   0
t Local Similarity:  99.7%          Mismatches:     1
ry Match:            62.5%          Indels:         0
                     2              Gaps:           0

10-821-670A-56 (1-328) x AR595949 (1-921)

        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
       501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy     243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy     263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy     283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy     303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy     323 TrpAlaSerValSerCys 328
           |||||||||||||||||
Db      21 TGGGCATCCGTGTCCTGC 4

RESULT 24
AR595959
LOCUS       AR595959                 1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              8.02e-243      Length:         1533
Score:                  205.00         Matches:        305
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            62.5%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AR595959 (1-1533)

Qy      23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy      43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy      63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy      83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy     103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy     123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
901 TGGGCATCCGTGTCCTGC 918
```

```
ULT 25
95960/c
US       AR595960                1533 bp    DNA     linear   PAT 15-DEC-2004
INITION  Sequence 45 from patent US 6818444.
ESSION   AR595960
SION     AR595960.1  GI:56646941
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 1533)
UTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL   Patent: US 6818444-A 45 16-NOV-2004;
         Heska Corporation; Fort Collins, CO
TURES             Location/Qualifiers
   source         1. .1533
                  /organism="unknown"
                  /mol_type="genomic DNA"
GIN

gnment Scores:
d. No.:              8.02e-243      Length:          1533
re:                  205.00         Matches:         305
cent Similarity:     99.7%          Conservative:    0
t Local Similarity:  99.7%          Mismatches:      1
ry Match:            62.5%          Indels:          0
                     2              Gaps:            0

10-821-670A-56 (1-328) x AR595960 (1-1533)
```

```
Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       323 TrpAlaSerValSerCys 328
             |||||||||||||||||
Db       633 TGGGCATCCGTGTCCTGC 616
```

```
RESULT 26
AF054607
LOCUS       AF054607                431 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p40 subunit mRNA, partial cds.
ACCESSION   AF054607
VERSION     AF054607.1  GI:3126822
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
```

```
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
          Felinae; Felis.
ERENCE    1  (bases 1 to 431)
UTHORS    Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
          Day,M.J.
ITLE      Cytokine mRNA expression in lesions in cats with chronic
          gingivostomatitis
OURNAL    Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
UBMED     10391845
ERENCE    2  (bases 1 to 431)
UTHORS    Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
          Harbour,D.A.
ITLE      Direct Submission
OURNAL    Submitted (19-MAR-1998) Clinical Veterinary Science, University of
          Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
TURES               Location/Qualifiers
  source            1. .431
                    /organism="Felis catus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9685"
                    /cell_line="FL4"
                    /cell_type="T cell"
                    /note="persistant FIV infection"
  CDS               <1. .>431
                    /codon_start=1
                    /product="interleukin 12 p40 subunit"
                    /protein_id="AAC15980.1"
                    /db_xref="GI:3126823"
                    /translation="CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEA
                    KNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYT
                    VECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRD"

IN

nment Scores:
i. No.:              1.83e-145       Length:          431
re:                  126.00          Matches:         126
cent Similarity:     100.0%          Conservative:    0
t Local Similarity:  100.0%          Mismatches:      0
ry Match:            38.4%           Indels:          0
                     14              Gaps:            0

10-821-670A-56 (1-328) x AF054607 (1-431)

       107 LysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLys 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        52 AAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAG 111

       127 IlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThr 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       112 ATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 171

       147 AlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGln 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       172 GCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAA 231

       167 GlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAsp 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       232 GGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGAT 291

       187 TyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSer 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       292 TATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGC 351

       207 LeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       352 CTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGC 411

       227 SerPheIleArgAsp 232
           ||||||||||||||||
       412 AGCTTCTTCATCAGGGAC 429

ULT 27
```

```
AX154603
LOCUS       AX154603                990 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 7 from Patent WO0140257.
ACCESSION   AX154603
VERSION     AX154603.1  GI:14536186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 7 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              2.34e-53        Length:          990
Score:                  52.00           Matches:         52
Percent Similarity:     100.0%          Conservative:    0
Best Local Similarity:  100.0%          Mismatches:      0
Query Match:            15.9%           Indels:          0
DB:                     2               Gaps:            0

US-10-821-670A-56 (1-328) x AX154603 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCTGACCCACCCAAGAACTTG 726

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGlu 254
              ||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTAAAGAATTCTCGACACGTGGAG 762

RESULT 28
AX154600
LOCUS       AX154600                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0140257.
ACCESSION   AX154600
VERSION     AX154600.1  GI:14536183
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 4 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              1.22e-49        Length:          984
Score:                  49.00           Matches:         49
Percent Similarity:     100.0%          Conservative:    0
Best Local Similarity:  100.0%          Mismatches:      0
Query Match:            14.9%           Indels:          0
```

```
                    2             Gaps:          0

10-821-670A-56 (1-328) x AX154600 (1-984)

       124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       370 AAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGG 429

       144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       430 TGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCT 489

       164 AspProGlnGlyValThrCysGlyAla 172
           ||||||||||||||||||||||||||||
       490 GACCCCCAAGGGGTGACTTGTGGAGCC 516

ULT 29
54599
JS       AX154599                 984 bp    DNA     linear   PAT 22-JUN-2001
INITION  Sequence 3 from Patent WO0140257.
ESSION   AX154599
SION     AX154599.1  GI:14536182
WORDS    .
RCE      synthetic construct
RGANISM  synthetic construct
         other sequences; artificial sequences.
ERENCE   1
UTHORS   Leong,S.R. and Punnonen,J.
ITLE     Cytokine polypeptides and nucleic acids
OURNAL   Patent: WO 0140257-A 3 07-JUN-2001;
         Maxygen, Inc. (US)
TURES             Location/Qualifiers
  source          1. .984
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="Synthetic Sequence"
GIN

gnment Scores:
d. No.:              5.78e-41       Length:        984
re:                  42.00          Matches:       42
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            12.8%          Indels:        0
                     2              Gaps:          0

10-821-670A-56 (1-328) x AX154599 (1-984)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACTTG 726

       243 GlnLeu 244
           ||||||
       727 CAGCTG 732

ULT 30
91829
JS       AY191829                 972 bp    mRNA    linear   SYN 04-FEB-2003
INITION  Synthetic construct evolved IL-12 p40 precursor, mRNA, partial cds.
ESSION   AY191829
SION     AY191829.1  GI:27729525
WORDS    .
RCE      synthetic construct
RGANISM  synthetic construct
         other sequences; artificial sequences.
ERENCE   1  (bases 1 to 972)
UTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
         Punnonen,J.
ITLE     Optimized expression and specific activity of IL-12 by directed
         molecular evolution
OURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
UBMED    12529500
ERENCE   2  (bases 1 to 972)
UTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
         Punnonen,J.
ITLE     Direct Submission
OURNAL   Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
         Drive, Redwood City, CA 94063, USA
TURES             Location/Qualifiers
     source       1. .972
                  /organism="synthetic construct"
                  /mol_type="mRNA"
                  /db_xref="taxon:32630"
     CDS          1. .>972
                  /codon_start=1
                  /transl_table=11
                  /product="evolved IL-12 p40 precursor"
                  /protein_id="AAO19112.1"
                  /db_xref="GI:27729526"
                  /translation="MCHQQLVISWFSLVLLASPLMAIWELKKDVYVVELDWYPNAPGE
                  TVVLTCDTPEEDGITWTLDQSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGEALSRSLL
                  LLHKKEDGIWSTDILKDQKEPKNKSFLKCEAKNYSGRFTCWWLTTISTDLKFSVKSSR
                  GSTDPRGVTCGTATLSEDLGEYKKYRVECQEGSACPAAEESLPIEVVLEAVHKLKYEN
                  YTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWGYPDTWSTPHSYFSLTFCIQVQGK
                  SKREKKDRIFTDKTSATVICRKNAKIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide  1. .66
     mat_peptide  67. .972
                  /product="evolved IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:              9.91e-40       Length:        972
Score:                  41.00          Matches:       41
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            12.5%          Indels:        0
DB:                     8              Gaps:          0

US-10-821-670A-56 (1-328) x AY191829 (1-972)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

Qy        257 Trp 257
              |||
Db        754 TGG 756

RESULT 31
AX154597
LOCUS       AX154597                 975 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0140257.
ACCESSION   AX154597
VERSION     AX154597.1  GI:14536180
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 1 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .975
                     /organism="synthetic construct"
```

```
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic Sequence"
IN

nment Scores:
. No.:              9.94e-40        Length:         975
e:                  41.00           Matches:        41
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            12.5%           Indels:         0
                    2               Gaps:           0

10-821-670A-56 (1-328) x AX154597 (1-975)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

       257 Trp 257
           |||
       754 TGG 756

ULT 32
07654
US        AB107654                 993 bp    mRNA    linear   MAM 29-APR-2004
INITION   Lama glama IL-12 p40 mRNA for interleukin 12 p40 subunit, complete
          cds.
ESSION    AB107654
SION      AB107654.1  GI:29603618
WORDS     .
RCE       Lama glama (llama)
RGANISM   Lama glama
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
          Camelidae; Lama.
ERENCE    1
UTHORS    Odbileg,R., Lee,S.I., Yoshida,R., Chang,K.S., Ohashi,K.,
          Sugimoto,C. and Onuma,M.
ITLE      Cloning and sequence analysis of llama cytokines related to
          cell-mediated immunity
URNAL     Vet. Immunol. Immunopathol. 99 (1-2), 1-10 (2004)
UBMED     15113649
RENCE     2  (bases 1 to 993)
THORS     Ohashi,K., Raadan,O. and Lee,S.
TLE       Direct Submission
URNAL     Submitted (04-APR-2003) Kazuhiko Ohashi, Graduate School of
          Veterinary Medicine, Hokkaido University, Department of Disease
          Control; Kita-ku Kita 18 Nishi 9, Sapporo, Hokkaido 060-0818, Japan
          (E-mail:okazu@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
          Fax:81-11-706-5217)
TURES               Location/Qualifiers
  source            1. .993
                    /organism="Lama glama"
                    /mol_type="mRNA"
                    /db_xref="taxon:9844"
                    /sex="Female"
                    /cell_type="PBMC"
                    /country="Japan"
  gene              1. .993
                    /gene="IL-12 p40"
  CDS               1. .993
                    /gene="IL-12 p40"
                    /codon_start=1
                    /product="interleukin 12 p40 subunit"
                    /protein_id="BAC75391.1"
                    /db_xref="GI:29603619"
                    /translation="MHPQQLVVSWFSLVLLASPIMAIWELEKNVYVVELDWYPDAPGE
                    TVVLTCDTPEEDGITWTSDHSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                    LLHKKEDGVWSTDILKKDQKEPKSKTFLKCEAKNYSGHFTCWWLTAVSTDLKFSVKSS
                    RGSSDPRGVTCGAATLSAERVGVEHRDSWKYTVECQEGSSCPAAEESLPIELVVEAVH
                    KLKYENYSSSFFIRDIIRPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFC
                    VQVQGKHKREKKDKLFVDQTSAKVTCPKDASIRVQARDRYYSSSWSEWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:              3.05e-37        Length:         993
Score:                  39.00           Matches:        39
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.9%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-56 (1-328) x AB107654 (1-993)

Qy        236 ProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluVal 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 CCAGACCCACCCAAGAATCTGCAGCTGAAGCCATTGAAGAATTCTCGGCACGTGGAGGTC 768

Qy        256 SerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPhe 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 AGCTGGGAGTACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACGTTT 825

RESULT 33
AY234218
LOCUS       AY234218                1005 bp    mRNA    linear   PRI 07-APR-2003
DEFINITION  Papio anubis interleukin-12 alpha p40 subunit precursor (IL12a)
            mRNA, complete cds.
ACCESSION   AY234218
VERSION     AY234218.1  GI:29569754
KEYWORDS    .
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Nonhuman primate cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2003) Pathology & Laboratory Medicine, Emory
            University School of Medicine, Woodruff Memorial Building Rm 2339,
            1639 Pierce Drive, Atlanta, GA 30322, USA
FEATURES              Location/Qualifiers
     source           1. .1005
                      /organism="Papio anubis"
                      /mol_type="mRNA"
                      /db_xref="taxon:9555"
     gene             1. .1005
                      /gene="IL12a"
     CDS              9. .995
                      /gene="IL12a"
                      /codon_start=1
                      /product="interleukin-12 alpha p40 subunit precursor"
                      /protein_id="AAO85331.1"
                      /db_xref="GI:29569755"
                      /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                      MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                      LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                      GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                      KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQAEVSWEYPDTWSTPHSYFSLTFCIQ
                      VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
     sig_peptide      9. .74
                      /gene="IL12a"
     mat_peptide      75. .992
                      /gene="IL12a"
                      /product="interleukin-12 alpha p40 subunit"
ORIGIN
```

gnment Scores:
d. No.: 3.09e-37 Length: 1005
re: 39.00 Matches: 39
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 11.9% Indels: 0
5 Gaps: 0

10-821-670A-56 (1-328) x AY234218 (1-1005)

```
213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
642 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 701

233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
702 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 758
```

ULT 34
19834
US CTU19834 1005 bp mRNA linear PRI 03-FEB-1996
INITION Cercocebus torquatus interleukin-12 alpha p40 subunit (IL-12a) mRNA, complete cds.
ESSION U19834
SION U19834.1 GI:644785
WORDS .
RCE Cercocebus torquatus (red-crowned mangabey)
RGANISM Cercocebus torquatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercocebus.
ERENCE 1 (bases 1 to 1005)
UTHORS Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
ITLE Comparative sequence analysis of cytokine genes from human and nonhuman primates
OURNAL J. Immunol. 155 (8), 3946-3954 (1995)
PUBMED 7561102
ERENCE 2 (bases 1 to 1005)
UTHORS Villinger,F.J.
ITLE Direct Submission
OURNAL Submitted (13-JAN-1995) Francois J. Villinger, Emory University, Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
TURES Location/Qualifiers
source 1. .1005
/organism="Cercocebus torquatus"
/mol_type="mRNA"
/sub_species="atys"
/db_xref="taxon:9530"
/clone="FPn IL-12a"
/cell_type="peripheral blood mononuclear cells"
/tissue_type="blood"
gene 1. .1005
/gene="IL-12a"
CDS 9. .995
/gene="IL-12a"
/function="NK cell stimulatory factor"
/codon_start=1
/product="interleukin-12 alpha p40 subunit"
/protein_id="AAA86701.1"
/db_xref="GI:644786"
/translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
LPHKKEDGIWSTDILKDQKEPKNETFLRCEAKNYSGRITCWWLSTISTDLTFSIISSR
GSSNPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWNEWTSVPCS"
GIN

gnment Scores:
d. No.: 3.09e-37 Length: 1005
re: 39.00 Matches: 39
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
Query Match: 11.9% Indels: 0
DB: 5 Gaps: 0

US-10-821-670A-56 (1-328) x CTU19834 (1-1005)

```
Qy  213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  642 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 701

Qy  233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  702 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 758
```

RESULT 35
MMU19841
LOCUS MMU19841 1080 bp mRNA linear PRI 03-FEB-1996
DEFINITION Macaca mulatta interleukin-12 alpha (IL-12a) mRNA, complete cds.
ACCESSION U19841
VERSION U19841.1 GI:644799
KEYWORDS .
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 1080)
AUTHORS Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
TITLE Comparative sequence analysis of cytokine genes from human and nonhuman primates
JOURNAL J. Immunol. 155 (8), 3946-3954 (1995)
PUBMED 7561102
REFERENCE 2 (bases 1 to 1080)
AUTHORS Villinger,F.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-1995) Francois J. Villinger, Emory University, Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES Location/Qualifiers
source 1. .1080
/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
/clone="RSo IL-12a clone 4"
/cell_type="peripheral blood mononuclear cells"
/tissue_type="blood"
gene 1. .1080
/gene="IL-12a"
CDS 13. .999
/gene="IL-12a"
/function="NK cell stimulatory factor"
/codon_start=1
/product="interleukin-12 alpha"
/protein_id="AAB60397.1"
/db_xref="GI:644800"
/translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
variation 329
/gene="IL-12a"
/replace="t"
variation 405
/gene="IL-12a"
/replace="c"
variation 519
/gene="IL-12a"
/replace="a"
variation 629
/gene="IL-12a"
/note="Leu to Pro"
/replace="c"
variation 665

```
                /gene="IL-12a"
                /note="Leu to Pro"
                /replace="c"
  variation     714
                /gene="IL-12a"
                /replace="g"
  variation     878
                /gene="IL-12a"
                /note="Ile to Thr"
                /replace="c"
  variation     895
                /gene="IL-12a"
                /note="Ser to Pro"
                /replace="c"
IN

nment Scores:
i. No.:              3.33e-37       Length:        1080
e:                   39.00          Matches:       39
ent Similarity:      100.0%         Conservative:  0
Local Similarity:    100.0%         Mismatches:    0
y Match:             11.9%          Indels:        0
                     5              Gaps:          0

0-821-670A-56 (1-328) x MMU19841 (1-1080)

       213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 705

       233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       706 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 762

LT 36
5965
S       AR595965                 921 bp    DNA     linear   PAT 15-DEC-2004
NITION  Sequence 52 from patent US 6818444.
SSION   AR595965
SION    AR595965.1  GI:56646946
WORDS   .
RCE     Unknown.
RGANISM Unknown.
        Unclassified.
ERENCE  1  (bases 1 to 921)
UTHORS  Wonderling,R.S. and Boroughs,K.L.
ITLE    Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL  Patent: US 6818444-A 52 16-NOV-2004;
        Heska Corporation; Fort Collins, CO
TURES             Location/Qualifiers
  source          1. .921
                  /organism="unknown"
                  /mol_type="genomic DNA"
IN

nment Scores:
i. No.:              8.52e-35       Length:        921
e:                   37.00          Matches:       37
ent Similarity:      100.0%         Conservative:  0
Local Similarity:    100.0%         Mismatches:    0
y Match:             11.3%          Indels:        0
                     2              Gaps:          0

0-821-670A-56 (1-328) x AR595965 (1-921)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651
```

```
RESULT 37
AR595966/c
LOCUS       AR595966                 921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 54 from patent US 6818444.
ACCESSION   AR595966
VERSION     AR595966.1  GI:56646947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 54 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              8.52e-35       Length:        921
Score:                  37.00          Matches:       37
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.3%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x AR595966 (1-921)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 38
BD171282
LOCUS       BD171282                 924 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171282
VERSION     BD171282.1  GI:28412572
KEYWORDS    JP 2002241398-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 924)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 2 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/2
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .924
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
```

```
d. No.:              8.55e-35        Length:         924
re:                  37.00           Matches:        37
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            11.3%           Indels:         0
                     2               Gaps:           0

10-821-670A-56 (1-328) x BD171282 (1-924)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       544 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 603

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
       604 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 654

ULT 39
95969
JS       AR595969                 987 bp    DNA     linear   PAT 15-DEC-2004
INITION  Sequence 58 from patent US 6818444.
ESSION   AR595969
SION     AR595969.1  GI:56646950
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 987)
UTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
URNAL    Patent: US 6818444-A 58 16-NOV-2004;
         Heska Corporation; Fort Collins, CO
TURES             Location/Qualifiers
  source          1. .987
                  /organism="unknown"
                  /mol_type="genomic DNA"
GIN

gnment Scores:
d. No.:              9.15e-35        Length:         987
re:                  37.00           Matches:        37
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            11.3%           Indels:         0
                     2               Gaps:           0

10-821-670A-56 (1-328) x AR595969 (1-987)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 40
95970/c
US       AR595970                 987 bp    DNA     linear   PAT 15-DEC-2004
INITION  Sequence 60 from patent US 6818444.
ESSION   AR595970
SION     AR595970.1  GI:56646951
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 987)
UTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
URNAL    Patent: US 6818444-A 60 16-NOV-2004;
         Heska Corporation; Fort Collins, CO
TURES             Location/Qualifiers
  source          1. .987
                  /organism="unknown"
                  /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:           9.15e-35        Length:         987
Score:               37.00           Matches:        37
Percent Similarity:  100.0%          Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:         11.3%           Indels:         0
DB:                  2               Gaps:           0

US-10-821-670A-56 (1-328) x AR595970 (1-987)

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 41
AR151061
LOCUS       AR151061                 990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6231850.
ACCESSION   AR151061
VERSION     AR151061.1  GI:15117111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:           9.18e-35        Length:         990
Score:               37.00           Matches:        37
Percent Similarity:  100.0%          Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:         11.3%           Indels:         0
DB:                  2               Gaps:           0

US-10-821-670A-56 (1-328) x AR151061 (1-990)

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 42
AR151071
LOCUS       AR151071                 990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6231850.
ACCESSION   AR151071
VERSION     AR151071.1  GI:15117121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
```

```
URNAL   Patent: US 6231850-A 11 15-MAY-2001;
TURES             Location/Qualifiers
  source          1. .990
                  /organism="unknown"
                  /mol_type="unassigned DNA"
IN

nment Scores:
. No.:            9.18e-35       Length:        990
e:                37.00          Matches:       37
ent Similarity:   100.0%         Conservative:  0
 Local Similarity: 100.0%        Mismatches:    0
y Match:          11.3%          Indels:        0
                  2              Gaps:          0

0-821-670A-56 (1-328) x AR151071 (1-990)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

LT 43
4653
S       BD014653                 990 bp    DNA     linear   PAT 27-AUG-2002
NITION  Process for producing highly pure protein, interleukin 12, protein
        inhibiting interleukin-12 activity, remedies for mammalian
        immunopathy and method of treating immunopathy.
ESSION  BD014653
SION    BD014653.1  GI:22555436
WORDS   JP 2001161378-A/1.
RCE     Canis sp.
RGANISM Canis sp.
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
        Canis.
ERENCE  1  (bases 1 to 990)
UTHORS  Okano,F.
ITLE    Process for producing highly pure protein, interleukin 12, protein
        inhibiting interleukin-12 activity, remedies for mammalian
        immunopathy and method of treating immunopathy
URNAL   Patent: JP 2001161378-A 1 19-JUN-2001;
        TORAY INDUSTRIES INC
ENT     OS   Canis sp. (dog)
        PN   JP 2001161378-A/1
        PD   19-JUN-2001
        PF   26-SEP-2000 JP 2000292946
        PI   FUMIYOSHI OKANO
        PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
        PC   A61P35/00,
        PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
        PC   C12R1:91),
        PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
        CC   Process for producing highly pure protein, interleukin 12,  CC
             protein
        CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
             immunopathy and
        CC   method of treating immunopathy
        FH   Key             Location/Qualifiers
        FT   CDS             (1). .(987)
        FT   mat_peptide     (67). .(987).
TURES             Location/Qualifiers
  source          1. .990
                  /organism="Canis sp."
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9616"
IN

nment Scores:
. No.:            9.18e-35       Length:        990
Score:                37.00          Matches:       37
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          11.3%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-56 (1-328) x BD014653 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 44
BD014663
LOCUS       BD014663                 990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014663
VERSION     BD014663.1  GI:22555446
KEYWORDS    JP 2001161378-A/11.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 11 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/11
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
            FT   mat_peptide     (67). .(987).
FEATURES              Location/Qualifiers
     source           1. .990
                      /organism="Canis sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:            9.18e-35       Length:        990
Score:                37.00          Matches:       37
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          11.3%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-56 (1-328) x BD014663 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 45
017
JS        E15017                    990 bp    DNA     linear   PAT 28-JUL-1999
INITION   Canine mRNA for interleukin 12 40kDa subunit,complete cds.
ESSION    E15017
SION      E15017.1  GI:5709700
WORDS     JP 1998036397-A/1.
RCE       Canis sp.
RGANISM   Canis sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
          Canis.
ERENCE    1  (bases 1 to 990)
UTHORS    Okano,F.
ITLE      CANINE INTERLEUKIN 12 AND ITS PRODUCTION
OURNAL    Patent: JP 1998036397-A 1 10-FEB-1998;
          TORAY IND INC
MENT      OS   Canis sp. (dog)
          PN   JP 1998036397-A/1
          PD   10-FEB-1998
          PF   08-NOV-1996 JP 1996296789
          PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
          OKANO FUMIYOSHI
          PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
            C12R1:91),
          PC   (C12P21/02,C12R1:91);
          CC   strandedness: Double;
          CC   topology: Linear;
          FH   Key             Location/Qualifiers
          FH
          FT   source          1. .990
          FT                   /organism='Canis sp.'
          FT                   /tissue_type='liver'
          FT   CDS             1. .990
          FT                   /product='interleukin 12 40kDa subunit'.
TURES               Location/Qualifiers
  source            1. .990
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
IN

gnment Scores:
d. No.:                9.18e-35       Length:          990
re:                    37.00          Matches:         37
cent Similarity:       100.0%         Conservative:    0
t Local Similarity:    100.0%         Mismatches:      0
ry Match:              11.3%          Indels:          0
                       2              Gaps:            0

10-821-670A-56 (1-328) x E15017 (1-990)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 46
16460
US        AR316460                  990 bp    mRNA    linear   PAT 17-AUG-2003
INITION   Sequence 1 from patent US 6562334.
ESSION    AR316460
SION      AR316460.1  GI:33695288
KEYWORDS  .
SOURCE    Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE 1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 1 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                9.18e-35       Length:          990
Score:                    37.00          Matches:         37
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              11.3%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-56 (1-328) x AR316460 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 47
AR316470
LOCUS       AR316470                  990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6562334.
ACCESSION   AR316470
VERSION     AR316470.1  GI:33695298
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 11 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                9.18e-35       Length:          990
Score:                    37.00          Matches:         37
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              11.3%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-56 (1-328) x AR316470 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

```
ULT 48
9100
JS        CFU49100                1015 bp    mRNA    linear   MAM 13-MAR-1996
INITION   Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ESSION    U49100
SION      U49100.1  GI:1223907
WORDS     .
RCE       Canis familiaris (dog)
RGANISM   Canis familiaris
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
          Canis.
ERENCE    1  (bases 1 to 1015)
UTHORS    Belke-Louis,G.F. and Buettner,M.
ITLE      Cloning and sequence analysis of the p35 and p40 subunits of canine
          interleukin-12
URNAL     Unpublished
ERENCE    2  (bases 1 to 1015)
UTHORS    Belke-Louis,G.F.
ITLE      Direct Submission
URNAL     Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
          Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
TURES               Location/Qualifiers
  source            1. .1015
                    /organism="Canis familiaris"
                    /mol_type="mRNA"
                    /db_xref="taxon:9615"
  CDS               1. .990
                    /codon_start=1
                    /product="interleukin-12 p40 subunit"
                    /protein_id="AAA92059.1"
                    /db_xref="GI:1223908"
                    /translation="MHPQQLVISWFSLVLLASSLMTIWELEKDVYVVELDWHPDAPGE
                    MVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLL
                    LIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                    GFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHK
                    LKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCV
                    QAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCS"
IN

nment Scores:
i. No.:              9.42e-35       Length:        1015
e:                   37.00          Matches:       37
ent Similarity:      100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
y Match:             11.3%          Indels:        0
                     14             Gaps:          0

0-821-670A-56 (1-328) x CFU49100 (1-1015)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 49
95973
JS        AR595973                1533 bp    DNA     linear   PAT 15-DEC-2004
INITION   Sequence 66 from patent US 6818444.
SSION     AR595973
SION      AR595973.1  GI:56646954
WORDS     .
CE        Unknown.
GANISM    Unknown.
          Unclassified.
RENCE     1  (bases 1 to 1533)
THORS     Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
URNAL     Patent: US 6818444-A 66 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .1533
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:           1.44e-34       Length:        1533
Score:               37.00          Matches:       37
Percent Similarity:  100.0%         Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:         11.3%          Indels:        0
DB:                  2              Gaps:          0

US-10-821-670A-56 (1-328) x AR595973 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 50
AR595974/c
LOCUS       AR595974                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .1533
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:           1.44e-34       Length:        1533
Score:               37.00          Matches:       37
Percent Similarity:  100.0%         Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:         11.3%          Indels:        0
DB:                  2              Gaps:          0

US-10-821-670A-56 (1-328) x AR595974 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 51
AR595971
LOCUS       AR595971                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

```
          Unclassified.
ERENCE    1  (bases 1 to 1599)
UTHORS    Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL    Patent: US 6818444-A 61 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
TURES               Location/Qualifiers
   source           1. .1599
                    /organism="unknown"
                    /mol_type="genomic DNA"
GIN

gnment Scores:
d. No.:                1.51e-34        Length:         1599
re:                    37.00           Matches:        37
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              11.3%           Indels:         0
                       2               Gaps:           0

10-821-670A-56 (1-328) x AR595971 (1-1599)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

JLT 52
95972/c
JS        AR595972                1599 bp    DNA     linear   PAT 15-DEC-2004
INITION   Sequence 63 from patent US 6818444.
ESSION    AR595972
SION      AR595972.1  GI:56646953
WORDS     .
RCE       Unknown.
RGANISM   Unknown.
          Unclassified.
ERENCE    1  (bases 1 to 1599)
UTHORS    Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL    Patent: US 6818444-A 63 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
TURES               Location/Qualifiers
   source           1. .1599
                    /organism="unknown"
                    /mol_type="genomic DNA"
GIN

gnment Scores:
d. No.:                1.51e-34        Length:         1599
re:                    37.00           Matches:        37
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              11.3%           Indels:         0
                       2               Gaps:           0

10-821-670A-56 (1-328) x AR595972 (1-1599)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

JLT 53
71281
JS        BD171281                2154 bp    DNA     linear   PAT 18-FEB-2003
INITION   Novel canine cytokine protein.
```

```
ACCESSION   BD171281
VERSION     BD171281.1  GI:28412571
KEYWORDS    JP 2002241398-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 2154)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 1 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/1
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .2154
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              2.06e-34        Length:         2154
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.3%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-56 (1-328) x BD171281 (1-2154)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 720

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 771

RESULT 54
AR596011
LOCUS       AR596011                2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 107 from patent US 6818444.
ACCESSION   AR596011
VERSION     AR596011.1  GI:56646992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 107 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .2267
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.17e-34        Length:         2267
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
```

```
y Match:            11.3%          Indels:        0
                    2              Gaps:          0

10-821-670A-56 (1-328) x AR596011 (1-2267)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

LT 55
6012/c
S       AR596012                2267 bp    DNA     linear   PAT 15-DEC-2004
INITION  Sequence 109 from patent US 6818444.
SSION   AR596012
SION    AR596012.1  GI:56646993
WORDS   .
CE      Unknown.
RGANISM  Unknown.
        Unclassified.
ERENCE  1  (bases 1 to 2267)
UTHORS  Wonderling,R.S. and Boroughs,K.L.
ITLE    Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL  Patent: US 6818444-A 109 16-NOV-2004;
        Heska Corporation; Fort Collins, CO
TURES           Location/Qualifiers
  source        1. .2267
                /organism="unknown"
                /mol_type="genomic DNA"
IN

gnment Scores:
i. No.:             2.17e-34       Length:        2267
e:                  37.00          Matches:       37
ent Similarity:     100.0%         Conservative:  0
 Local Similarity:  100.0%         Mismatches:    0
y Match:            11.3%          Indels:        0
                    2              Gaps:          0

10-821-670A-56 (1-328) x AR596012 (1-2267)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
      1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

LT 56
1134
S       AF091134                446 bp    mRNA    linear   MAM 04-AUG-1999
INITION  Canis familiaris interleukin-12 p40 mRNA, partial cds.
SSION   AF091134
SION    AF091134.1  GI:5690205
WORDS   .
RCE     Canis familiaris (dog)
RGANISM  Canis familiaris
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
        Canis.
ERENCE  1  (bases 1 to 446)
UTHORS  German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J.
ITLE    Cloning and sequencing of canine IL-12 p40 mRNA
OURNAL  Unpublished
ERENCE  2  (bases 1 to 446)
UTHORS  German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J.
ITLE    Direct Submission
OURNAL  Submitted (12-SEP-1998) Department of Clinical Veterinary Science,
        University of Bristol, Langford House, Langford, Bristol, North
        Somerset BS40 5DU, United Kingdom
FEATURES            Location/Qualifiers
     source         1. .446
                    /organism="Canis familiaris"
                    /mol_type="mRNA"
                    /db_xref="taxon:9615"
     CDS            <1. .>446
                    /note="Il-12 p40"
                    /codon_start=1
                    /product="interleukin-12 p40"
                    /protein_id="AAD46992.1"
                    /db_xref="GI:5690206"
                    /translation="LGAGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIW
                    STDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTC
                    GAVTLSAERVRVDNRDYNKYTVECQEGSACPSAEESLPIEVVVDAIP"
ORIGIN

Alignment Scores:
Pred. No.:          6.97e-34       Length:        446
Score:              36.00          Matches:       36
Percent Similarity: 100.0%         Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:        11.0%          Indels:        0
DB:                 14             Gaps:          0

US-10-821-670A-56 (1-328) x AF091134 (1-446)

Qy      119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      151 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 210

Qy      139 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db      211 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 258

RESULT 57
AF333121
LOCUS       AF333121                452 bp    mRNA    linear   MAM 06-FEB-2001
DEFINITION  Canis familiaris interleukin 12 subunit p40 mRNA, partial cds.
ACCESSION   AF333121
VERSION     AF333121.1  GI:12667429
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Expression of canine interleukin-12 subunit p40 mRNA in a
            continuous macrophage cell line
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JAN-2001) Department of Veterinary Pathology,
            Justus-Liebig-University of Giessen, Frankfurter Strasse 96,
            Giessen 35392, Germany
FEATURES            Location/Qualifiers
     source         1. .452
                    /organism="Canis familiaris"
                    /mol_type="mRNA"
                    /db_xref="taxon:9615"
                    /cell_line="DH 82"
                    /cell_type="macrophage"
                    /note="amplified using primer pair p77s/p34as"
     CDS            <1. .>452
                    /codon_start=2
                    /product="interleukin 12 subunit p40"
                    /protein_id="AAK01441.1"
                    /db_xref="GI:12667430"
                    /translation="TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK
                    GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST
```

DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
GIN

gnment Scores:
d. No.: 7.07e-34 Length: 452
re: 36.00 Matches: 36
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 11.0% Indels: 0
14 Gaps: 0

10-821-670A-56 (1-328) x AF333121 (1-452)

119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
212 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 271

139 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
272 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 319

ULT 58
49536
US AF349536 588 bp mRNA linear MAM 17-MAY-2001
INITION Canis familiaris interleukin-12 subunit p40 mRNA, partial cds.
ESSION AF349536
SION AF349536.1 GI:14133584
WORDS .
RCE Canis familiaris (dog)
RGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
ERENCE 1 (bases 1 to 588)
UTHORS Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
ITLE Sequence of canine interleukin-12-p40 mRNA in DH82-cells
OURNAL Unpublished
ERENCE 2 (bases 1 to 588)
UTHORS Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
ITLE Direct Submission
OURNAL Submitted (15-FEB-2001) Institute of Pathology,
Justus-Liebig-University, Frankfurter Str. 96, Giessen 35392,
Germany
TURES Location/Qualifiers
source 1. .588
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/cell_line="DH82"
CDS <1. .>588
/codon_start=3
/product="interleukin-12 subunit p40"
/protein_id="AAK54070.1"
/db_xref="GI:14133585"
/translation="QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVV
LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIH
KKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFS
DPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
GIN

gnment Scores:
d. No.: 9.29e-34 Length: 588
re: 36.00 Matches: 36
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 11.0% Indels: 0
14 Gaps: 0

10-821-670A-56 (1-328) x AF349536 (1-588)

119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
348 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 407

Qy 139 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
Db 408 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 455

RESULT 59
BD021808
LOCUS BD021808 906 bp DNA linear PAT 27-AUG-2002
DEFINITION Natural killer stimulatory factor.
ACCESSION BD021808
VERSION BD021808.1 GI:22563031
KEYWORDS JP 2001245678-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 906)
AUTHORS Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
Hewick,R.M.
TITLE Natural killer stimulatory factor
JOURNAL Patent: JP 2001245678-A 1 11-SEP-2001;
GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT OS Unidentified
PN JP 2001245678-A/1
PD 11-SEP-2001
PF 10-JAN-2001 JP 2001002839
PR 10-NOV-1988 US 269945,07-FEB-1989 US 307817 PI
GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C PI
CLARK,
PI GORDON G WONG,RODNEY M HEWICK
PC C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
PC A61P43/00,
PC C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
Natural killer stimulatory factor
FH Key Location/Qualifiers
FT source 1. .906
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1. .906
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.: 2.52e-32 Length: 906
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-56 (1-328) x BD021808 (1-906)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
Db 678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
Db 738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 60
BD021809
LOCUS BD021809 906 bp DNA linear PAT 27-AUG-2002
DEFINITION Natural killer stimulatory factor.
ACCESSION BD021809
VERSION BD021809.1 GI:22563032
KEYWORDS JP 2001245678-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 906)
AUTHORS Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and

```
        Hewick,R.M.
ITLE    Natural killer stimulatory factor
OURNAL  Patent: JP 2001245678-A 2 11-SEP-2001;
        GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
IENT    OS   Unidentified
        PN   JP 2001245678-A/2
        PD   11-SEP-2001
        PF   10-JAN-2001 JP 2001002839
        PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
        GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
        CLARK,
        PI   GORDON G WONG,RODNEY M HEWICK
        PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
        PC   A61P43/00,
        PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
        Natural killer stimulatory factor
        FH   Key             Location/Qualifiers
        FT   source          1. .906
        FT                   /organism='Unidentified'.
TURES           Location/Qualifiers
  source        1. .906
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
IN

nment Scores:
. No.:              2.52e-32        Length:         906
e:                  35.00           Matches:        35
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            10.7%           Indels:         0
                    2               Gaps:           0

0-821-670A-56 (1-328) x BD021809 (1-906)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

ULT 61
54602
JS      AX154602                975 bp    DNA     linear   PAT 22-JUN-2001
INITION Sequence 6 from Patent WO0140257.
ESSION  AX154602
SION    AX154602.1  GI:14536185
WORDS   .
RCE     synthetic construct
RGANISM synthetic construct
        other sequences; artificial sequences.
ERENCE  1
UTHORS  Leong,S.R. and Punnonen,J.
ITLE    Cytokine polypeptides and nucleic acids
OURNAL  Patent: WO 0140257-A 6 07-JUN-2001;
        Maxygen, Inc. (US)
TURES           Location/Qualifiers
  source        1. .975
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic Sequence"
IN

nment Scores:
. No.:              2.72e-32        Length:         975
e:                  35.00           Matches:        35
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            10.7%           Indels:         0
DB:                 2               Gaps:           0

US-10-821-670A-56 (1-328) x AX154602 (1-975)

Qy      128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      382 TTTCTAAAGTGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGGTGGCTGACGGCA 441

Qy      148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
            ||||||||||||||||||||||||||||||||||||||||||||
Db      442 ATCAGTACTGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

RESULT 62
AR008950
LOCUS       AR008950                987 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5756085.
ACCESSION   AR008950
VERSION     AR008950.1  GI:3967755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 1 26-MAY-1998;
FEATURES            Location/Qualifiers
     source         1. .987
                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.76e-32        Length:         987
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-56 (1-328) x AR008950 (1-987)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 63
BD007070
LOCUS       BD007070                987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007070
VERSION     BD007070.1  GI:18635441
KEYWORDS    JP 2001503257-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 1 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
```

```
          PC   C12N15/00,A61K37/02
          CC   Strandedness: Single;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers
          FT   source          1. .987
          FT                   /organism='Unidentified'.
TURES             Location/Qualifiers
  source          1. .987
                  /organism="unidentified"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32644"
GIN

gnment Scores:
d. No.:               2.76e-32       Length:         987
re:                   35.00          Matches:        35
cent Similarity:      100.0%         Conservative:   0
t Local Similarity:   100.0%         Mismatches:     0
ry Match:             10.7%          Indels:         0
                      2              Gaps:           0

10-821-670A-56 (1-328) x BD007070 (1-987)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ULT 64
07076
JS        BD007076                 987 bp    DNA     linear   PAT 31-JAN-2002
INITION   Gene expression and delivery systems and uses.
ESSION    BD007076
SION      BD007076.1  GI:18635447
WORDS     JP 2001503258-A/1.
RCE       unidentified
RGANISM   unidentified
          unclassified sequences.
ERENCE    1  (bases 1 to 987)
UTHORS    Nodosutoromu,J., Freemark,B. and Dishupande,D.
ITLE      Gene expression and delivery systems and uses
OURNAL    Patent: JP 2001503258-A 1 13-MAR-2001;
          BARENTISU INC
MENT      OS   Unidentified
          PN   JP 2001503258-A/1
          PD   13-MAR-2001
          PF   10-OCT-1997 JP 1998519520
          PR   18-OCT-1996 US    60/028687
          PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
          C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
          C12N15/00
          CC   Strandedness: Single;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers
          FT   source          1. .987
          FT                   /organism='Unidentified'.
TURES             Location/Qualifiers
  source          1. .987
                  /organism="unidentified"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32644"
GIN

gnment Scores:
d. No.:               2.76e-32       Length:         987
re:                   35.00          Matches:        35
cent Similarity:      100.0%         Conservative:   0
t Local Similarity:   100.0%         Mismatches:     0
ry Match:             10.7%          Indels:         0
                      2              Gaps:           0
```

```
US-10-821-670A-56 (1-328) x BD007076 (1-987)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 65
BD007077
LOCUS       BD007077                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007077
VERSION     BD007077.1  GI:18635448
KEYWORDS    JP 2001503258-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 2 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/2
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .987
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              2.76e-32       Length:         987
Score:                  35.00          Matches:        35
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            10.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x BD007077 (1-987)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 66
BD007078
LOCUS       BD007078                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007078
VERSION     BD007078.1  GI:18635449
KEYWORDS    JP 2001503258-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
```

```
        unclassified sequences.
ERENCE  1  (bases 1 to 987)
THORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
ITLE    Gene expression and delivery systems and uses
URNAL   Patent: JP 2001503258-A 3 13-MAR-2001;
        BARENTISU INC
MENT    OS   Unidentified
        PN   JP 2001503258-A/3
        PD   13-MAR-2001
        PF   10-OCT-1997 JP 1998519520
        PR   18-OCT-1996 US    60/028687
        PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
        C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
        C12N15/00
        CC   Strandedness: Single;
        CC   Topology: Linear;
        FH   Key             Location/Qualifiers
        FT   source          1. .987
        FT                   /organism='Unidentified'.
TURES             Location/Qualifiers
  source          1. .987
                  /organism="unidentified"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32644"
IN

nment Scores:
i. No.:              2.76e-32       Length:        987
e:                   35.00          Matches:       35
ent Similarity:      100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
y Match:             10.7%          Indels:        0
                     2              Gaps:          0

10-821-670A-56 (1-328) x BD007078 (1-987)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

LT 67
6034
S       BD136034                987 bp    DNA     linear   PAT 18-SEP-2002
NITION  Interferon alpha plasmid and delivery system and method of
        preparing and using the same.
SSION   BD136034
ION     BD136034.1  GI:23230979
ORDS    JP 2002506647-A/1.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
ERENCE  1  (bases 1 to 987)
THORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
ITLE    Interferon alpha plasmid and delivery system and method of
        preparing and using the same
URNAL   Patent: JP 2002506647-A 1 05-MAR-2002;
        VALENTIS INC
MENT    OS   Homo sapiens (human)
        PN   JP 2002506647-A/1
        PD   05-MAR-2002
        PF   12-MAR-1999 JP 2000536861
        PR   19-MAR-1998 US    60/078654
        PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
        PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
        PC   C12N1/15,
        PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
         C12N5/00
        CC   Interferon alpha plasmid and delivery system and method of  CC
             preparing and
        CC   using the same
        FH   Key             Location/Qualifiers
        FT   source          1. .987
        FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              2.76e-32       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x BD136034 (1-987)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||
Db         706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 68
BD136035
LOCUS       BD136035                987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136035
VERSION     BD136035.1  GI:23230980
KEYWORDS    JP 2002506647-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 2 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/2
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: all codons optimized
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              2.76e-32       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
```

```
:t Local Similarity:  100.0%          Mismatches:    0
ry Match:             10.7%           Indels:        0
                      2               Gaps:          0

10-821-670A-56 (1-328) x BD136035 (1-987)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

JLT 69
36036
JS       BD136036                 987 bp    DNA     linear   PAT 18-SEP-2002
INITION  Interferon alpha plasmid and delivery system and method of
         preparing and using the same.
'ESSION  BD136036
:SION    BD136036.1  GI:23230981
'WORDS   JP 2002506647-A/3.
'RCE     synthetic construct
'RGANISM synthetic construct
         other sequences; artificial sequences.
ERENCE   1  (bases 1 to 987)
'UTHORS  Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
ITLE     Interferon alpha plasmid and delivery system and method of
         preparing and using the same
'OURNAL  Patent: JP 2002506647-A 3 05-MAR-2002;
         VALENTIS INC
'MENT    OS   Artificial Sequence
         PN   JP 2002506647-A/3
         PD   05-MAR-2002
         PF   12-MAR-1999 JP 2000536861
         PR   19-MAR-1998 US    60/078654
         PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
         PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
         PC   C12N1/15,
         PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
          C12N5/00
         CC   Sequence source: most codons optimized
         FH   Key             Location/Qualifiers
         FT   source          1. .987
         FT                   /organism='Artificial Sequence'.
TURES              Location/Qualifiers
  source           1. .987
                   /organism="synthetic construct"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:32630"
IN

gnment Scores:
d. No.:               2.76e-32       Length:        987
re:                   35.00          Matches:       35
cent Similarity:      100.0%         Conservative:  0
t Local Similarity:   100.0%         Mismatches:    0
ry Match:             10.7%          Indels:        0
                      2              Gaps:          0

10-821-670A-56 (1-328) x BD136036 (1-987)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

JLT 70
03342
JS       CQ803342                 987 bp    DNA     linear   PAT 10-MAY-2004
```

```
DEFINITION  Sequence 2 from Patent WO2004035799.
ACCESSION   CQ803342
VERSION     CQ803342.1  GI:47110208
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 2 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                2.76e-32       Length:        987
Score:                    35.00          Matches:       35
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              10.7%          Indels:        0
DB:                       2              Gaps:          0

US-10-821-670A-56 (1-328) x CQ803342 (1-987)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 71
CS131491
LOCUS       CS131491                 987 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 10 from Patent WO2005066348.
ACCESSION   CS131491
VERSION     CS131491.1  GI:71794159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 10 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HuIL12 p40 subunit"
ORIGIN

Alignment Scores:
Pred. No.:                2.76e-32       Length:        987
Score:                    35.00          Matches:       35
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              10.7%          Indels:        0
DB:                       2              Gaps:          0

US-10-821-670A-56 (1-328) x CS131491 (1-987)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ULT 72
591
JS       I28591                  987 bp    DNA     linear   PAT 06-FEB-1997
INITION  Sequence 1 from patent US 5573764.
ESSION   I28591
SION     I28591.1  GI:1819367
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 987)
UTHORS   Sykes,M. and Wolf,S.F.
ITLE     Use of interleukin-12 to prevent graft versus host disease
URNAL    Patent: US 5573764-A 1 12-NOV-1996;
TURES             Location/Qualifiers
  source          1. .987
                  /organism="unknown"
                  /mol_type="unassigned DNA"
IN

gnment Scores:
.. No.:              2.76e-32       Length:         987
e:                   35.00          Matches:        35
ent Similarity:      100.0%         Conservative:   0
 Local Similarity:   100.0%         Mismatches:     0
y Match:             10.7%          Indels:         0
                     2              Gaps:           0

0-821-670A-56 (1-328) x I28591 (1-987)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ULT 73
34633
JS       AX154633                987 bp    DNA     linear   PAT 22-JUN-2001
INITION  Sequence 37 from Patent WO0140257.
ESSION   AX154633
SION     AX154633.1  GI:14536197
WORDS    .
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1
UTHORS   Leong,S.R. and Punnonen,J.
ITLE     Cytokine polypeptides and nucleic acids
URNAL    Patent: WO 0140257-A 37 07-JUN-2001;
         Maxygen, Inc. (US)
TURES             Location/Qualifiers
  source          1. .987
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
IN

nment Scores:
.. No.:              2.76e-32       Length:         987
e:                   35.00          Matches:        35
ent Similarity:      100.0%         Conservative:   0
Best Local Similarity:  100.0%      Mismatches:     0
Query Match:            10.7%       Indels:         0
DB:                     2           Gaps:           0

US-10-821-670A-56 (1-328) x AX154633 (1-987)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 74
AF180563
LOCUS       AF180563                1007 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P40 mRNA, complete cds.
ACCESSION   AF180563
VERSION     AF180563.1  GI:5923854
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
     source          1. .1007
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="peripheral mononuclear"
     CDS             7. .993
                     /note="NKSF/CLMF; IL12p40; 40kD"
                     /codon_start=1
                     /product="interleukin 12, P40"
                     /protein_id="AAD56386.1"
                     /db_xref="GI:5923855"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:              2.82e-32       Length:         1007
Score:                  35.00          Matches:        35
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            10.7%          Indels:         0
DB:                     5              Gaps:           0

US-10-821-670A-56 (1-328) x AF180563 (1-1007)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||||
Db      712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756
```

```
ULT 75
46353
US       AB246353                1008 bp    mRNA    linear   MAM 13-JAN-2006
INITION  Bubalus bubalis IL-12p40 mRNA for interleukin-12p40, complete cds.
ESSION   AB246353
SION     AB246353.1  GI:84871717
WORDS    .
RCE      Bubalus bubalis (water buffalo)
RGANISM  Bubalus bubalis
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
         Pecora; Bovidae; Bovinae; Bubalus.
ERENCE   1
UTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
ITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
         buffalo and other bubaline breeds by molecular cloning, sequencing
         and phylogenetics
OURNAL   Unpublished
ERENCE   2  (bases 1 to 1008)
UTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
ITLE     Direct Submission
OURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
         Veterinary Medicine, Hokkaido University, Department of Disease
         Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
         9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
         Tel:81-11-706-5216, Fax:81-11-706-5217)
TURES             Location/Qualifiers
  source          1. .1008
                  /organism="Bubalus bubalis"
                  /mol_type="mRNA"
                  /db_xref="taxon:89462"
                  /sex="female"
                  /cell_type="PBMC"
                  /note="Bulgarian Murrah buffalo - crossbreed between
                  Mediterranean and Indian buffalo both are Riverine type
                  water buffalo"
  gene            1. .1008
                  /gene="IL-12p40"
  CDS             1. .984
                  /gene="IL-12p40"
                  /codon_start=1
                  /product="interleukin-12p40"
                  /protein_id="BAE75858.1"
                  /db_xref="GI:84871718"
                  /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
                  TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                  LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                  GSSDPRGVTCEAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                  LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                  QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
IN

nment Scores:
1. No.:              2.82e-32        Length:         1008
re:                  35.00           Matches:        35
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            10.7%           Indels:         0
                     14              Gaps:           0

10-821-670A-56 (1-328) x AB246353 (1-1008)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       649 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCA 708

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       709 GACCCACCCAAGAACCTGCAACTGAAACCATTAAAGAATTCTCGG 753

ULT 76
98121
JS       AY198121                1012 bp    mRNA    linear   MAM 09-JUN-2005
```

```
DEFINITION  Bubalus bubalis interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
ACCESSION   AY198121
VERSION     AY198121.1  GI:28192687
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
  TITLE     Interleukin-12 subunits p35 and p40 of Indian water buffalo
            (Bubalus bubalis) maintain high sequence homology with those of
            other ruminants
  JOURNAL   Eur. J. Immunogenet. 32 (3), 179-186 (2005)
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E. and Rasool,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-2002) Animal Biotechnology, Rajiv Gandhi Center
            for Biotechnology, Jagathy, Thycaud PO, Trivandrum, Kerala 695014,
            India
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
     CDS             1. .984
                     /note="cytokine; 40 kDa subunit"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAO25629.1"
                     /db_xref="GI:28192688"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSADPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:              2.83e-32        Length:         1012
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-56 (1-328) x AY198121 (1-1012)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCA 708

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        709 GACCCACCCAAGAACCTGCAACTGAAACCATTAAAGAATTCTCGG 753

RESULT 77
AR052857
LOCUS       AR052857                1018 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 194 from patent US 5833975.
ACCESSION   AR052857
VERSION     AR052857.1  GI:5977719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
```

```
URNAL   Patent: US 5833975-A 194 10-NOV-1998;
TURES             Location/Qualifiers
  source          1. .1018
                  /organism="unknown"
                  /mol_type="unassigned DNA"
IN

nment Scores:
.. No.:               2.85e-32       Length:        1018
e:                    35.00          Matches:       35
ent Similarity:       100.0%         Conservative:  0
  Local Similarity:   100.0%         Mismatches:    0
y Match:              10.7%          Indels:        0
                      2              Gaps:          0

 0-821-670A-56 (1-328) x AR052857 (1-1018)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

JLT 78
38169
JS       AR288169              1018 bp    mRNA    linear   PAT 12-JUN-2003
INITION  Sequence 194 from patent US 6537594.
SSION    AR288169
SION     AR288169.1  GI:31675448
WORDS    .
CE       Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 1018)
UTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
TLE      Vaccina virus comprising cytokine and/or tumor associated antigen
         genes
URNAL    Patent: US 6537594-A 194 25-MAR-2003;
         Virogenetics Corporation; Troy, NY
TURES             Location/Qualifiers
  source          1. .1018
                  /organism="unknown"
                  /mol_type="mRNA"
IN

nment Scores:
.. No.:               2.85e-32       Length:        1018
e:                    35.00          Matches:       35
ent Similarity:       100.0%         Conservative:  0
  Local Similarity:   100.0%         Mismatches:    0
y Match:              10.7%          Indels:        0
                      2              Gaps:          0

 0-821-670A-56 (1-328) x AR288169 (1-1018)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

JLT 79
57156
JS       AR567156              1018 bp    mRNA    linear   PAT 08-OCT-2004
INITION  Sequence 194 from patent US 6780407.
SSION    AR567156
SION     AR567156.1  GI:53984798
WORDS    .
CE       Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 194 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES            Location/Qualifiers
     source         1. .1018
                    /organism="unknown"
                    /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.85e-32       Length:        1018
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x AR567156 (1-1018)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 80
CQ829448
LOCUS       CQ829448               1029 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 7 from Patent WO2004052929.
ACCESSION   CQ829448
VERSION     CQ829448.1  GI:49732784
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 7 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES            Location/Qualifiers
     source         1. .1029
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="cDNA for beta chain of IL-12"
ORIGIN

Alignment Scores:
Pred. No.:              2.88e-32       Length:        1029
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x CQ829448 (1-1029)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 720

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 765

RESULT 81
```

```
)74723
JS        BC074723                1046 bp    mRNA    linear   PRI 28-JUL-2005
INITION   Homo sapiens interleukin 12B (natural killer cell stimulatory
          factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
          (cDNA clone MGC:103792 IMAGE:30915173), complete cds.
ESSION    BC074723
SION      BC074723.2  GI:50960609
WORDS     MGC.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 1046)
UTHORS    Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
          Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
          Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
          Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
          Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
          Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
          Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
          Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
          Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
          McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
          Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
          Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
          Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
          Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
          Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
          Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
          Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
          Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
ONSRTM    Mammalian Gene Collection Program Team
ITLE      Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences
OURNAL    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
UBMED     12477932
ERENCE    2  (bases 1 to 1046)
UTHORS    .
ONSRTM    NIH MGC Project
ITLE      Direct Submission
OURNAL    Submitted (25-JUN-2004) National Institutes of Health, Mammalian
          Gene Collection (MGC), Bethesda, MD 20892-2590, USA
EMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
MENT      On Aug 4, 2004 this sequence version replaced gi:49901500.
          Contact: MGC help desk
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
          Center
          cDNA Library Preparation: British Columbia Cancer Research Center
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Genome Sequence Centre,
          BC Cancer Agency, Vancouver, BC, Canada
          info@bcgsc.bc.ca
          Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
          Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
          Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
          Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
          Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
          Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
          Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
          Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
          Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRBU Plate: 1 Row: A Column: 6.
TURES                Location/Qualifiers
  source             1. .1046
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:103792 IMAGE:30915173"
                     /tissue_type="Brain, PCR rescued clones"
                     /clone_lib="NIH_MGC_272"
                     /lab_host="DH10B"
                     /note="Vector: pCR4 Topo TA with reversed insert"
  gene               1. .1046
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
  CDS                32. .1018
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH74723.1"
                     /db_xref="GI:50960610"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:                2.93e-32        Length:          1046
Score:                    35.00           Matches:         35
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              10.7%           Indels:          0
DB:                       5               Gaps:            0

US-10-821-670A-56 (1-328) x BC074723 (1-1046)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 82
BC067498
LOCUS       BC067498                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79355 IMAGE:6971868), complete cds.
ACCESSION   BC067498
VERSION     BC067498.1  GI:45768642
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
```

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
)NSRTM Mammalian Gene Collection Program Team
ITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
)URNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
)UBMED 12477932
ERENCE 2 (bases 1 to 1073)
UTHORS .
)NSRTM NIH MGC Project
ITLE Direct Submission
)URNAL Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
MARK NIH-MGC Project URL: http://mgc.nci.nih.gov
ENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497437.

URES Location/Qualifiers
source 1. .1073
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:79355 IMAGE:6971868"
/tissue_type="PCR rescued clones"
/clone_lib="NIH_MGC_195"
/lab_host="DH10B"
/note="Vector: pDNR-Dual"
gene 1. .1073
/gene="IL12B"
/note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
/db_xref="GeneID:3593"
/db_xref="MIM:161561"
CDS 5. .991
/gene="IL12B"
/codon_start=1
/product="interleukin 12B, precursor"
/protein_id="AAH67498.1"
/db_xref="GI:45768643"
/db_xref="GeneID:3593"
/db_xref="MIM:161561"
/translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"

IN

nment Scores:
.. No.: 3.01e-32 Length: 1073
e: 35.00 Matches: 35
ent Similarity: 100.0% Conservative: 0
Local Similarity: 100.0% Mismatches: 0
y Match: 10.7% Indels: 0
5 Gaps: 0

0-821-670A-56 (1-328) x BC067498 (1-1073)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754
```

RESULT 83
BC067499
LOCUS BC067499 1073 bp mRNA linear PRI 28-JUL-2005
DEFINITION Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA (cDNA clone MGC:79356 IMAGE:6971869), complete cds.
ACCESSION BC067499
VERSION BC067499.1 GI:45768645
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1073)
AUTHORS .
CONSRTM NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497437.

FEATURES Location/Qualifiers
source 1. .1073
/organism="Homo sapiens"

```
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79356 IMAGE:6971869"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67499.1"
                     /db_xref="GI:45768646"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
GIN

gnment Scores:
d. No.:              3.01e-32        Length:         1073
re:                  35.00           Matches:        35
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            10.7%           Indels:         0
                     5               Gaps:           0

10-821-670A-56 (1-328) x BC067499 (1-1073)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

JLT 84
67500
JS       BC067500                1073 bp    mRNA    linear   PRI 28-JUL-2005
INITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
         factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
         (cDNA clone MGC:79358 IMAGE:6971872), complete cds.
ESSION   BC067500
SION     BC067500.1  GI:45768649
WORDS    MGC.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 1073)
UTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
         Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
         Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
         Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
         Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
         Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
         Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
         Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
         Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
         McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
         Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
         Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
         Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
         Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
         Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
         Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
         Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
         Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM  Mammalian Gene Collection Program Team
  TITLE    Generation and initial analysis of more than 15,000 full-length
           human and mouse cDNA sequences
  JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED  12477932
REFERENCE  2  (bases 1 to 1073)
  AUTHORS  .
  CONSRTM  NIH MGC Project
  TITLE    Direct Submission
  JOURNAL  Submitted (19-MAR-2004) National Institutes of Health, Mammalian
           Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT    Contact: MGC help desk
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Sequencing Group at the Stanford Human Genome
           Center, Stanford University School of Medicine, Stanford, CA  94305
           Web site:       http://www-shgc.stanford.edu
           Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
           Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
           R. M.

           Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Series: IRAK Plate: 172 Row: d Column: 21
           This clone was selected for full length sequencing because it
           passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79358 IMAGE:6971872"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67500.1"
                     /db_xref="GI:45768650"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:           3.01e-32        Length:         1073
Score:               35.00           Matches:        35
Percent Similarity:  100.0%          Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:         10.7%           Indels:         0
DB:                  5               Gaps:           0
```

```
0-821-670A-56 (1-328) x BC067500 (1-1073)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

LT 85
7501
S       BC067501                1073 bp    mRNA    linear   PRI 28-JUL-2005
NITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
        factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
        (cDNA clone MGC:79359 IMAGE:6971873), complete cds.
SSION   BC067501
ION     BC067501.1  GI:45767736
ORDS    MGC.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 1073)
THORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
        Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
        Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
        Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
        Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
        Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
        Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
        Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
        Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
        McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
        Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
        Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
        Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
        Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
        Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
        Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
        Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
        Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
NSRTM   Mammalian Gene Collection Program Team
TLE     Generation and initial analysis of more than 15,000 full-length
        human and mouse cDNA sequences
URNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
UBMED   12477932
RENCE   2  (bases 1 to 1073)
THORS   .
NSRTM   NIH MGC Project
TLE     Direct Submission
URNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
        Gene Collection (MGC), Bethesda, MD 20892-2590, USA
MARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
ENT     Contact: MGC help desk
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: Narayan Bhat
        cDNA Library Preparation: Bhat Laboratory
        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
        DNA Sequencing by: Sequencing Group at the Stanford Human Genome
        Center, Stanford University School of Medicine, Stanford, CA  94305
        Web site:       http://www-shgc.stanford.edu
        Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
        Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
        R. M.

        Clone distribution: MGC clone distribution information can be found
        through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
        Series: IRAK Plate: 172 Row: d Column: 22
        This clone was selected for full length sequencing because it
        passed the following selection criteria: matched mRNA gi: 24497437.

FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79359 IMAGE:6971873"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67501.1"
                     /db_xref="GI:45767737"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:                3.01e-32        Length:          1073
Score:                    35.00           Matches:         35
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              10.7%           Indels:          0
DB:                       5               Gaps:            0

US-10-821-670A-56 (1-328) x BC067501 (1-1073)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 86
BC067502
LOCUS       BC067502                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79360 IMAGE:6971874), complete cds.
ACCESSION   BC067502
VERSION     BC067502.1  GI:45768652
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
```

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
ONSRTM Mammalian Gene Collection Program Team
ITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
OURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
ERENCE 2 (bases 1 to 1073)
UTHORS .
ONSRTM NIH MGC Project
ITLE Direct Submission
OURNAL Submitted (19-MAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
EMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
MENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 24497437.

```
URES            Location/Qualifiers
  source        1. .1073
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="MGC:79360 IMAGE:6971874"
                /tissue_type="PCR rescued clones"
                /clone_lib="NIH_MGC_195"
                /lab_host="DH10B"
                /note="Vector: pDNR-Dual"
  gene          1. .1073
                /gene="IL12B"
                /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                /db_xref="GeneID:3593"
                /db_xref="MIM:161561"
  CDS           5. .991
                /gene="IL12B"
                /codon_start=1
                /product="interleukin 12B, precursor"
                /protein_id="AAH67502.1"
                /db_xref="GI:45768653"
                /db_xref="GeneID:3593"
                /db_xref="MIM:161561"
                /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
IN

nment Scores:
i. No.:              3.01e-32        Length:         1073
re:                  35.00           Matches:        35
cent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            10.7%        Indels:         0
DB:                     5            Gaps:           0

US-10-821-670A-56 (1-328) x BC067502 (1-1073)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||||
Db      710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 87
AR393788
LOCUS       AR393788               1389 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6617135.
ACCESSION   AR393788
VERSION     AR393788.1  GI:40120790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1389)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 4 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
     source          1. .1389
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.93e-32        Length:         1389
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-56 (1-328) x AR393788 (1-1389)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 88
AX084106
LOCUS       AX084106               1389 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 4 from Patent WO0110912.
ACCESSION   AX084106
VERSION     AX084106.1  GI:13185656
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 4 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .1389
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
```

```
                /note="human p40-IL-2 fusion protein coding sequence"
:IN

:nment Scores:
l. No.:              3.93e-32       Length:        1389
:e:                  35.00          Matches:       35
:ent Similarity:     100.0%         Conservative:  0
: Local Similarity:  100.0%         Mismatches:    0
:y Match:            10.7%          Indels:        0
                     2              Gaps:          0

0-821-670A-56 (1-328) x AX084106 (1-1389)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

'LT 89
5800
'S       BD165800                1397 bp    DNA     linear   PAT 17-JAN-2003
'NITION  Antibody against cytotoxic lymphocyte maturing factors.
'SSION   BD165800
.ION     BD165800.1  GI:27871612
'ORDS    JP 2002167400-A/1.
.CE      unidentified
.GANISM  unidentified
         unclassified sequences.
:RENCE   1  (bases 1 to 1397)
'THORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
         Podlanski,F.J. and Stern,A.S.
 TLE     Antibody against cytotoxic lymphocyte maturing factors
'URNAL   Patent: JP 2002167400-A 1 11-JUN-2002;
         PROTEIN DESIGN LABS INC
!ENT     OS   Homo sapiens (human)
         PN   JP 2002167400-A/1
         PD   11-JUN-2002
         PF   14-AUG-2001 JP 2001246031
         PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
         27-AUG-1990 US       572284
         PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
         PI   GUBLER,
         PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
         PI   ALVIN SETH STERN
         PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
           Antibody against cytotoxic lymphocyte maturing factors FH   Key
                 Location/Qualifiers
         FT   CDS              (41). .(1024).
'URES              Location/Qualifiers
 source            1. .1397
                   /organism="unidentified"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:32644"
:IN

:nment Scores:
l. No.:              3.95e-32       Length:        1397
'e:                  35.00          Matches:       35
:ent Similarity:     100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
:y Match:            10.7%          Indels:        0
                     2              Gaps:          0

0-821-670A-56 (1-328) x BD165800 (1-1397)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
Db    746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 90
AR091391
LOCUS       AR091391                1399 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from patent US 5994104.
ACCESSION   AR091391
VERSION     AR091391.1  GI:10018146
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1399)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 3 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1399
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.96e-32       Length:        1399
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x AR091391 (1-1399)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 91
HUMCLMF40
LOCUS       HUMCLMF40               1399 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human cytotoxic lymphocyte maturation factor 40 kDa subunit mRNA,
            complete cds.
ACCESSION   M65272 M38443 M38444
VERSION     M65272.1  GI:180625
KEYWORDS    cytotoxic lymphocyte maturation factor 40 kDa subunit; interleukin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1399)
  AUTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
            Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
            and Gately,M.K.
  TITLE     Coexpression of two distinct genes is required to generate secreted
            bioactive cytotoxic lymphocyte maturation factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
   PUBMED   1674604
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .1399
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             43. .1029
                     /codon_start=1
                     /product="cytotoxic lymphocyte maturation factor 40 kDa
                     subunit"
                     /protein_id="AAA35695.1"
```

```
                /db_xref="GI:180626"
                /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
GIN

gnment Scores:
d. No.:              3.96e-32       Length:        1399
re:                  35.00          Matches:       35
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            10.7%          Indels:        0
                     5              Gaps:          0

10-821-670A-56 (1-328) x HUMCLMF40 (1-1399)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

JLT 92
91395
JS       AR091395              1560 bp    DNA     linear   PAT 07-SEP-2000
INITION  Sequence 11 from patent US 5994104.
ESSION   AR091395
SION     AR091395.1  GI:10018150
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 1560)
UTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
ITLE     Interleukin-12 fusion protein
OURNAL   Patent: US 5994104-A 11 30-NOV-1999;
TURES             Location/Qualifiers
  source          1. .1560
                  /organism="unknown"
                  /mol_type="unassigned DNA"
GIN

gnment Scores:
d. No.:              4.43e-32       Length:        1560
re:                  35.00          Matches:       35
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            10.7%          Indels:        0
                     2              Gaps:          0

10-821-670A-56 (1-328) x AR091395 (1-1560)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       583 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 642

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       643 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 687

JLT 93
91394
JS       AR091394              1623 bp    DNA     linear   PAT 07-SEP-2000
INITION  Sequence 9 from patent US 5994104.
ESSION   AR091394
SION     AR091394.1  GI:10018149
WORDS    .
RCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1623
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.62e-32       Length:        1623
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x AR091394 (1-1623)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 94
CQ715179
LOCUS       CQ715179               2307 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 1113 from Patent WO02068579.
ACCESSION   CQ715179
VERSION     CQ715179.1  GI:42276036
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 1113 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .2307
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              6.65e-32       Length:        2307
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x CQ715179 (1-2307)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         648 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 707

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         708 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 752
```

```
LT 95
2684
S       AR082684                2362 bp    DNA     linear   PAT 01-SEP-2000
NITION  Sequence 1 from patent US 5976539.
SSION   AR082684
ION     AR082684.1  GI:10009474
ORDS    .
CE      Unknown.
GANISM  Unknown.
        Unclassified.
RENCE   1  (bases 1 to 2362)
THORS   Scott,P. and Trinchieri,G.
TLE     Compositions and methods for use of IL-12 as an adjuvant
URNAL   Patent: US 5976539-A 1 02-NOV-1999;
URES            Location/Qualifiers
 source         1. .2362
                /organism="unknown"
                /mol_type="unassigned DNA"
IN

nment Scores:
. No.:              6.82e-32       Length:        2362
e:                  35.00          Matches:       35
ent Similarity:     100.0%         Conservative:  0
 Local Similarity:  100.0%         Mismatches:    0
y Match:            10.7%          Indels:        0
                    2              Gaps:          0

0-821-670A-56 (1-328) x AR082684 (1-2362)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

LT 96
2960
S       AR122960                2362 bp    DNA     linear   PAT 16-MAY-2001
NITION  Sequence 1 from patent US 6168923.
SSION   AR122960
ION     AR122960.1  GI:14107926
ORDS    .
CE      Unknown.
GANISM  Unknown.
        Unclassified.
RENCE   1  (bases 1 to 2362)
THORS   Scott,P. and Trinchieri,G.
TLE     Compositions and methods for use of IL-12 as an adjuvant
URNAL   Patent: US 6168923-A 1 02-JAN-2001;
URES            Location/Qualifiers
 source         1. .2362
                /organism="unknown"
                /mol_type="unassigned DNA"
IN

nment Scores:
. No.:              6.82e-32       Length:        2362
e:                  35.00          Matches:       35
ent Similarity:     100.0%         Conservative:  0
 Local Similarity:  100.0%         Mismatches:    0
y Match:            10.7%          Indels:        0
                    2              Gaps:          0

0-821-670A-56 (1-328) x AR122960 (1-2362)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 97
I28325
LOCUS       I28325                  2362 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5571515.
ACCESSION   I28325
VERSION     I28325.1  GI:1819101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2362)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5571515-A 1 05-NOV-1996;
FEATURES            Location/Qualifiers
     source         1. .2362
                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.82e-32       Length:        2362
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x I28325 (1-2362)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 98
AR309636
LOCUS       AR309636                2362 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6555658.
ACCESSION   AR309636
VERSION     AR309636.1  GI:31701687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2362)
  AUTHORS   Trinchieri,G., Perussia,B., Clark,S.C., Wong,G.G., Hewick,R. and
            Kobayashi,M.
  TITLE     Antibodies to natural killer stimulatory factor
  JOURNAL   Patent: US 6555658-A 3 29-APR-2003;
            Wyeth and The Wistar Institute; Madison, NJ
FEATURES            Location/Qualifiers
     source         1. .2362
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.82e-32       Length:        2362
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x AR309636 (1-2362)
```

```
       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

JLT 99
770
JS       I89770                  2362 bp    DNA     linear   PAT 10-AUG-1998
INITION  Sequence 1 from patent US 5723127.
ESSION   I89770
SION     I89770.1  GI:3409710
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 2362)
UTHORS   Scott,P. and Trinchieri,G.
ITLE     Compositions and methods for use of IL-12 as an adjuvant
OURNAL   Patent: US 5723127-A 1 03-MAR-1998;
TURES             Location/Qualifiers
  source          1. .2362
                  /organism="unknown"
                  /mol_type="unassigned DNA"
GIN

gnment Scores:
i. No.:              6.82e-32       Length:        2362
re:                  35.00          Matches:       35
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            10.7%          Indels:        0
                     2              Gaps:          0

10-821-670A-56 (1-328) x I89770 (1-2362)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

JLT 100
36048
JS       BD136048                5686 bp    DNA     linear   PAT 18-SEP-2002
INITION  Interferon alpha plasmid and delivery system and method of
         preparing and using the same.
ESSION   BD136048
SION     BD136048.1  GI:23230993
WORDS    JP 2002506647-A/15.
RCE      synthetic construct
RGANISM  synthetic construct
         other sequences; artificial sequences.
ERENCE   1  (bases 1 to 5686)
UTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
ITLE     Interferon alpha plasmid and delivery system and method of
         preparing and using the same
OURNAL   Patent: JP 2002506647-A 15 05-MAR-2002;
         VALENTIS INC
MENT     OS   Artificial Sequence
         PN   JP 2002506647-A/15
         PD   05-MAR-2002
         PF   12-MAR-1999 JP 2000536861
         PR   19-MAR-1998 US    60/078654
         PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
         PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
         PC   C12N1/15,
         PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
         C12N5/00
         CC   Sequence source: synthetic construct
         FH   Key             Location/Qualifiers
         FT   source          1. .5686
         FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .5686
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              1.7e-31        Length:        5686
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x BD136048 (1-5686)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3864 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3923

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db       3924 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3968


Search completed: June 10, 2006, 12:08:56
Job time : 7487.55 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

on: June 10, 2006, 01:23:11 ; Search time 794.721 Seconds
(without alignments)
4316.416 Million cell updates/sec

le: US-10-821-670A-56
fect score: 328
uence: 1 MHPQQLVIAWFSLVLLAPPL.....VQARDRYYSSSWSNWASVSC 328

ring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

rched: 5244920 seqs, 3486124231 residues

d size: 1

al number of hits satisfying chosen parameters: 10484873

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Listing first 200 summaries

mand line parameters:
DEL=frame+_p2n.model -DEV=xlh
/abss/ABSSWEB_spool/US10821670/runat_07062006_110446_27507/app_query.fasta_1
=N_Geneseq -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rng -MINMATCH=0.1
OPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
ANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
IGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
XLEN=2000000000 -HOST=abss05h
ER=US10821670_@CGN_1_1_1666_@runat_07062006_110446_27507 -NCPU=6 -ICPU=3
MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
N_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
APOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

abase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt No.	Score	% Query Match	Length	DB	ID	Description
1	328	100.0	985	6	ABK98962	Abk98962 Feline in
2	328	100.0	985	6	ABK98961	Abk98961 Feline in
3	328	100.0	985	14	ADV34707	Adv34707 Feline N-
c 4	328	100.0	985	14	ADV34709	Adv34709 Feline N-
5	328	100.0	987	6	ABK98944	Abk98944 Feline in
c 6	328	100.0	987	6	ABK98945	Abk98945 Feline in
7	328	100.0	987	14	ADV34682	Adv34682 Feline si
c 8	328	100.0	987	14	ADV34684	Adv34684 Feline si
9	328	100.0	990	4	AAF26082	Aaf26082 Feline IL
10	328	100.0	990	4	AAF26085	Aaf26085 Feline IL
11	328	100.0	4522	4	AAF26076	Aaf26076 Feline IL
12	328	100.0	4522	4	AAF26094	Aaf26094 Plasmid p
13	316	96.3	2193	2	AAV56625	Aav56625 Feline FL
14	306	93.3	921	2	AAV56627	Aav56627 Feline FL
15	306	93.3	921	2	AAV56626	Aav56626 Feline FL
16	216	65.9	1599	6	ABK98950	Abk98950 Feline in
c 17	216	65.9	1599	6	ABK98951	Abk98951 Feline in
18	216	65.9	1599	14	ADV34691	Adv34691 Feline si
c 19	216	65.9	1599	14	ADV34693	Adv34693 Feline si
20	205	62.5	921	6	ABK98942	Abk98942 Feline in
c 21	205	62.5	921	6	ABK98943	Abk98943 Feline in
c 22	205	62.5	921	14	ADV34681	Adv34681 Feline si
23	205	62.5	921	14	ADV34679	Adv34679 Feline si
c 24	205	62.5	1533	6	ABK98954	Abk98954 Feline in
25	205	62.5	1533	6	ABK98953	Abk98953 Feline in
c 26	205	62.5	1533	14	ADV34697	Adv34697 Feline si
27	205	62.5	1533	14	ADV34695	Adv34695 Feline si
28	52	15.9	990	5	AAD15209	Aad15209 Modified
29	49	14.9	984	5	AAD15206	Aad15206 Modified
30	42	12.8	984	5	AAD15205	Aad15205 Modified
31	41	12.5	975	5	AAD15203	Aad15203 Modified
32	37	11.3	921	6	ABK98959	Abk98959 Canine in
c 33	37	11.3	921	6	ABK98960	Abk98960 Canine in
c 34	37	11.3	921	14	ADV34706	Adv34706 Canine si
35	37	11.3	921	14	ADV34704	Adv34704 Canine si
36	37	11.3	924	2	AAX18177	Aax18177 Canine ma
37	37	11.3	987	6	ABK98963	Abk98963 Canine in
c 38	37	11.3	987	6	ABK98964	Abk98964 Canine in
c 39	37	11.3	987	14	ADV34712	Adv34712 Canine si
40	37	11.3	987	14	ADV34710	Adv34710 Canine si
41	37	11.3	990	2	AAV13816	Aav13816 Canine IL
42	37	11.3	990	2	AAV13817	Aav13817 Canine IL
43	37	11.3	990	2	AAX03162	Aax03162 Nucleic a
44	37	11.3	990	2	AAX03152	Aax03152 Nucleic a
45	37	11.3	990	2	AAX35625	Aax35625 Nucleic a
46	37	11.3	990	2	AAX35615	Aax35615 Nucleic a
47	37	11.3	990	4	AAI64378	Aai64378 Canine co
48	37	11.3	990	4	AAI64388	Aai64388 Canine co
49	37	11.3	990	11	ADZ25698	Adz25698 Canine in
50	37	11.3	1015	13	ADT04849	Adt04849 Canine in
51	37	11.3	1533	6	ABK98967	Abk98967 Canine in
c 52	37	11.3	1533	6	ABK98968	Abk98968 Canine in
c 53	37	11.3	1533	14	ADV34718	Adv34718 Canine si
54	37	11.3	1533	14	ADV34716	Adv34716 Canine si
55	37	11.3	1599	6	ABK98965	Abk98965 Canine in
c 56	37	11.3	1599	6	ABK98966	Abk98966 Canine in
c 57	37	11.3	1599	14	ADV34715	Adv34715 Canine si
58	37	11.3	1599	14	ADV34713	Adv34713 Canine si
59	37	11.3	2154	2	AAX18176	Aax18176 Canine fu
c 60	37	11.3	2267	6	ABK99006	Abk99006 Canine in
61	37	11.3	2267	6	ABK99005	Abk99005 Canine in
62	37	11.3	2267	14	ADV34757	Adv34757 Canine si
c 63	37	11.3	2267	14	ADV34759	Adv34759 Canine si
64	35	10.7	906	2	AAQ04701	Aaq04701 Sequence
65	35	10.7	975	5	AAD15208	Aad15208 Modified
66	35	10.7	979	2	AAQ12149	Aaq12149 Cytotoxic
67	35	10.7	984	12	ADG39430	Adg39430 Human CLM
68	35	10.7	987	2	AAQ97484	Aaq97484 Human int
69	35	10.7	987	2	AAV07273	Aav07273 Human Int
70	35	10.7	987	2	AAV07217	Aav07217 DNA encod
71	35	10.7	987	2	AAZ40406	Aaz40406 Human int
72	35	10.7	987	2	AAZ40404	Aaz40404 Human int
73	35	10.7	987	2	AAZ40405	Aaz40405 Human int
74	35	10.7	987	5	AAD15210	Aad15210 Human cyt
75	35	10.7	987	12	ADF77278	Adf77278 Human IL-

76	35	10.7	987	12	ADF77263	Adf77263 Human IL-
77	35	10.7	987	12	ADF77277	Adf77277 Human IL-
78	35	10.7	987	12	ADF77276	Adf77276 Human IL-
79	35	10.7	987	12	ADO07653	Ado07653 Human int
80	35	10.7	987	13	ADS00006	Ads00006 Human int
81	35	10.7	987	14	ADV42753	Adv42753 Human psy
82	35	10.7	987	14	ADW97242	Adw97242 Human p40
83	35	10.7	987	14	AEB48822	Aeb48822 Human int
84	35	10.7	1007	5	AAD18585	Aad18585 Human int
85	35	10.7	1018	2	AAQ67879	Aaq67879 EPV 42 kD
86	35	10.7	1018	2	AAZ08510	Aaz08510 EPV 42 kD
87	35	10.7	1018	13	ADR21886	Adr21886 EPV 42kDa
88	35	10.7	1029	12	ADP88402	Adp88402 Human int
89	35	10.7	1389	4	AAF76880	Aaf76880 Human p40
90	35	10.7	1397	2	AAT77849	Aat77849 40 kDa su
91	35	10.7	1397	2	AAT97969	Aat97969 40 kDa su
92	35	10.7	1397	2	AAV00401	Aav00401 40 kDa su
93	35	10.7	1397	2	AAV37767	Aav37767 Cytotoxic
94	35	10.7	1397	12	ADG39387	Adg39387 Human cyt
95	35	10.7	1397	12	ADO03758	Ado03758 Human CLM
96	35	10.7	1399	3	AAZ40021	Aaz40021 Human p40
97	35	10.7	1399	14	ADY86632	Ady86632 Human int
98	35	10.7	2300	3	AAA92406	Aaa92406 Human int
99	35	10.7	2336	14	AEE03207	Aee03207 Human int
100	35	10.7	2347	12	ACF57534	Acf57534 Human IL1
101	35	10.7	2347	12	ADJ62892	Adj62892 Human int
102	35	10.7	2347	14	ADZ26728	Adz26728 Human IL1
103	35	10.7	2362	2	AAQ23586	Aaq23586 Natural k
104	35	10.7	2362	2	AAT48098	Aat48098 Human int
105	35	10.7	2362	2	AAV42535	Aav42535 Human int
106	35	10.7	2362	2	AAV15227	Aav15227 Heterodim
107	35	10.7	2362	3	AAZ28862	Aaz28862 Human int
108	35	10.7	2362	4	AAF56280	Aaf56280 IL-12 vac
109	35	10.7	5686	2	AAZ40415	Aaz40415 Plasmid p
110	35	10.7	5686	12	ADF77239	Adf77239 Human IL-
111	35	10.7	6139	3	AAZ40023	Aaz40023 Interleuk
12	35	10.7	11569	10	ADG25150	Adg25150 Vector pA
13	34	10.4	945	12	ADF77264	Adf77264 Human IL-
14	32	9.8	985	10	ADK98707	Adk98707 Human int
15	28	8.5	969	5	AAD15207	Aad15207 Modified
16	28	8.5	984	2	AAT50759	Aat50759 Sequence
17	28	8.5	984	5	AAD15204	Aad15204 Modified
18	28	8.5	1019	3	AAA70709	Aaa70709 Bovine in
19	28	8.5	2390	12	ADM29103	Adm29103 Human int
20	23	7.0	987	2	AAV83199	Aav83199 Interleuk
21	23	7.0	987	6	ACC47592	Acc47592 Human int
22	23	7.0	1007	10	ACD26421	Acd26421 cDNA enco
23	23	7.0	1580	12	ADQ14472	Adq14472 DNA encod
24	23	7.0	2318	8	ACA61267	Aca61267 DNA encod
25	23	7.0	2318	10	ABX33940	Abx33940 Human cDN
26	23	7.0	4727	14	AEA40942	Aea40942 T-DNA reg
27	23	7.0	8578	6	AAD31546	Aad31546 pIRES-hB7
128	23	7.0	8578	6	AAD31545	Aad31545 pIRES-hB7
129	23	7.0	8608	6	AAD31548	Aad31548 pIRES-hB7
130	23	7.0	8623	6	AAD31547	Aad31547 pIRES-hB7
131	23	7.0	8629	6	AAD31552	Aad31552 pIRES-IL1
132	23	7.0	8638	6	AAD31549	Aad31549 pIRES-hB7
133	23	7.0	8644	6	AAD31551	Aad31551 pIRES-IL1
134	23	7.0	8659	6	AAD31550	Aad31550 pIRES-IL1
135	23	7.0	11453	10	ADG25152	Adg25152 Vector pS
136	22	6.7	18110	6	ABK15357	Abk15357 Human int
137	22	6.7	18340	5	AAD19368	Aad19368 Mammalian
138	20	6.1	270	12	ACH83638	Ach83638 Human gen
139	20	6.1	399	14	AEE14792	Aee14792 Hamster S
140	20	6.1	399	14	AEE11150	Aee11150 Hamster c
41	20	6.1	556	12	ACH69938	Ach69938 Human gen
142	19	5.8	948	12	ADI28579	Adi28579 Duck inte
143	19	5.8	948	12	ADI28581	Adi28581 Turkey in
144	19	5.8	948	12	ADI28576	Adi28576 Chicken i
45	17	5.2	73	4	AAS15322	Aas15322 Mouse IL-
146	17	5.2	600	2	AAX78397	Aax78397 IL-12p40
147	17	5.2	600	2	AAX25947	Aax25947 Interleuk
48	17	5.2	1008	13	ADS00008	Ads00008 Murine in
149	17	5.2	1008	14	ADW97243	Adw97243 Murine p4
150	17	5.2	1056	2	AAV28472	Aav28472 Murine in
151	17	5.2	1061	2	AAT35200	Aat35200 Mouse int
152	17	5.2	1409	4	AAF76879	Aaf76879 Murine p4
153	17	5.2	1472	4	AAF76878	Aaf76878 Murine p4
154	17	5.2	1569	4	AAF76888	Aaf76888 Single-ch
155	17	5.2	1610	12	ADQ14470	Adq14470 DNA encod
156	17	5.2	1840	8	ACA61265	Aca61265 DNA encod
157	17	5.2	2013	4	AAF76887	Aaf76887 Murine p3
158	17	5.2	2334	14	AEE03206	Aee03206 Murine in
159	17	5.2	2438	12	ADO43004	Ado43004 DNA encod
160	17	5.2	2709	4	AAF76889	Aaf76889 Coding se
161	17	5.2	5252	12	ADO07652	Ado07652 Tricistro
162	17	5.2	5966	2	AAZ40417	Aaz40417 Plasmid p
163	17	5.2	5966	12	ADF77241	Adf77241 Mouse IL-
164	17	5.2	5985	12	ADQ82718	Adq82718 Anticance
165	17	5.2	6295	2	AAV02043	Aav02043 Plasmid p
166	17	5.2	7287	2	AAV02042	Aav02042 Plasmid p
167	17	5.2	9049	12	ADO07661	Ado07661 Viral vec
168	17	5.2	10633	12	ADO07660	Ado07660 Viral vec
169	17	5.2	11458	10	ADG25151	Adg25151 Vector pA
170	17	5.2	11746	12	ADO07659	Ado07659 Viral vec
171	17	5.2	28191	14	AEE03204	Aee03204 Adenovira
172	17	5.2	28892	14	AEE03202	Aee03202 Adenovira
173	17	5.2	38246	12	ADO07662	Ado07662 Viral vec
174	13	4.0	987	2	AAV31480	Aav31480 Human int
175	13	4.0	987	2	AAZ40422	Aaz40422 Human int
176	13	4.0	987	12	ADF77256	Adf77256 Human IL-
177	12	3.7	38	2	AAV56630	Aav56630 Feline FL
178	12	3.7	200	2	AAV03357	Aav03357 Homo sapi
c 179	10	3.0	30	3	AAA48905	Aaa48905 Probe 12.
180	10	3.0	21925	10	ADC87602	Adc87602 Human GPC
181	10	3.0	26184	10	ADC87236	Adc87236 Human GPC
182	9	2.7	28	6	ABK98985	Abk98985 Feline PC
183	9	2.7	28	14	ADV34735	Adv34735 Feline IL
184	9	2.7	30	5	AAD19247	Aad19247 Mammalian
185	9	2.7	31	14	ADW78364	Adw78364 Hybridizi
186	9	2.7	37	6	ABK98987	Abk98987 Feline PC
187	9	2.7	37	14	ADV34737	Adv34737 Feline IL
188	9	2.7	353	5	ABV07469	Abv07469 Human pro
189	9	2.7	419	5	AAD19240	Aad19240 Mammalian
190	9	2.7	419	5	AAD19239	Aad19239 Mammalian
191	9	2.7	426	5	ABV37403	Abv37403 Human pro
c 192	9	2.7	463	4	AAH08718	Aah08718 Human cDN
193	9	2.7	532	3	AAC04020	Aac04020 Human sec
c 194	9	2.7	664	4	AAL25132	Aal25132 Human bre
195	9	2.7	858	11	ACN88481	Acn88481 Breast ca
196	9	2.7	1974	4	AAH13637	Aah13637 Human cDN
197	9	2.7	2162	10	ADC30563	Adc30563 Human nov
198	9	2.7	2256	5	ABV22512	Abv22512 Human pro
199	9	2.7	2256	5	ABV28327	Abv28327 Human pro
200	9	2.7	2256	5	ABV24801	Abv24801 Human pro

ALIGNMENTS

RESULT 1
ABK98962/c
ID ABK98962 standard; cDNA; 985 BP.
XX
AC ABK98962;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 3; Page 75-76; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

gnment Scores:

i. No.:	0	Length:	985
re:	328.00	Matches:	328
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	100.0%	Indels:	0
	6	Gaps:	0

10-821-670A-56 (1-328) x ABK98962 (1-985)

```
          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy      141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy      161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||
Db       25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 2
ABK98961
ID ABK98961 standard; cDNA; 985 BP.
XX
AC ABK98961;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69311.
XX

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 3; Page 73-74; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

nment Scores:

i. No.:	0	Length:	985
e:	328.00	Matches:	328
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	100.0%	Indels:	0
	6	Gaps:	0

0-821-670A-56 (1-328) x ABK98961 (1-985)

```
        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

       21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

       41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

       61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

       81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

      101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

      121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

      141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

      161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984
```

RESULT 3
ADV34707
ID ADV34707 standard; cDNA; 985 BP.
XX
AC ADV34707;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .984
FT   /*tag= a
FT   /product= "PCaIL-12P40-N328 protein"
FT   /partial
FT   /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34708.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40

subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline N-terminal single chain IL-12p40 protein encoding cDNA.

Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

gnment Scores:

i. No.:	0	Length:	985
re:	328.00	Matches:	328
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	100.0%	Indels:	0
	14	Gaps:	0

10-821-670A-56 (1-328) x ADV34707 (1-985)

```
          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||
Db      961 AGCAACTGGGCATCCGTGTCCTGC 984
```

RESULT 4
ADV34709/c
ID ADV34709 standard; DNA; 985 BP.
XX
AC ADV34709;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 57; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline N-terminal single chain IL-12p40
CC complementary DNA.
XX
SQ Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	985
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x ADV34709 (1-985)

```
  1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

 21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

 41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

 61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

 81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

321 SerAsnTrpAlaSerValSerCys 328
    |||||||||||||||||||||||
 25 AGCAACTGGGCATCCGTGTCCTGC 2
```

LT 5
8944
ABK98944 standard; cDNA; 987 BP.

ABK98944;

XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69303.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 51-53; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	987
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x ABK98944 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

 81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

321 SerAsnTrpAlaSerValSerCys 328
    |||||||||||||||||||||||
961 AGCAACTGGGCATCCGTGTCCTGC 984
```

JLT 6
98945/c
ABK98945 standard; cDNA; 987 BP.

ABK98945;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12p40-987 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 54; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	987
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x ABK98945 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
```

```
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

  161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

  181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

  201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

  221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

  241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

  261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

  281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

  301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

  321 SerAsnTrpAlaSerValSerCys 328
      |||||||||||||||||||||||
   27 AGCAACTGGGCATCCGTGTCCTGC 4
```

```
LT 7
4682
 ADV34682 standard; cDNA; 987 BP.

 ADV34682;

 24-FEB-2005  (first entry)

 Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.

 DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
 infectious disease; antimicrobial; gene; ss.

 Felis catus.

 Key             Location/Qualifiers
 CDS             1. .987
                 /*tag=  a
                 /product= "PFeIL-12p40 329 protein "
                 /partial
                 /note= "No stop codon"

 US2004248261-A1.

 09-DEC-2004.

 09-APR-2004; 2004US-00821670.

 04-AUG-2000; 2000US-0223016P.
 27-JUL-2001; 2001US-00917265.

 (WOND/) WONDERLING R S.
 (BORO/) BOROUGHS K L.

 PI   Wonderling RS,  Boroughs KL;
 XX
 DR   WPI; 2005-020565/02.
 DR   P-PSDB; ADV34683.
 XX
 PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
 PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
 PT   vaccine against infectious diseases in feline animals.
 XX
 PS   Claim 23; SEQ ID NO 29; 103pp; English.
 XX
 CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
 CC   subunit protein and their encoding nucleic acid molecules and a nucleic
 CC   acid linker. The invention also provides the feline caspase (casp)-1,
 CC   feline IL-18 single chain and canine IL-12 single chain proteins and
 CC   their nucleic acid molecules. The nucleic acid molecule is useful in
 CC   preparing a vaccine against infectious diseases in feline animals. The
 CC   present sequence is the feline single chain IL-12p40 subunit protein
 CC   encoding full-length cDNA.
 XX
 SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

 Alignment Scores:
 Pred. No.:                0              Length:          987
 Score:                    328.00         Matches:         328
 Percent Similarity:       100.0%         Conservative:    0
 Best Local Similarity:    100.0%         Mismatches:      0
 Query Match:              100.0%         Indels:          0
 DB:                       14             Gaps:            0

 US-10-821-670A-56 (1-328) x ADV34682 (1-987)

 Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

 Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

 Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

 Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

 Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

 Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

 Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

 Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

 Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

 Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

 Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
```

```
601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

321 SerAsnTrpAlaSerValSerCys 328
961 AGCAACTGGGCATCCGTGTCCTGC 984
```

JLT 8
34684/c
ADV34684 standard; DNA; 987 BP.

ADV34684;

24-FEB-2005 (first entry)

Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Felis catus.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 3; SEQ ID NO 31; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12p40 subunit full-length complementary DNA.

SQ Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	987
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x ADV34684 (1-987)

```
Qy    1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuAlaProProLeu 20
Db  987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy   21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
Db  927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy   41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
Db  867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy   61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db  807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy   81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
Db  747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy  101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
Db  687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy  121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db  627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy  141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
Db  567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy  161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
Db  507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy  181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db  447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy  201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db  387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy  221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
Db  327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy  241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
Db  267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy  261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
Db  207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy  281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
Db  147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy  301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
```

```
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

   321 SerAsnTrpAlaSerValSerCys 328
       |||||||||||||||||||||||
    27 AGCAACTGGGCATCCGTGTCCTGC 4

LT 9
6082
 AAF26082 standard; DNA; 990 BP.

 AAF26082;

 24-APR-2001  (first entry)

 Feline IL-12p40 encoding DNA SEQ ID 8.

 Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
 interleukin; antiviral; cytotoxic immune response; Th1 response; ds.

 Felis sp.

 WO200104280-A2.

 18-JAN-2001.

 08-JUL-2000; 2000WO-DE002262.

 08-JUL-1999;   99CH-00001258.

 (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
 (UYZU-) UNIV ZUERICH.

 Leutenegger C,  Schroff M,  Wittig B,  Lutz H;

 WPI; 2001-147190/15.

 Vaccine for treating or preventing lentivirus infection in cats, contains
 nucleic acid sequence encoding viral protein under control of eukaryotic
 promoter.

 Claim 14; Page 36; 37pp; German.

 This invention describes a novel vaccine (A) for prevention or treatment
 of lentivirus infection in felines which comprises an immunizing nucleic
 acid sequence (I) that contains, or comprises, at least part of a gene
 encoding a protein (II) of the virus, under control of a eukaryotic
 promoter functional in the relevant animal. (II) is especially the
 envelope (env) protein. The invention also describes (1) vaccine (A)
 containing an immunizing protein, or fragment, from a lentivirus plus at
 least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
 lentivirus protein, or fragment, especially derived from feline immune
 deficiency virus (FIV), by expressing the corresponding nucleic acid
 sequence in a host cell. The products of the invention have antiviral
 activity. The vaccine (A) and related protein-based vaccines, are
 particularly used to treat or prevent lentivirus infections in domestic
 cats, especially feline immune deficiency virus (FIV). Vaccination with
 (A) allows differentiation between vaccinated and infected animals, from
 the antibody status. The vaccines may be formulated with an adjuvant
 (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
 immune response, particularly a Th1 response

 Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

nment Scores:
.. No.:              0              Length:        990
e:                   328.00         Matches:       328
ent Similarity:      100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
y Match:             100.0%         Indels:        0
                     4              Gaps:          0

 0-821-670A-56 (1-328) x AAF26082 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 10
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
```

AAF26085;

24-APR-2001 (first entry)

Feline IL-12p40 encoding DNA.

Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection; immunostimulant; tumor; antiviral; antitumor; interferon-gamma; Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.

Felis sp.

WO200104155-A2.

18-JAN-2001.

08-JUL-2000; 2000WO-DE002263.

08-JUL-1999; 99CH-00001259.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.
(REGC) UNIV CALIFORNIA.

Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;

WPI; 2001-147178/15.

Recombinant feline interleukin-12, useful as immunostimulant and for treating e.g. viral infections in cats, and related nucleic acid constructs.

Claim 3; Page 30; 35pp; German.

This invention describes a novel feline interleukin-12 (fIL-12) polypeptide (I) that is expressed, by recombinant gene expression in eukaryotic or prokaryotic cells, in the form of both polypeptide chains of subunits p35 and p40. These proteins are formed so that, in equimolar concentrations and in presence of an immunizing antigen, they can be administered to carnivores, particularly domestic cats. The invention also describes a nucleic acid construct (II) encoding fIL-12 containing sequences at least 95% identical with the p40- and p35-encoding sequences (A, 990 bp and B, 669 bp respectively), reproduced in the specification, as immunostimulants for immunization against infectious diseases and/or for treating infections or tumors in felines, especially domestic cats. The products of the invention have immunostimulatory, antiviral and antitumor activity. Nucleic acid constructs that encode (II) are useful as adjuvants for prophylactic immunization against viral diseases and for treating diseases associated with a Th1 defect. IL-12 induces synthesis of interferon gamma (Th1 response). The feline interleukin-12 polypeptide is useful for carnivores, and particularly domestic cats in the following: (i) as immunostimulant, for preventative or therapeutic use; and (ii) treating tumors and autoimmune diseases, or diseases associated with a Th1 defect, especially pre-existing infections by feline immune deficiency virus (FIV), feline leukemia virus and corona virus

Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

gnment Scores:

d. No.:	0	Length:	990
re:	328.00	Matches:	328
cent Similarity:	100.0%	Conservative:	0
c Local Similarity:	100.0%	Mismatches:	0
ry Match:	100.0%	Indels:	0
	4	Gaps:	0

10-821-670A-56 (1-328) x AAF26085 (1-990)

```
          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
```

```
Db        61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy       161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy       321 SerAsnTrpAlaSerValSerCys 328
             |||||||||||||||||||||||
Db       961 AGCAACTGGGCATCCGTGTCCTGC 984
```

RESULT 11
AAF26076
ID AAF26076 standard; DNA; 4522 BP.
XX
AC AAF26076;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA SEQ ID 2.
XX

Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection; interleukin; antiviral; cytotoxic immune response; Th1 response; ds.

Felis sp.

WO200104280-A2.

18-JAN-2001.

08-JUL-2000; 2000WO-DE002262.

08-JUL-1999; 99CH-00001258.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.

Leutenegger C, Schroff M, Wittig B, Lutz H;

WPI; 2001-147190/15.

Vaccine for treating or preventing lentivirus infection in cats, contains nucleic acid sequence encoding viral protein under control of eukaryotic promoter.

Disclosure; Page 29-31; 37pp; German.

This invention describes a novel vaccine (A) for prevention or treatment of lentivirus infection in felines which comprises an immunizing nucleic acid sequence (I) that contains, or comprises, at least part of a gene encoding a protein (II) of the virus, under control of a eukaryotic promoter functional in the relevant animal. (II) is especially the envelope (env) protein. The invention also describes (1) vaccine (A) containing an immunizing protein, or fragment, from a lentivirus plus at least one of interleukin (IL)-12 and/or -16; and (2) preparation of a lentivirus protein, or fragment, especially derived from feline immune deficiency virus (FIV), by expressing the corresponding nucleic acid sequence in a host cell. The products of the invention have antiviral activity. The vaccine (A) and related protein-based vaccines, are particularly used to treat or prevent lentivirus infections in domestic cats, especially feline immune deficiency virus (FIV). Vaccination with (A) allows differentiation between vaccinated and infected animals, from the antibody status. The vaccines may be formulated with an adjuvant (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic immune response, particularly a Th1 response

Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

nment Scores:

.. No.:	0	Length:	4522
e:	328.00	Matches:	328
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	100.0%	Indels:	0
	4	Gaps:	0

0-821-670A-56 (1-328) x AAF26076 (1-4522)

```
        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

       21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

       41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

       61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy       81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy      101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy      121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy      141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy      161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||
Db     4007 AGCAACTGGGCATCCGTGTCCTGC 4030
```

RESULT 12
AAF26094
ID AAF26094 standard; DNA; 4522 BP.
XX
AC AAF26094;
XX
DT 24-APR-2001 (first entry)
XX
DE Plasmid pMol-fil12p40 DNA SEQ ID 10.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.

08-JUL-1999; 99CH-00001259.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.
(REGC) UNIV CALIFORNIA.

Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;

WPI; 2001-147178/15.

Recombinant feline interleukin-12, useful as immunostimulant and for treating e.g. viral infections in cats, and related nucleic acid constructs.

Example 1c; Page 33-35; 35pp; German.

This invention describes a novel feline interleukin-12 (fIL-12) polypeptide (I) that is expressed, by recombinant gene expression in eukaryotic or prokaryotic cells, in the form of both polypeptide chains of subunits p35 and p40. These proteins are formed so that, in equimolar concentrations and in presence of an immunizing antigen, they can be administered to carnivores, particularly domestic cats. The invention also describes a nucleic acid construct (II) encoding fIL-12 containing sequences at least 95% identical with the p40- and p35-encoding sequences (A, 990 bp and B, 669 bp respectively), reproduced in the specification, as immunostimulants for immunization against infectious diseases and/or for treating infections or tumors in felines, especially domestic cats. The products of the invention have immunostimulatory, antiviral and antitumor activity. Nucleic acid constructs that encode (II) are useful as adjuvants for prophylactic immunization against viral diseases and for treating diseases associated with a Th1 defect. IL-12 induces synthesis of interferon gamma (Th1 response). The feline interleukin-12 polypeptide is useful for carnivores, and particularly domestic cats in the following: (i) as immunostimulant, for preventative or therapeutic use; and (ii) treating tumors and autoimmune diseases, or diseases associated with a Th1 defect, especially pre-existing infections by feline immune deficiency virus (FIV), feline leukemia virus and corona virus

Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

gnment Scores:			
i. No.:	0	Length:	4522
re:	328.00	Matches:	328
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	100.0%	Indels:	0
	4	Gaps:	0

10-821-670A-56 (1-328) x AAF26094 (1-4522)

```
          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGC 4030
```

RESULT 13
AAV56625
ID AAV56625 standard; cDNA; 2193 BP.
XX
AC AAV56625;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp40 cDNA.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX

FH	Key	Location/Qualifiers
FT	CDS	64. .1053
FT		/*tag= a
FT	sig_peptide	64. .129
FT		/*tag= b
FT	mat_peptide	130. .1050
FT		/*tag= c
FT		/product= "FLAFp40"
FT		/note= "feline cytokine"

XX
PN WO9746583-A1.
XX

11-DEC-1997.

29-MAY-1997; 97WO-JP001824.

04-JUN-1996; 96JP-00165249.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;

WPI; 1998-042118/04.
P-PSDB; AAW76173.

Novel feline cytokine protein - useful for treating feline auto:immune diseases, e.g. those caused by feline herpes virus or feline calcivirus.

Claim 19; Page 52-54; 94pp; Japanese.

This sequence encodes a novel feline cytokine protein, FLAFp40. This protein can be used in the production of a FLAFp35/FLAFp40 heterodimer which can potentiate the cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins are used for treatment of feline autoimmune diseases e.g. as caused by feline herpes virus or feline calcivirus

Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 U; 0 Other;

nment Scores:

.. No.:	4.65e-313	Length:	2193
e:	316.00	Matches:	316
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	96.3%	Indels:	0
	2	Gaps:	0

0-821-670A-56 (1-328) x AAV56625 (1-2193)

```
       13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

       33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

       53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

       73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

       93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

      113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

      133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

      153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

      173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

Qy      193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

Qy      213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy      233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy      253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

Qy      273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

Qy      293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

Qy      313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 1047
```

RESULT 14
AAV56627
ID AAV56627 standard; cDNA; 921 BP.
XX
AC AAV56627;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp40 cDNA mature transcript #2.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76174.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 21; Page 56-57; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC This protein can be used in the production of a FLAFp35/FLAFp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC feline autoimmune diseases e.g. as caused by feline herpes virus or
CC feline calcivirus
XX
SQ Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 U; 0 Other;

Alignment Scores:

d. No.:	3.5e-303	Length:	921
re:	306.00	Matches:	306
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	93.3%	Indels:	0
	2	Gaps:	0

10-821-670A-56 (1-328) x AAV56627 (1-921)

```
 23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

 43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
901 TGGGCATCCGTGTCCTGC 918
```

RESULT 15
AAV56626
ID AAV56626 standard; cDNA; 921 BP.
XX
AC AAV56626;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp40 cDNA mature transcript #1.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76174.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 20; Page 55; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC This protein can be used in the production of a FLAFp35/FLAFp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC feline autoimmune diseases e.g. as caused by feline herpes virus or
CC feline calcivirus
XX
SQ Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.5e-303	Length:	921
Score:	306.00	Matches:	306
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	93.3%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-56 (1-328) x AAV56626 (1-921)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
```

```
      123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

      143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

      163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

      243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

      323 TrpAlaSerValSerCys 328
          |||||||||||||||||
      901 TGGGCATCCGTGTCCTGC 918

LT 16
8950
 ABK98950 standard; cDNA; 1599 BP.

 ABK98950;

 21-OCT-2002  (first entry)

 Feline interleukin-12 nFeIL-12-1599 coding strand.

 Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
 canine IL-12; autoimmune disease; allergic reaction; infectious disease;
 tumour development; inflammatory disease; graft rejection; gene; ss.

 Felis catus.

 US2002052030-A1.

 02-MAY-2002.

 27-JUL-2001; 2001US-00917265.

 04-AUG-2000; 2000US-0223016P.

 (WOND/) WONDERLING R S.
 (BORO/) BOROUGHS K L.

 Wonderling RS,  Boroughs KL;

XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.53e-211       Length:         1599
Score:                  216.00          Matches:        316
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            65.9%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-56 (1-328) x ABK98950 (1-1599)

Qy          12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy          32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy          52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy          72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy          92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy         112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy         132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy         152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy         172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy         192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
```

```
      574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

      212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
      634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

      232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
      694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

      252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
      754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

      272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
      814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

      292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
      874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

      312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
      934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 984

JLT 17
98951/c
  ABK98951 standard; cDNA; 1599 BP.

  ABK98951;

  21-OCT-2002  (first entry)

  Feline interleukin-12 nFeIL-12-1599 complementary strand.

  Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
  canine IL-12; autoimmune disease; allergic reaction; infectious disease;
  tumour development; inflammatory disease; graft rejection; ss.

  Felis catus.

  US2002052030-A1.

  02-MAY-2002.

  27-JUL-2001; 2001US-00917265.

  04-AUG-2000; 2000US-0223016P.

  (WOND/) WONDERLING R S.
  (BORO/) BOROUGHS K L.

  Wonderling RS,  Boroughs KL;

  WPI; 2002-573554/61.

  Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
  chain and canine IL-12 single chain proteins, useful for treating and
  preventing autoimmune diseases, inflammatory diseases and/or graft
  rejection in animals.

  Claim 6; Page 61-62; 106pp; English.

  The present invention discloses new feline interleukin 18 (IL-18), feline
  caspase-1, feline IL-12 single chain and canine IL-12 single chain
  proteins. A composition comprising a feline IL-18, feline caspase-1,
  feline IL-12 single chain or canine IL-12 single chain proteins, a
  nucleic acid encoding these proteins, mimetopes of these proteins,
  multimeric forms of these proteins, an antibody against these proteins,
  or an inhibitor identified by its ability to inhibit the activity of
  these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.53e-211       Length:         1599
Score:                  216.00          Matches:        316
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            65.9%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-56 (1-328) x ABK98951 (1-1599)

Qy          12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
Db        1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

Qy          32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
Db        1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

Qy          52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
Db        1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

Qy          72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
Db        1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

Qy          92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
Db        1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

Qy         112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
Db        1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

Qy         132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
Db        1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

Qy         152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
Db        1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

Qy         172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
Db        1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy         192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
Db        1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy         212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
Db         966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy         232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
Db         906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy         252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
Db         846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy         272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
Db         786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727
```

```
      292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

      312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 616

LT 18
4691
 ADV34691 standard; cDNA; 1599 BP.

 ADV34691;

 24-FEB-2005  (first entry)

 Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.

 DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
 infectious disease; antimicrobial; gene; ss.

 Felis catus.

 Key             Location/Qualifiers
 CDS             1. .1599
                 /*tag= a
                 /product= "PFeIL-12p533 protein"
                 /partial
                 /note= "No stop codon"

 US2004248261-A1.

 09-DEC-2004.

 09-APR-2004; 2004US-00821670.

 04-AUG-2000; 2000US-0223016P.
 27-JUL-2001; 2001US-00917265.

 (WOND/) WONDERLING R S.
 (BORO/) BOROUGHS K L.

 Wonderling RS,  Boroughs KL;

 WPI; 2005-020565/02.
 P-PSDB; ADV34692.

 New nucleic acid molecule comprising a sequence encoding a feline p35 or
 p40 subunit protein and a nucleic acid linker, useful in preparing a
 vaccine against infectious diseases in feline animals.

 Claim 24; SEQ ID NO 38; 103pp; English.

 The present invention relates to the feline interleukin (IL)-12p35 or p40
 subunit protein and their encoding nucleic acid molecules and a nucleic
 acid linker. The invention also provides the feline caspase (casp)-1,
 feline IL-18 single chain and canine IL-12 single chain proteins and
 their nucleic acid molecules. The nucleic acid molecule is useful in
 preparing a vaccine against infectious diseases in feline animals. The
 present sequence is the feline single chain IL-12 protein encoding cDNA.

 Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

nment Scores:
.. No.:              8.53e-211      Length:         1599
e:                   216.00         Matches:        316
ent Similarity:      99.7%          Conservative:   0
 Local Similarity:   99.7%          Mismatches:     1
y Match:             65.9%          Indels:         0
                     14             Gaps:           0

 0-821-670A-56 (1-328) x ADV34691 (1-1599)

Qy          12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy          32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy          52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy          72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy          92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy         112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy         132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy         152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy         172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy         192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy         212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy         232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy         252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy         272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy         292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

Qy         312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 984

RESULT 19
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
```

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Felis catus.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 3; SEQ ID NO 40; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12 complementary DNA.

Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

gnment Scores:

i. No.:	8.53e-211	Length:	1599
re:	216.00	Matches:	316
cent Similarity:	99.7%	Conservative:	0
t Local Similarity:	99.7%	Mismatches:	1
ry Match:	65.9%	Indels:	0
	14	Gaps:	0

10-821-670A-56 (1-328) x ADV34693 (1-1599)

```
Qy        12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

Qy        32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

Qy        52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

Qy        72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

Qy        92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

Qy       112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

Qy       132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

Qy       152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

Qy       172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy       192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy       212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy       232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy       252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy       272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

Qy       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 616
```

RESULT 20
ABK98942
ID ABK98942 standard; cDNA; 921 BP.
XX
AC ABK98942;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-921 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69302.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and

preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 1; Page 49-50; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

nment Scores:

.. No.:	9.2e-200	Length:	921
e:	205.00	Matches:	305
ent Similarity:	99.7%	Conservative:	0
Local Similarity:	99.7%	Mismatches:	1
y Match:	62.5%	Indels:	0
	6	Gaps:	0

0-821-670A-56 (1-328) x ABK98942 (1-921)

```
       23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

       43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

       63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

       83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

      103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

      123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

      143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

      163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
      421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy    243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy    263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy    283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy    303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy    323 TrpAlaSerValSerCys 328
          |||||||||||||||||
Db    901 TGGGCATCCGTGTCCTGC 918
```

RESULT 21
ABK98943/c
ID ABK98943 standard; cDNA; 921 BP.
XX
AC ABK98943;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-921 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 51; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

gnment Scores:

d. No.:	9.2e-200	Length:	921
re:	205.00	Matches:	305
cent Similarity:	99.7%	Conservative:	0
t Local Similarity:	99.7%	Mismatches:	1
ry Match:	62.5%	Indels:	0
	6	Gaps:	0

10-821-670A-56 (1-328) x ABK98943 (1-921)

```
 23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

 43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

323 TrpAlaSerValSerCys 328
    ||||||||||||||||||
```

Db 21 TGGGCATCCGTGTCCTGC 4

RESULT 22
ADV34681/c
ID ADV34681 standard; DNA; 921 BP.
XX
AC ADV34681;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p40 complementary DNA, nFeIL-12p40 921.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 28; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p40 subunit
CC complementary DNA.
XX
SQ Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.2e-200	Length:	921
Score:	205.00	Matches:	305
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	62.5%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x ADV34681 (1-921)

```
Qy  23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy  43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy  63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy  83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
```

```
      741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

      103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

      123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

      143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

      163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
          ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
      501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

      243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

      323 TrpAlaSerValSerCys 328
          |||||||||||||||||
       21 TGGGCATCCGTGTCCTGC 4

LT 23
4679
 ADV34679 standard; cDNA; 921 BP.

 ADV34679;

 24-FEB-2005  (first entry)

 Feline single chain mature IL-12p40 protein cDNA, nFeIL-12p40 921.

 DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
 infectious disease; antimicrobial; gene; ss.

 Felis catus.

 Key             Location/Qualifiers
 CDS             1. .921
                 /*tag=  a
                 /product= "PFeIL-12p40 307 protein"
                 /partial
                 /note= "No start and stop codon"

 PN   US2004248261-A1.
 XX
 PD   09-DEC-2004.
 XX
 PF   09-APR-2004; 2004US-00821670.
 XX
 PR   04-AUG-2000; 2000US-0223016P.
 PR   27-JUL-2001; 2001US-00917265.
 XX
 PA   (WOND/) WONDERLING R S.
 PA   (BORO/) BOROUGHS K L.
 XX
 PI   Wonderling RS,  Boroughs KL;
 XX
 DR   WPI; 2005-020565/02.
 DR   P-PSDB; ADV34680.
 XX
 PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
 PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
 PT   vaccine against infectious diseases in feline animals.
 XX
 PS   Claim 23; SEQ ID NO 26; 103pp; English.
 XX
 CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
 CC   subunit protein and their encoding nucleic acid molecules and a nucleic
 CC   acid linker. The invention also provides the feline caspase (casp)-1,
 CC   feline IL-18 single chain and canine IL-12 single chain proteins and
 CC   their nucleic acid molecules. The nucleic acid molecule is useful in
 CC   preparing a vaccine against infectious diseases in feline animals. The
 CC   present sequence is the feline single chain mature IL-12p40 subunit
 CC   protein encoding cDNA.
 XX
 SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

 Alignment Scores:
 Pred. No.:                 9.2e-200        Length:          921
 Score:                     205.00          Matches:         305
 Percent Similarity:        99.7%           Conservative:    0
 Best Local Similarity:     99.7%           Mismatches:      1
 Query Match:               62.5%           Indels:          0
 DB:                        14              Gaps:            0

 US-10-821-670A-56 (1-328) x ADV34679 (1-921)

 Qy          23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

 Qy          43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

 Qy          63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 Qy          83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

 Qy         103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

 Qy         123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

 Qy         143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

 Qy         163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
```

```
421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
901 TGGGCATCCGTGTCCTGC 918
```

JLT 24
98954/c
ABK98954 standard; cDNA; 1533 BP.

ABK98954;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12-1533 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 66-67; 106pp; English.

CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.5e-199	Length:	1533
Score:	205.00	Matches:	305
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	62.5%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x ABK98954 (1-1533)

```
Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
Db      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
Db      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814
```

```
      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

      323 TrpAlaSerValSerCys 328
          |||||||||||||||||
      633 TGGGCATCCGTGTCCTGC 616

LT 25
8953
 ABK98953 standard; cDNA; 1533 BP.

 ABK98953;

 21-OCT-2002  (first entry)

 Feline interleukin-12 nFeIL-12-1533 coding strand.

 Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
 canine IL-12; autoimmune disease; allergic reaction; infectious disease;
 tumour development; inflammatory disease; graft rejection; gene; ss.

 Felis catus.

 US2002052030-A1.

 02-MAY-2002.

 27-JUL-2001; 2001US-00917265.

 04-AUG-2000; 2000US-0223016P.

 (WOND/) WONDERLING R S.
 (BORO/) BOROUGHS K L.

 Wonderling RS,  Boroughs KL;

 WPI; 2002-573554/61.
 P-PSDB; ABG69307.

 Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
 chain and canine IL-12 single chain proteins, useful for treating and
 preventing autoimmune diseases, inflammatory diseases and/or graft
 rejection in animals.

 Claim 6; Page 63-64; 106pp; English.

 The present invention discloses new feline interleukin 18 (IL-18), feline
 caspase-1, feline IL-12 single chain and canine IL-12 single chain
 proteins. A composition comprising a feline IL-18, feline caspase-1,
 feline IL-12 single chain or canine IL-12 single chain proteins, a
 nucleic acid encoding these proteins, mimetopes of these proteins,
 multimeric forms of these proteins, an antibody against these proteins,
 or an inhibitor identified by its ability to inhibit the activity of
 these proteins, can be used to treat or prevent autoimmune diseases,
 allergic reactions, infectious diseases, tumour development, inflammatory
 diseases and/or graft rejection in animals. The present nucleic acid
 sequence represents a feline interleukin 12 DNA sequence, as described in
 the invention

 Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

nment Scores:
.. No.:              1.5e-199        Length:         1533
e:                   205.00          Matches:        305
```

```
Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            62.5%          Indels:        0
DB:                     6              Gaps:          0

US-10-821-670A-56 (1-328) x ABK98953 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCys 328
              |||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGC 918

RESULT 26
ADV34697/c
```

ADV34697 standard; DNA; 1533 BP.

ADV34697;

24-FEB-2005 (first entry)

Feline single chain IL-12 complementary DNA, nFeIL-12 1533.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Felis catus.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 3; SEQ ID NO 45; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12 complementary DNA.

Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

gnment Scores:

d. No.:	1.5e-199	Length:	1533
re:	205.00	Matches:	305
cent Similarity:	99.7%	Conservative:	0
: Local Similarity:	99.7%	Mismatches:	1
ty Match:	62.5%	Indels:	0
	14	Gaps:	0

10-821-670A-56 (1-328) x ADV34697 (1-1533)

```
Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       323 TrpAlaSerValSerCys 328
             ||||||||||||||||||
Db       633 TGGGCATCCGTGTCCTGC 616
```

RESULT 27
ADV34695
ID ADV34695 standard; cDNA; 1533 BP.
XX
AC ADV34695;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .1533
FT		/*tag= a
FT		/product= "PFeIL-12 511 protein"
FT		/partial
FT		/note= "No start and stop codon"

XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.

```
04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS,  Boroughs KL;

WPI; 2005-020565/02.
P-PSDB; ADV34696.

New nucleic acid molecule comprising a sequence encoding a feline p35 or
p40 subunit protein and a nucleic acid linker, useful in preparing a
vaccine against infectious diseases in feline animals.

Claim 24; SEQ ID NO 43; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40
subunit protein and their encoding nucleic acid molecules and a nucleic
acid linker. The invention also provides the feline caspase (casp)-1,
feline IL-18 single chain and canine IL-12 single chain proteins and
their nucleic acid molecules. The nucleic acid molecule is useful in
preparing a vaccine against infectious diseases in feline animals. The
present sequence is the feline single chain IL-12 protein encoding cDNA.

Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

nment Scores:
.. No.:              1.5e-199       Length:        1533
e:                   205.00         Matches:       305
ent Similarity:      99.7%          Conservative:  0
 Local Similarity:   99.7%          Mismatches:    1
y Match:             62.5%          Indels:        0
                     14             Gaps:          0

0-821-670A-56 (1-328) x ADV34695 (1-1533)

       23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

       43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

       63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

       83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

      103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

      123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

      143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

      163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
          ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
      421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy       323 TrpAlaSerValSerCys 328
             |||||||||||||||||
Db       901 TGGGCATCCGTGTCCTGC 918

RESULT 28
AAD15209
ID   AAD15209 standard; DNA; 990 BP.
XX
AC   AAD15209;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone R16-51.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08602.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
```

and p35 polypeptides), useful for treating various diseases e.g. diabetic retinopathy and cancer.

Claim 1; Page 137-138; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is a modified human p40 protein encoding DNA

Sequence 990 BP; 270 A; 250 C; 254 G; 216 T; 0 U; 0 Other;

gnment Scores:

i. No.:	4.56e-43	Length:	990
re:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	15.9%	Indels:	0
	5	Gaps:	0

10-821-670A-56 (1-328) x AAD15209 (1-990)

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCTGACCCACCCAAGAACTTG 726

      243 GlnLeuLysProLeuLysAsnSerArgHisValGlu 254
          ||||||||||||||||||||||||||||||||||
      727 CAGCTGAAGCCATTAAAGAATTCTCGACACGTGGAG 762
```

JLT 29
15206
AAD15206 standard; DNA; 984 BP.

AAD15206;

01-NOV-2001 (first entry)

Modified human cytokine p40 encoding DNA from clone B1-81.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p40; mutant; ds.

Homo sapiens.
Synthetic.

Key	Location/Qualifiers
CDS	1. .984
	/*tag= a
	/product= "Modified p40 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .981
	/*tag= c
	/product= "Mature modified p40 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08599.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 1; Page 137; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p40 protein encoding
CC DNA
XX
SQ Sequence 984 BP; 272 A; 254 C; 247 G; 211 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.35e-40	Length:	984
Score:	49.00	Matches:	49
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.9%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-56 (1-328) x AAD15206 (1-984)

```
Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGG 429

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCT 489

Qy        164 AspProGlnGlyValThrCysGlyAla 172
              ||||||||||||||||||||||||||
Db        490 GACCCCCAAGGGGTGACTTGTGGAGCC 516
```

RESULT 30
AAD15205
ID AAD15205 standard; DNA; 984 BP.
XX
AC AAD15205;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p40 encoding DNA from clone B2-52.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p40; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .984
FT		/*tag= a
FT		/product= "Modified p40 protein precursor"
FT	sig_peptide	1. .66

```
                /*tag=  b
mat_peptide     67. .981
                /*tag=  c
                /product= "Mature modified p40 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999;   99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR,  Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08598.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
and p35 polypeptides), useful for treating various diseases e.g. diabetic
retinopathy and cancer.

Claim 1; Page 136-137; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine
polypeptides (i.e. modified p40 and p35 polypeptides). The modified
cytokine polypeptides have T-cell proliferative and interferon (IFN)-
gamma induction activities. The polypeptides and polynucleotides of the
invention are useful for treating various diseases e.g. bacterial
infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
polynucleotide may also be useful as a vaccine adjuvant, to enhance a
vaccinated host's cell-mediated immunity for protective response to a
pathogen. The present sequence is a modified human p40 protein encoding
DNA

Sequence 984 BP; 267 A; 246 C; 254 G; 217 T; 0 U; 0 Other;

nment Scores:
.. No.:              7.87e-33        Length:         984
e:                   42.00           Matches:        42
ent Similarity:      100.0%          Conservative:   0
 Local Similarity:   100.0%          Mismatches:     0
y Match:             12.8%           Indels:         0
                     5               Gaps:           0

0-821-670A-56 (1-328) x AAD15205 (1-984)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACTTG 726

      243 GlnLeu 244
          ||||||
      727 CAGCTG 732

LT 31
5203
 AAD15203 standard; DNA; 975 BP.

 AAD15203;

 01-NOV-2001  (first entry)

 Modified human cytokine p40 encoding DNA from clone C2-22.

 Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
```

```
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .975
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .972
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08596.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 975 BP; 269 A; 252 C; 250 G; 204 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.25e-32        Length:         975
Score:                  41.00           Matches:        41
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.5%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-56 (1-328) x AAD15203 (1-975)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

Qy        257 Trp 257
              |||
Db        754 TGG 756
```

JLT 32
98959
ABK98959 standard; cDNA; 921 BP.

ABK98959;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12p40-921 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69310.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 1; Page 71; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

gnment Scores:

i. No.:	9.73e-28	Length:	921
re:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	6	Gaps:	0

10-821-670A-56 (1-328) x ABK98959 (1-921)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651
```

JLT 33

ABK98960/c
ID ABK98960 standard; cDNA; 921 BP.
XX
AC ABK98960;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p40-921 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 73; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.73e-28	Length:	921
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x ABK98960 (1-921)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271
```

RESULT 34
ADV34706/c
ID ADV34706 standard; DNA; 921 BP.

ADV34706;

24-FEB-2005 (first entry)

Canine single chain mature IL-12p40 complementary DNA, nCaIL-12p40 921.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Canis familiaris.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Disclosure; SEQ ID NO 54; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the canine single chain IL-12p40 subunit reverse complementary DNA.

Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

nment Scores:
.. No.: 9.73e-28 Length: 921
e: 37.00 Matches: 37
ent Similarity: 100.0% Conservative: 0
Local Similarity: 100.0% Mismatches: 0
y Match: 11.3% Indels: 0
14 Gaps: 0

0-821-670A-56 (1-328) x ADV34706 (1-921)

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

LT 35
4704
ADV34704 standard; cDNA; 921 BP.

ADV34704;

24-FEB-2005 (first entry)

Canine single chain mature IL-12p40 protein cDNA, nCaIL-12p40 921.

KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 1. .921
FT /*tag= a
FT /product= "PCaIL-12P40 307 protein"
FT /partial
FT /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34705.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 52; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p40 subunit protein
CC encoding cDNA.
XX
SQ Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.73e-28 Length: 921
Score: 37.00 Matches: 37
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.3% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-56 (1-328) x ADV34704 (1-921)

Qy 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
Db 541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
Db 601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 36
AAX18177
ID AAX18177 standard; cDNA; 924 BP.
XX
AC AAX18177;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine mature CLAF p40 subunit coding sequence.

CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog; viral disease; canine distemper; canine parvovirus; autoimmune disease; canine infectious hepatitis; ds.

Canis sp.

WO9855511-A1.

10-DEC-1998.

26-MAY-1998; 98WO-JP002295.

03-JUN-1997; 97JP-00161936.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Imamura T, Maeda H, Tokiyoshi S, Eda Y;

WPI; 1999-070260/06.
P-PSDB; AAW74323.

Canine cytokine protein which activates canine cytotoxic T lymphocytes - is useful for treatment of viral and autoimmune diseases in dogs.

Claim 8; Page 32; 51pp; Japanese.

This sequence encodes the canine lymphocyte activation factor (CLAF) of the invention. CLAF activates lymphocytes, especially canine cytotoxic T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies recognising it may be used in the treatment of viral diseases in dogs (such as canine distemper, canine parvovirus and canine infectious hepatitis). The antibodies may also be used in isolation of CLAF from culture of the transformant host cells by affinity chromatography. The p40 homodimer can be used for the treatment of autoimmune diseases in dogs

Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 U; 0 Other;

gnment Scores:
i. No.: 9.76e-28 Length: 924
re: 37.00 Matches: 37
cent Similarity: 100.0% Conservative: 0
: Local Similarity: 100.0% Mismatches: 0
ry Match: 11.3% Indels: 0
2 Gaps: 0

10-821-670A-56 (1-328) x AAX18177 (1-924)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 603

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 654
```

JLT 37
98963
ABK98963 standard; cDNA; 987 BP.

ABK98963;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12p40-987 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

Canis familiaris.

PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69312.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 76-77; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.04e-27 Length: 987
Score: 37.00 Matches: 37
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.3% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-56 (1-328) x ABK98963 (1-987)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

RESULT 38
ABK98964/c
ID ABK98964 standard; cDNA; 987 BP.
XX
AC ABK98964;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p40-987 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 4; Page 78; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

nment Scores:

.. No.:	1.04e-27	Length:	987
e:	37.00	Matches:	37
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	11.3%	Indels:	0
	6	Gaps:	0

0-821-670A-56 (1-328) x ABK98964 (1-987)

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271
```

LT 39
4712/c
ADV34712 standard; DNA; 987 BP.

ADV34712;

24-FEB-2005 (first entry)

Canine single chain IL-12p40 complementary DNA, nCaIL-12p40 987.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Canis familiaris.

US2004248261-A1.

09-DEC-2004.

PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 60; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p40 subunit full-length
CC complementary DNA.
XX
SQ Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.04e-27	Length:	987
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x ADV34712 (1-987)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271
```

RESULT 40
ADV34710
ID ADV34710 standard; cDNA; 987 BP.
XX
AC ADV34710;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p40 full-length cDNA, nCaIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Canis familiaris.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .987
FT		/*tag= a
FT		/product= "PCaIL-12P40-329 protein"
FT		/partial
FT		/note= "No stop codon"

XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.
P-PSDB; ADV34711.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 4; SEQ ID NO 58; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the canine single chain IL-12p40 subunit protein encoding full-length cDNA.

Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

gnment Scores:

i. No.:	1.04e-27	Length:	987
re:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	14	Gaps:	0

10-821-670A-56 (1-328) x ADV34710 (1-987)

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

JLT 41
13816
AAV13816 standard; cDNA to mRNA; 990 BP.

AAV13816;

14-MAY-1998 (first entry)

Canine IL-12 P40 subunit cDNA.

Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour; antiviral; vaccine adjuvant; ds.

Canis sp.

Key	Location/Qualifiers
CDS	1. .990
	/*tag= a
	/product= "interleukin-12_P40_subunit"

JP10036397-A.

10-FEB-1998.

08-NOV-1996; 96JP-00296789.

XX
PR 08-NOV-1995; 95JP-00289729.
PR 23-MAY-1996; 96JP-00128104.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.
DR P-PSDB; AAW41790.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT activities are expected.
XX
PS Claim 8; Page 8; 12pp; Japanese.
XX
CC The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC antiviral activating factor and the expression of class II MHC molecules
CC in canine tumour cells, stimulating proliferation of canine blastogenic
CC lymphocytes and activating canine leukocytes to inhibit canine tumour
CC cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.04e-27	Length:	990
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-56 (1-328) x AAV13816 (1-990)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

RESULT 42
AAV13817
ID AAV13817 standard; cDNA to mRNA; 990 BP.
XX
AC AAV13817;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit cDNA.
XX
KW Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .990
FT /*tag= a
FT /product= "interleukin-12_P40_subunit"
XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-00296789.
XX
PR 08-NOV-1995; 95JP-00289729.
PR 23-MAY-1996; 96JP-00128104.
XX
PA (TORA) TORAY IND INC.

```
WPI; 1998-174914/16.
P-PSDB; AAW41791.

Canine interleukin 12 - comprises P40 and P35 subunits; useful in
veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
activities are expected.

Claim 10; Page 10-11; 12pp; Japanese.

The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
antiviral activating factor and the expression of class II MHC molecules
in canine tumour cells, stimulating proliferation of canine blastogenic
lymphocytes and activating canine leukocytes to inhibit canine tumour
cells. The canine IL-12 can be used in veterinary medicines, e.g.
antitumour, antivirus and vaccine adjuvant activities are expected

Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

nment Scores:
.. No.:              1.04e-27       Length:         990
e:                   37.00          Matches:        37
ent Similarity:      100.0%         Conservative:   0
 Local Similarity:   100.0%         Mismatches:     0
y Match:             11.3%          Indels:         0
                     2              Gaps:           0

0-821-670A-56 (1-328) x AAV13817 (1-990)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

LT 43
3162
 AAX03162 standard; cDNA to mRNA; 990 BP.

 AAX03162;

 30-MAR-1999  (first entry)

 Nucleic acid encoding canine interleukin 12.

 Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
 skin disease; viral infection; allergic disease; breast tumour;
 oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
 othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
 otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
 allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
 dog Parvovirus infection; distemper virus; cat plaque virus infection;
 feline leukaemia; allergy; pollinosis; ds.

 Canis sp.

 Key             Location/Qualifiers
 CDS             1. .990
                 /*tag=  a
                 /product= "interleukin_12"

 WO9851327-A1.

 19-NOV-1998.

 07-MAY-1998;   98WO-JP002031.

 16-MAY-1997;   97JP-00127690.

 (TORA ) TORAY IND INC.
```

```
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84373.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.04e-27       Length:         990
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            11.3%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AAX03162 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 44
AAX03152
ID   AAX03152 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03152;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
```

19-NOV-1998.

07-MAY-1998; 98WO-JP002031.

16-MAY-1997; 97JP-00127690.

(TORA) TORAY IND INC.

Okano F, Satoh M, Yamada K;

WPI; 1999-070100/06.
P-PSDB; AAW84371.

New therapeutic and prophylactic agents - comprise genetically-engineered canine interleukin 12, used to treat, e.g. canine and feline immunological diseases.

Claim 1; Page 23-25; 45pp; Japanese.

The present sequence encodes a canine interleukin 12 (IL-12) protein. The IL-12 protein can be used in therapeutic or prophylactic agents. The agents can be used to prevent and treat canine and feline immunological diseases including dog and cat tumours, skin diseases, viral infections and allergic diseases, especially tumours, breast tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma, othematoma, pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin diseases, otitis externa, dermatitis, eczema, fungal diseases of the skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis and hair loss; infections; dog Parvovirus infection and distemper virus, cat plaque virus infection and feline leukaemia, and allergic diseases, e.g. pollinosis

Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

gnment Scores:

i. No.:	1.04e-27	Length:	990
ce:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
c Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	2	Gaps:	0

10-821-670A-56 (1-328) x AAX03152 (1-990)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

JLT 45
35625
AAX35625 standard; cDNA to mRNA; 990 BP.

AAX35625;

09-JUL-1999 (first entry)

Nucleic acid encoding canine Interleukin-12 (IL-12).

Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer; tumour; skin disease; infectious disease; allergic disease; ds.

Canis sp.

Key	Location/Qualifiers
CDS	1. .990
	/*tag= a

JP11106350-A.

PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-00133345.
XX
PR 16-MAY-1997; 97JP-00127690.
PR 07-AUG-1997; 97JP-00213755.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR P-PSDB; AAY02342.
XX
PT A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT prevention and treatment of dog and cat immune diseases.
XX
PS Claim 1; Page 14-15; 16pp; Japanese.
XX
CC The present sequence encodes canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment of dog
CC and cat immune diseases. The treatment used an agent comprising dog IL-12
CC (CaIL12) proteins to form a heterodimer. The agent is useful for
CC preventing and treating dog and cat immune diseases, including tumours,
CC skin diseases, infectious diseases and allergic diseases
XX
SQ Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.04e-27	Length:	990
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-56 (1-328) x AAX35625 (1-990)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

RESULT 46
AAX35615
ID AAX35615 standard; cDNA to mRNA; 990 BP.
XX
AC AAX35615;
XX
DT 09-JUL-1999 (first entry)
XX
DE Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .990
FT /*tag= a
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-00133345.
XX
PR 16-MAY-1997; 97JP-00127690.
PR 07-AUG-1997; 97JP-00213755.
XX
PA (TORA) TORAY IND INC.

```
WPI; 1999-308068/26.
P-PSDB; AAY02339.

A prevention and treating agent containing interleukin 12 (CaIL12) - for
prevention and treatment of dog and cat immune diseases.

Claim 1; Page 12; 16pp; Japanese.

The present sequence encodes canine interleukin-12 (IL-12). The
specification describes a method for the prevention and treatment of dog
and cat immune diseases. The treatment used an agent comprising dog IL-12
(CaIL12) proteins to form a heterodimer. The agent is useful for
preventing and treating dog and cat immune diseases, including tumours,
skin diseases, infectious diseases and allergic diseases

Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

nment Scores:
. No.:              1.04e-27       Length:        990
e:                  37.00          Matches:       37
ent Similarity:     100.0%         Conservative:  0
 Local Similarity:  100.0%         Mismatches:    0
y Match:            11.3%          Indels:        0
                    2              Gaps:          0

0-821-670A-56 (1-328) x AAX35615 (1-990)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

LT 47
4378
 AAI64378 standard; DNA; 990 BP.

 AAI64378;

 23-NOV-2001  (first entry)

 Canine coding sequence #1.

 Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.

 Canis familiaris.

 Key             Location/Qualifiers
 CDS             1. .990
                 /*tag=  a
                 /product= "Canine protein #1"
 sig_peptide     1. .66
                 /*tag=  b
 mat_peptide     67. .987
                 /*tag=  c

 JP2001161378-A.

 19-JUN-2001.

 26-SEP-2000; 2000JP-00292946.

 01-OCT-1999;   99JP-00281234.

 (TORA ) TORAY IND INC.

 WPI; 2001-592466/67.
 P-PSDB; AAG66480.

 Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.04e-27       Length:        990
Score:                  37.00          Matches:       37
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.3%          Indels:        0
DB:                     4              Gaps:          0

US-10-821-670A-56 (1-328) x AAI64378 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 48
AAI64388
ID   AAI64388 standard; DNA; 990 BP.
XX
AC   AAI64388;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66482.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 16-17; 21pp; Japanese.
```

The present invention relates to a method for the preparation of a highly pure protein in which interleukin 12 (IL12) and/or a protein inhibiting the activity of IL12 is contacted to an ion exchanging carrier and/or a pigment carrier to get IL12 and/or a protein inhibiting the activity of IL12. The protein is used as a preventive agent for dog immunopathy. The present sequence was used in the method of the present invention

Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

gnment Scores:

d. No.:	1.04e-27	Length:	990
re:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	4	Gaps:	0

10-821-670A-56 (1-328) x AAI64388 (1-990)

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

JLT 49
25698
ADZ25698 standard; cDNA; 990 BP.

ADZ25698;

16-JUN-2005 (first entry)

Canine interleukin 12 P40 encoding cDNA SEQ ID NO:3.

interleukin-12; antiviral; gene; ss.

Canis sp.

Key	Location/Qualifiers
CDS	1. .990
	/*tag= b
	/product= "interleukin-12 P40"
sig_peptide	1. .66
	/*tag= a
mat_peptide	67. .987
	/*tag= c
	/product= "interleukin-12 P40"

JP2003284585-A.

07-OCT-2003.

28-MAR-2002; 2002JP-00090161.

28-MAR-2002; 2002JP-00090161.

(TORA) TORAY IND INC.

WPI; 2003-885430/82.
P-PSDB; ADZ25702.

Large scale production of interleukin-12 for pharmaceutical applications, comprises infecting an insect cell with a recombinant virus containing gene encoding IL-12, and producing IL-12 by carrying out spinner culture of insect cell.

Example; SEQ ID NO 3; 8pp; Japanese.

The invention related to the large scale production of interleukin-12 (IL-12), which involves infecting an insect cell with a recombinant virus containing a gene encoding IL-12, and producing IL-12 by carrying out spinner culture of insect cell. The method is useful for producing IL-12, preferably canine IL-12. IL-12 has pharmaceutical applications. The present sequence encodes canine IL-12 P40, which is used in the exemplification of the present invention.

SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.04e-27	Length:	990
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	11	Gaps:	0

US-10-821-670A-56 (1-328) x ADZ25698 (1-990)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

RESULT 50
ADT04849
ID ADT04849 standard; DNA; 1015 BP.
XX
AC ADT04849;
XX
DT 13-JAN-2005 (first entry)
XX
DE Canine interleukin-12 (IL-12) p40 DNA.
XX
KW gene expression; insect; ds; interleukin-12; IL-12.
XX
OS Canis familiaris.
XX
PN JP2004290182-A.
XX
PD 21-OCT-2004.
XX
PF 06-FEB-2004; 2004JP-00030183.
XX
PR 10-MAR-2003; 2003JP-00062907.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 2004-740760/73.
XX
PT Novel gene vector for expression in insect useful for expression of
PT foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
PS Claim 4; SEQ ID NO 5; 13pp; Japanese.
XX
CC The invention relates to a novel gene vector for expression in an insect
CC comprising at least two promoters, particularly the polyhedrin promoter
CC and p10 promoter. The vector contains at least two types of foreign
CC protein expression gene and the gene product of the vector is produced
CC using a gene recombinant baculovirus, particularly a recombinant silkworm
CC nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC silkworm. The vector of the invention may be useful for expression of a
CC foreign gene, such as canine interleukin 12. Within the vector, two types
CC of foreign protein expression genes are integrated simultaneously for
CC their simultaneous expression. The current sequence is that of the canine
CC interleukin-12 (IL-12) p40 DNA of the invention.
XX
SQ Sequence 1015 BP; 285 A; 251 C; 254 G; 225 T; 0 U; 0 Other;

Alignment Scores:

```
. No.:              1.07e-27        Length:         1015
e:                  37.00           Matches:        37
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            11.3%           Indels:         0
                    13              Gaps:           0

0-821-670A-56 (1-328) x ADT04849 (1-1015)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

LT 51
8967
 ABK98967 standard; cDNA; 1533 BP.

 ABK98967;

 21-OCT-2002  (first entry)

 Canine interleukin-12 nCaIL-12-1533 coding strand.

 Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
 canine IL-12; autoimmune disease; allergic reaction; infectious disease;
 tumour development; inflammatory disease; graft rejection; gene; ss.

 Canis familiaris.

 US2002052030-A1.

 02-MAY-2002.

 27-JUL-2001; 2001US-00917265.

 04-AUG-2000; 2000US-0223016P.

 (WOND/) WONDERLING R S.
 (BORO/) BOROUGHS K L.

 Wonderling RS,  Boroughs KL;

 WPI; 2002-573554/61.
 P-PSDB; ABG69314.

 Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
 chain and canine IL-12 single chain proteins, useful for treating and
 preventing autoimmune diseases, inflammatory diseases and/or graft
 rejection in animals.

 Claim 6; Page 83-85; 106pp; English.

 The present invention discloses new feline interleukin 18 (IL-18), feline
 caspase-1, feline IL-12 single chain and canine IL-12 single chain
 proteins. A composition comprising a feline IL-18, feline caspase-1,
 feline IL-12 single chain or canine IL-12 single chain proteins, a
 nucleic acid encoding these proteins, mimetopes of these proteins,
 multimeric forms of these proteins, an antibody against these proteins,
 or an inhibitor identified by its ability to inhibit the activity of
 these proteins, can be used to treat or prevent autoimmune diseases,
 allergic reactions, infectious diseases, tumour development, inflammatory
 diseases and/or graft rejection in animals. The present nucleic acid
 sequence represents a canine interleukin 12 DNA sequence, as described in
 the invention

 Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

nment Scores:
. No.:              1.59e-27        Length:         1533
Score:              37.00           Matches:        37
Percent Similarity: 100.0%          Conservative:   0
Best Local Similarity: 100.0%       Mismatches:     0
Query Match:        11.3%           Indels:         0
DB:                 6               Gaps:           0

US-10-821-670A-56 (1-328) x ABK98967 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 52
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 86-87; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          1.59e-27        Length:         1533
Score:              37.00           Matches:        37
Percent Similarity: 100.0%          Conservative:   0
```

```
: Local Similarity:  100.0%        Mismatches:    0
:y Match:            11.3%         Indels:        0
                     6             Gaps:          0

10-821-670A-56 (1-328) x ABK98968 (1-1533)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

JLT 53
34718/c
  ADV34718 standard; DNA; 1533 BP.

  ADV34718;

  24-FEB-2005  (first entry)

  Canine single chain IL-12 complementary DNA, nCaIL-12 1533.

  DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
  infectious disease; antimicrobial; ds.

  Canis familiaris.

  US2004248261-A1.

  09-DEC-2004.

  09-APR-2004; 2004US-00821670.

  04-AUG-2000; 2000US-0223016P.
  27-JUL-2001; 2001US-00917265.

  (WOND/) WONDERLING R S.
  (BORO/) BOROUGHS K L.

  Wonderling RS,  Boroughs KL;

  WPI; 2005-020565/02.

  New nucleic acid molecule comprising a sequence encoding a feline p35 or
  p40 subunit protein and a nucleic acid linker, useful in preparing a
  vaccine against infectious diseases in feline animals.

  Example 4; SEQ ID NO 68; 103pp; English.

  The present invention relates to the feline interleukin (IL)-12p35 or p40
  subunit protein and their encoding nucleic acid molecules and a nucleic
  acid linker. The invention also provides the feline caspase (casp)-1,
  feline IL-18 single chain and canine IL-12 single chain proteins and
  their nucleic acid molecules. The nucleic acid molecule is useful in
  preparing a vaccine against infectious diseases in feline animals. The
  present sequence is the canine single chain IL-12 complementary DNA.

  Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

gnment Scores:
d. No.:              1.59e-27      Length:          1533
re:                  37.00         Matches:         37
:ent Similarity:     100.0%        Conservative:    0
: Local Similarity:  100.0%        Mismatches:      0
ry Match:            11.3%         Indels:          0
                     14            Gaps:            0

10-821-670A-56 (1-328) x ADV34718 (1-1533)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy         223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 54
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:           1.59e-27      Length:          1533
Score:               37.00         Matches:         37
Percent Similarity:  100.0%        Conservative:    0
Best Local Similarity: 100.0%      Mismatches:      0
Query Match:         11.3%         Indels:          0
DB:                  14            Gaps:            0

US-10-821-670A-56 (1-328) x ADV34716 (1-1533)

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
      541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

LT 55
8965
 ABK98965 standard; cDNA; 1599 BP.

 ABK98965;

 21-OCT-2002  (first entry)

 Canine interleukin-12 nCaIL-12-1599 coding strand.

 Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
 canine IL-12; autoimmune disease; allergic reaction; infectious disease;
 tumour development; inflammatory disease; graft rejection; gene; ss.

 Canis familiaris.

 US2002052030-A1.

 02-MAY-2002.

 27-JUL-2001; 2001US-00917265.

 04-AUG-2000; 2000US-0223016P.

 (WOND/) WONDERLING R S.
 (BORO/) BOROUGHS K L.

 Wonderling RS,  Boroughs KL;

 WPI; 2002-573554/61.
 P-PSDB; ABG69313.

 Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
 chain and canine IL-12 single chain proteins, useful for treating and
 preventing autoimmune diseases, inflammatory diseases and/or graft
 rejection in animals.

 Claim 6; Page 79-80; 106pp; English.

 The present invention discloses new feline interleukin 18 (IL-18), feline
 caspase-1, feline IL-12 single chain and canine IL-12 single chain
 proteins. A composition comprising a feline IL-18, feline caspase-1,
 feline IL-12 single chain or canine IL-12 single chain proteins, a
 nucleic acid encoding these proteins, mimetopes of these proteins,
 multimeric forms of these proteins, an antibody against these proteins,
 or an inhibitor identified by its ability to inhibit the activity of
 these proteins, can be used to treat or prevent autoimmune diseases,
 allergic reactions, infectious diseases, tumour development, inflammatory
 diseases and/or graft rejection in animals. The present nucleic acid
 sequence represents a canine interleukin 12 DNA sequence, as described in
 the invention

 Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

nment Scores:
.. No.:              1.65e-27        Length:         1599
e:                   37.00           Matches:        37
ent Similarity:      100.0%          Conservative:   0
 Local Similarity:   100.0%          Mismatches:     0
y Match:             11.3%           Indels:         0
                     6               Gaps:           0

0-821-670A-56 (1-328) x ABK98965 (1-1599)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 56
ABK98966/c
ID   ABK98966 standard; cDNA; 1599 BP.
XX
AC   ABK98966;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 82-83; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.65e-27        Length:         1599
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.3%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-56 (1-328) x ABK98966 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||
      933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

JLT 57
34715/c
  ADV34715 standard; DNA; 1599 BP.

  ADV34715;

  24-FEB-2005  (first entry)

  Canine single chain IL-12 complementary DNA, nCaIL-12 1599.

  DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
  infectious disease; antimicrobial; ds.

  Canis familiaris.

  US2004248261-A1.

  09-DEC-2004.

  09-APR-2004; 2004US-00821670.

  04-AUG-2000; 2000US-0223016P.
  27-JUL-2001; 2001US-00917265.

  (WOND/) WONDERLING R S.
  (BORO/) BOROUGHS K L.

  Wonderling RS,  Boroughs KL;

  WPI; 2005-020565/02.

  New nucleic acid molecule comprising a sequence encoding a feline p35 or
  p40 subunit protein and a nucleic acid linker, useful in preparing a
  vaccine against infectious diseases in feline animals.

  Example 4; SEQ ID NO 63; 103pp; English.

  The present invention relates to the feline interleukin (IL)-12p35 or p40
  subunit protein and their encoding nucleic acid molecules and a nucleic
  acid linker. The invention also provides the feline caspase (casp)-1,
  feline IL-18 single chain and canine IL-12 single chain proteins and
  their nucleic acid molecules. The nucleic acid molecule is useful in
  preparing a vaccine against infectious diseases in feline animals. The
  present sequence is the canine single chain IL-12 complementary DNA.

  Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

gnment Scores:
d. No.:                 1.65e-27        Length:         1599
re:                     37.00           Matches:        37
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               11.3%           Indels:         0
                        14              Gaps:           0

10-821-670A-56 (1-328) x ADV34715 (1-1599)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

JLT 58
34713
  ADV34713 standard; cDNA; 1599 BP.

  ADV34713;

XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.65e-27        Length:         1599
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.3%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-56 (1-328) x ADV34713 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 59
AAX18176
ID   AAX18176 standard; cDNA; 2154 BP.
XX
AC   AAX18176;
```

07-MAY-1999 (first entry)

Canine full length CLAF p40 subunit coding sequence.

CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog; viral disease; canine distemper; canine parvovirus; autoimmune disease; canine infectious hepatitis; ds.

Canis sp.

WO9855511-A1.

10-DEC-1998.

26-MAY-1998; 98WO-JP002295.

03-JUN-1997; 97JP-00161936.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Imamura T, Maeda H, Tokiyoshi S, Eda Y;

WPI; 1999-070260/06.
P-PSDB; AAW74322.

Canine cytokine protein which activates canine cytotoxic T lymphocytes - is useful for treatment of viral and autoimmune diseases in dogs.

Claim 8; Page 30-31; 51pp; Japanese.

This sequence encodes the canine lymphocyte activation factor (CLAF) of the invention. CLAF activates lymphocytes, especially canine cytotoxic T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies recognising it may be used in the treatment of viral diseases in dogs (such as canine distemper, canine parvovirus and canine infectious hepatitis). The antibodies may also be used in isolation of CLAF from culture of the transformant host cells by affinity chromatography. The p40 homodimer can be used for the treatment of autoimmune diseases in dogs

Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 U; 0 Other;

nment Scores:
. No.: 2.2e-27 Length: 2154
e: 37.00 Matches: 37
ent Similarity: 100.0% Conservative: 0
Local Similarity: 100.0% Mismatches: 0
y Match: 11.3% Indels: 0
2 Gaps: 0

0-821-670A-56 (1-328) x AAX18176 (1-2154)

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
661 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 720

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
721 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 771

LT 60
9006/c
ABK99006 standard; cDNA; 2267 BP.

ABK99006;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12p40-2267 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease;

KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 4; Page 99-100; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.31e-27 Length: 2267
Score: 37.00 Matches: 37
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.3% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-56 (1-328) x ABK99006 (1-2267)

Qy 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
Db 1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
Db 1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

RESULT 61
ABK99005
ID ABK99005 standard; cDNA; 2267 BP.
XX
AC ABK99005;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p40-2267 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX

Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69317.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 4; Page 97-98; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

gnment Scores:

i. No.:	2.31e-27	Length:	2267
re:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	6	Gaps:	0

10-821-670A-56 (1-328) x ABK99005 (1-2267)

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870
```

JLT 62
34757
ADV34757 standard; cDNA; 2267 BP.

ADV34757;

24-FEB-2005 (first entry)

Canine single chain IL-12p40 protein cDNA, nCaIL-12p40 2267.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; gene; ss.

Canis familiaris.

FH Key Location/Qualifiers
FT CDS 154. .1143
FT /*tag= a
FT /product= "PCaIL-12p40 329 protein"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34758.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 107; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p40 subunit protein
CC encoding cDNA.
XX
SQ Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.31e-27	Length:	2267
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x ADV34757 (1-2267)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870
```

RESULT 63
ADV34759/c
ID ADV34759 standard; DNA; 2267 BP.
XX
AC ADV34759;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p40 complementary DNA, nCaIL-12p35 2267.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 4; SEQ ID NO 109; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the canine single chain IL-12p40 subunit complementary DNA.

Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

nment Scores:
.. No.: 2.31e-27 Length: 2267
e: 37.00 Matches: 37
ent Similarity: 100.0% Conservative: 0
Local Similarity: 100.0% Mismatches: 0
y Match: 11.3% Indels: 0
14 Gaps: 0

0-821-670A-56 (1-328) x ADV34759 (1-2267)

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
     1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398
```

LT 64
4701
AAQ04701 standard; DNA; 906 BP.

AAQ04701;

25-MAR-2003 (revised)
11-OCT-1990 (first entry)

Sequence encoding natural killer cell stimulatory factor (NKSF).

Natural killer cell stimulatory factor; NKSF; cancer; leukopaenia; anaemia; radiation; bone marrow transplantation; ds.

Homo sapiens.

WO9005147-A.

17-MAY-1990.

10-NOV-1988; 88US-00269945.

10-NOV-1988; 88US-00269945.

PR 07-FEB-1989; 89US-00307817.
XX
PA (GEMY) GENETICS INST INC.
PA (WIST-) WISTAR INST.
XX
PI Trinchieri G, Perussia B, Kobayashi M, Clark SC, Wong GG;
XX
DR WPI; 1990-178800/23.
DR P-PSDB; AAR05171.
XX
PT New natural killer cell stimulatory factor - useful for treating cancer
PT and e.g. leukopenia, bacterial and viral infections, anaemia and B or T
PT cell deficiencies.
XX
PS Claim 16; Page 60; 69pp; English.
XX
CC Natural killer cell stimulatory factor (NKSF) is useful in treating
CC cancer and other disease states which respond to NK cell activity. Such
CC states may arise from immune or haematopoietic-cell deficiency following
CC a bone marrow translpantation, exposure to radiation and disease.
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 906 BP; 244 A; 220 C; 238 G; 204 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.07e-25 Length: 906
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-56 (1-328) x AAQ04701 (1-906)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782
```

RESULT 65
AAD15208
ID AAD15208 standard; DNA; 975 BP.
XX
AC AAD15208;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p40 encoding DNA from clone A16-94.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p40; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .975
FT /*tag= a
FT /product= "Modified p40 protein precursor"
FT sig_peptide 1. .66
FT /*tag= b
FT mat_peptide 67. .972
FT /*tag= c
FT /product= "Mature modified p40 protein"
XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR, Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08601.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides), useful for treating various diseases e.g. diabetic retinopathy and cancer.

Claim 1; Page 137; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is a modified human p40 protein encoding DNA

Sequence 975 BP; 261 A; 250 C; 255 G; 209 T; 0 U; 0 Other;

gnment Scores:
i. No.: 1.15e-25 Length: 975
re: 35.00 Matches: 35
cent Similarity: 100.0% Conservative: 0
: Local Similarity: 100.0% Mismatches: 0
ry Match: 10.7% Indels: 0
5 Gaps: 0

10-821-670A-56 (1-328) x AAD15208 (1-975)

128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
382 TTTCTAAAGTGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGGTGGCTGACGGCA 441

148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
|||||||||||||||||||||||||||||||||||||||||||||
442 ATCAGTACTGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

ULT 66
12149
AAQ12149 standard; DNA; 979 BP.

AAQ12149;

10-SEP-1991 (first entry)

Cytotoxic lymphocyte maturation factor (40 kD subunit) gene.

Cytotoxic lymphocyte maturation factor; CLMF; probe; antitumour; monoclonal antibodies; T cell; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 41. .979
/*tag= a
/product= "CLMP"
sig_peptide 41. .106
/*tag= b
/note= "hydrophobic signal peptide"
mat_peptide 107. .979
/*tag= c
XX
PN EP433827-A.
XX
PD 26-JUN-1991.
XX
PF 09-DEC-1990; 90EP-00123670.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YCE;
PI Podlaski FJ, Stern AS;
XX
DR WPI; 1991-186715/26.
DR P-PSDB; AAR12493.
XX
PT New cytotoxic lymphocyte maturation factor - used as antitumour agent and
PT monoclonal antibodies used in transplantation to block proliferation and
PT activation of cytotoxic T cells.
XX
PS Disclosure; Fig 25 (a-c); 90pp; English.
XX
CC The natural CLMF protein is a 75 kD heterodimer comprising two
CC polypeptide subunits, a 40 kD and a 35 kD subunit (AAQ12150). The
CC subunits are bonded together via one or more disulfide bonds. The CLMF
CC can interact with IL-2 to synergistically induce the cytolytic activity
CC of Lymphokine Activated Killer (LAK) cells. It is also capable of
CC stimulating T-cell growth. It can be used for the prepn. of LAK- and T-
CC cell activator and antitumour compsns. and for stimulating Natural Killer
CC (NK) cells
XX
SQ Sequence 979 BP; 261 A; 245 C; 257 G; 216 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.15e-25 Length: 979
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-56 (1-328) x AAQ12149 (1-979)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
|||||||||||||||||||||||||||||||||||||||||||
Db 746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 67
ADG39430
ID ADG39430 standard; DNA; 984 BP.
XX
AC ADG39430;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human CLMF 40 kDa subunit DNA.
XX
KW human; cytotoxic lymphocyte maturation factor; CLMF;
KW activated T-cell stimulator; natural killer cell stimulator;
KW immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 67. .984

```
                /*tag=  a
                /partial
                /product= "CLMF 40 kDa subunit"
                /note= "No start or stop codon given"

 US2003204059-A1.

 30-OCT-2003.

 08-OCT-2002; 2002US-00267565.

 22-DEC-1989;   89US-00455708.
 09-MAY-1990;   90US-00520935.
 27-AUG-1990;   90US-00572284.
 24-MAR-1992;   92US-00857023.
 02-MAR-1994;   94US-00205011.
 02-JUN-1995;   95US-00459151.
 22-SEP-1999;   99US-00401839.

 (HOFF ) HOFFMANN LA ROCHE & CIE SA F.

 Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
 Chizzonite RA,  Pan YE;

 WPI; 2004-010534/01.
 P-PSDB; ADG39429.

 Novel protein comprising cytotoxic lymphocyte maturation factor in
 substantially pure form or protein which exhibits cytotoxic lymphocyte
 maturation factor activity, useful as antitumor and immunoenhancing
 agent.

 Claim 17; Page 28-29; 74pp; English.

 The invention relates to a protein which comprises a cytotoxic lymphocyte
 maturation factor (CLMF). The protein is useful for stimulating activated
 T-cells which involves treating T-cells with the protein. The method
 further involves treating the activated T-cells with IL2 or its
 biologically active fragment. The protein is useful for stimulating
 natural killer cells which involves treating the natural killer cells
 with the protein. The protein has immunoenhancing and antitumour effects
 when used as single therapeutic agent in vivo. The present sequence is
 used in the exemplification of the present invention.

 Sequence 984 BP; 263 A; 243 C; 258 G; 220 T; 0 U; 0 Other;

nment Scores:
. No.:               1.16e-25        Length:         984
e:                   35.00           Matches:        35
ent Similarity:      100.0%          Conservative:   0
 Local Similarity:   100.0%          Mismatches:     0
y Match:             10.7%           Indels:         0
                     12              Gaps:           0

0-821-670A-56 (1-328) x ADG39430 (1-984)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

LT 68
7484
 AAQ97484 standard; cDNA; 987 BP.

 AAQ97484;

 25-MAR-2003  (revised)
 22-DEC-1995  (first entry)

DE   Human interleukin-12 40 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Wolf SF,  Sykes M;
XX
DR   WPI; 1995-269273/35.
DR   P-PSDB; AAR79186.
XX
PT   Control of graft versus host disease using interleukin 12 - partic.
PT   admin. at the time of bone marrow transplant.
XX
PS   Disclosure; Page 21-22; 32pp; English.
XX
CC   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC   12 is a heterodimeric cytokine which was originally identified as a
CC   factor which induces gamma-interferon from T cells and natural killer
CC   cells as set forth in PCT/US91/06332, published April 2 1992, and
CC   incorporated by reference. EP 433827, published June 26 1991, disclosed
CC   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC   is defined as a heterodimeric glycoprotein comprised of two covalently
CC   linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC   subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:               1.16e-25        Length:         987
Score:                   35.00           Matches:        35
Percent Similarity:      100.0%          Conservative:   0
Best Local Similarity:   100.0%          Mismatches:     0
Query Match:             10.7%           Indels:         0
DB:                      2               Gaps:           0

US-10-821-670A-56 (1-328) x AAQ97484 (1-987)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||
Db         706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 69
AAV07273
ID   AAV07273 standard; cDNA; 987 BP.
XX
AC   AAV07273;
XX
DT   25-SEP-1998  (first entry)
```

Human Interleukin-12 p40 gene.

IL-12 subunit; expression construct; treatment; asthma; microbial infection; viral infection; cancer; Human; Interleukin; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .987
	/*tag= a
	/product= "IL-12 p40"

WO9817689-A2.

30-APR-1998.

10-OCT-1997; 97WO-US018779.

18-OCT-1996; 96US-0028676P.

(GENE-) GENEMEDICINE INC.

Nordstrom J, Freimark B, Deshpande D;

WPI; 1998-261428/23.
P-PSDB; AAW51311.

Constructs for expression of interleukin-12 sub-units - are used for delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral infections and certain cancers.

Claim 1; Page 34; 80pp; English.

The IL-12 subunits AAV07273 and AAV07274 can be expressed using an appropriate expression construct engineered into a plasmid. The plasmids can provide for efficient expression of IL-12 subunits. The products can be used for the treatment of asthma, microbial and viral infections and certain cancers

Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

gnment Scores:			
l. No.:	1.16e-25	Length:	987
re:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	10.7%	Indels:	0
	2	Gaps:	0

10-821-670A-56 (1-328) x AAV07273 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

JLT 70
07217
AAV07217 standard; DNA; 987 BP.

AAV07217;

12-AUG-1998 (first entry)

DNA encoding human interleukin-12 40kDa subunit.

Interleukin-12; IL-12; graft-versus-host disease; GVHD. bone marrow transplantation; graft-versus-leukemia; ss.

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a
FT /product= "Interleukin-12_40kDa_subunit"
XX
PN US5756085-A.
XX
PD 26-MAY-1998.
XX
PF 30-APR-1996; 96US-00640386.
XX
PR 21-JAN-1994; 94US-00186529.
XX
PA (GEMY) GENETICS INST INC.
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Sykes M, Wolf SF;
XX
DR WPI; 1998-321459/28.
DR P-PSDB; AAW51221.
XX
PT Therapy of graft-versus-host disease - by administration of interleukin-
PT 12 to maintain and/or promote graft-versus-leukaemia effects.
XX
PS Disclosure; Col 17-20; 20pp; English.
XX
CC The invention relates to a method for the treatment or prevention of
CC graft-versus-host disease (GVHD) which comprises the administration of
CC interleukin-12 (IL-12) at the time of bone-marrow transplantation to
CC maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC 0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC the bone marrow transplant. IL-12 is administered daily until there is an
CC improvement in the condition. Administration is oral, cutaneous,
CC subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC intravenous. The present sequence encodes the human interleukin-12 40kDa
CC subunit
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1.16e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-56 (1-328) x AAV07217 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 71
AAZ40406
ID AAZ40406 standard; DNA; 987 BP.
XX
AC AAZ40406;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human interleukin 12 p40 subunit semi-optimised coding sequence.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer; ss.
XX

Homo sapiens.

WO9947678-A2.

23-SEP-1999.

12-MAR-1999; 99WO-US005394.

19-MAR-1998; 98US-0078654P.

(GENE-) GENEMEDICINE INC.

Nordstrom J, Pericle F, Rolland A, Ralston R;

WPI; 1999-562116/47.
P-PSDB; AAY42487.

New plasmids containing an interferon-alpha coding sequence, used for the treatment of a mammalian condition or disease, particularly cancer.

Claim 11; Page 43-45; 137pp; English.

This sequence represents a semi-optimised coding region for the human interleukin 12 p40 subunit. The invention relates to a novel plasmid comprising a cytomegalovirus (CMV) promoter transcriptionally linked with an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-untranslated region (UTR). The plasmids can be used for treating a mammalian condition or disease, particularly cancer

Sequence 987 BP; 216 A; 330 C; 296 G; 145 T; 0 U; 0 Other;

nment Scores:

.. No.:	1.16e-25	Length:	987
e:	35.00	Matches:	35
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	10.7%	Indels:	0
	2	Gaps:	0

0-821-670A-56 (1-328) x AAZ40406 (1-987)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750
```

LT 72
0404
AAZ40404 standard; DNA; 987 BP.

AAZ40404;

15-FEB-2000 (first entry)

Human interleukin 12 p40 subunit wild type coding sequence.

Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV; promoter; growth hormone; untranslated region; UTR; mammal; disease; cancer; ss.

Homo sapiens.

WO9947678-A2.

23-SEP-1999.

12-MAR-1999; 99WO-US005394.

19-MAR-1998; 98US-0078654P.

PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR P-PSDB; AAY42487.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX
PS Claim 11; Page 43-45; 137pp; English.
XX
CC This sequence represents the wild type coding region for the human
CC interleukin 12 p40 subunit. The invention relates to a novel plasmid
CC comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC untranslated region (UTR). The plasmids can be used for treating a
CC mammalian condition or disease, particularly cancer
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.16e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-56 (1-328) x AAZ40404 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 73
AAZ40405
ID AAZ40405 standard; DNA; 987 BP.
XX
AC AAZ40405;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human interleukin 12 p40 subunit optimised coding sequence.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9947678-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005394.
XX
PR 19-MAR-1998; 98US-0078654P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR P-PSDB; AAY42487.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX

Claim 11; Page 43-45; 137pp; English.

This sequence represents an optimised coding region for the human interleukin 12 p40 subunit. The invention relates to a novel plasmid comprising a cytomegalovirus (CMV) promoter transcriptionally linked with an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-untranslated region (UTR). The plasmids can be used for treating a mammalian condition or disease, particularly cancer

Sequence 987 BP; 220 A; 324 C; 318 G; 125 T; 0 U; 0 Other;

gnment Scores:

d. No.:	1.16e-25	Length:	987
re:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	10.7%	Indels:	0
	2	Gaps:	0

10-821-670A-56 (1-328) x AAZ40405 (1-987)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750
```

JLT 74
15210
AAD15210 standard; DNA; 987 BP.

AAD15210;

01-NOV-2001 (first entry)

Human cytokine p40 DNA.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p40; ds.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .987
	/*tag= a
	/product= "p40 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .984
	/*tag= c
	/product= "Mature p40 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR, Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08603.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides), useful for treating various diseases e.g. diabetic retinopathy and cancer.

PS Claim 5; Page 142; 223pp; English.

CC The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is human p40 protein encoding DNA

SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.16e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-56 (1-328) x AAD15210 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 75
ADF77278
ID ADF77278 standard; DNA; 987 BP.
XX
AC ADF77278;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p40 subunit optimised DNA #2.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; Page 14-15; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,

comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 987 BP; 216 A; 331 C; 294 G; 145 T; 0 U; 1 Other;

nment Scores:

.. No.:	1.16e-25	Length:	987
e:	35.00	Matches:	35
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	10.7%	Indels:	0
	12	Gaps:	0

0-821-670A-56 (1-328) x ADF77278 (1-987)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750
```

LT 76
7263
ADF77263 standard; DNA; 987 BP.

ADF77263;

26-FEB-2004 (first entry)

Human IL-12 p40 subunit optimised DNA #4.

ds; human; interferon alpha expression plasmid; tumour; IL-12.

Synthetic.
Homo sapiens.

US2003181405-A1.

25-SEP-2003.

29-APR-2002; 2002US-00136837.

12-MAR-1999; 99US-00268135.

(NORD/) NORDSTROM J L.
(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

Nordstrom JL, Pericle F, Rolland A, Ralston RO;

WPI; 2004-020834/02.

A mammalian interferon alpha expression plasmid is useful in gene therapy to deliver interferon alpha to cells to modulate tumor activity in the treatment of cancer.

Disclosure; SEQ ID NO 32; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 987 BP; 272 A; 138 C; 164 G; 413 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.16e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-56 (1-328) x ADF77263 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CATAAATTAAAATATGAAAATTATACTTCTTCTTTTTTTATTCGTGATATTATTAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GATCCTCCTAAAAATTTACAATTAAAACCTTTAAAAAATTCTCGT 750
```

RESULT 77
ADF77277
ID ADF77277 standard; DNA; 987 BP.
XX
AC ADF77277;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p40 subunit optimised DNA #1.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; Page 14-15; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,
CC comprising a promoter and a synthetic 5' intron transcriptionally linked
CC with an interferon alpha coding sequence and a 3' untranslated region.
CC The mammalian interferon alpha expression plasmid is useful for treating
CC tumour growth. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 987 BP; 220 A; 325 C; 317 G; 125 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.16e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	12	Gaps:	0

10-821-670A-56 (1-328) x ADF77277 (1-987)

```
       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750
```

JLT 78
77276
ADF77276 standard; DNA; 987 BP.

ADF77276;

26-FEB-2004 (first entry)

Human IL-12 p40 subunit DNA.

ds; human; interferon alpha expression plasmid; tumour; IL-12.

Homo sapiens.

US2003181405-A1.

25-SEP-2003.

29-APR-2002; 2002US-00136837.

12-MAR-1999; 99US-00268135.

(NORD/) NORDSTROM J L.
(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

Nordstrom JL, Pericle F, Rolland A, Ralston RO;

WPI; 2004-020834/02.

A mammalian interferon alpha expression plasmid is useful in gene therapy to deliver interferon alpha to cells to modulate tumor activity in the treatment of cancer.

Disclosure; Page 14-15; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 987 BP; 264 A; 243 C; 258 G; 221 T; 0 U; 1 Other;

gnment Scores:			
i. No.:	1.16e-25	Length:	987
re:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	10.7%	Indels:	0
	12	Gaps:	0

10-821-670A-56 (1-328) x ADF77276 (1-987)

```
       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 79
ADO07653
ID ADO07653 standard; DNA; 987 BP.
XX
AC ADO07653;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human interleukin-12 40kDa coding sequence.
XX
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS Homo sapiens.
XX
PN WO2004035799-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011252.
XX
PR 11-OCT-2002; 2002DE-01048141.
XX
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI Waehler R, Schnieders F;
XX
DR WPI; 2004-357221/33.
XX
PT Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
PS Claim 4; Fig 19; 129pp; German.
XX
CC The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a human interleukin-12 coding sequence used in the
CC exemplification of the invention.
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1.16e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-56 (1-328) x ADO07653 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 80
ADS00006
ID ADS00006 standard; DNA; 987 BP.
XX
AC ADS00006;
XX
DT 16-DEC-2004 (first entry)
XX

Human interleukin-23 (IL-23) p40 subunit DNA.

tumour; interleukin-23; IL-23; cytostatic; immunostimulant; cancer;
p40 subunit; ds; gene.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .987
	/*tag= a
	/product= "Human interleukin-23 (IL-23) p40 subunit protein"

JP2004262797-A.

24-SEP-2004.

28-FEB-2003; 2003JP-00052999.

28-FEB-2003; 2003JP-00052999.

(CHIB-) CHIBA PREFECTURE.

WPI; 2004-665614/65.
P-PSDB; ADS00010.

Novel anti-tumor agent comprising interleukin-23 gene, or cell transduced with interleukin-23 gene, as active ingredient, useful for activating anti-tumor immune response and treating tumor.

Disclosure; SEQ ID NO 2; 23pp; Japanese.

The invention relates to a novel anti-tumour agent comprising an interleukin-23 (IL-23) gene, or a cell transduced with an IL-23 gene, as an active ingredient. The molecules of the invention demonstrate cytostatic and immunostimulant activities and may be useful within an anti-tumour agent which activates an anti-tumour immune response. The agent is safe when used in cancer treatment, may be combined with other treatments and induces tumour-specific acquired immunity. The current sequence is that of the human interleukin-23 (IL-23) p40 subunit DNA of the invention.

Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

nment Scores:

. No.:	1.16e-25	Length:	987
e:	35.00	Matches:	35
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	10.7%	Indels:	0
	13	Gaps:	0

0-821-670A-56 (1-328) x ADS00006 (1-987)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

LT 81
2753
ADV42753 standard; cDNA; 987 BP.

ADV42753;

10-MAR-2005 (first entry)

Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 381.

microarray; psychoneuroendocrinimmune; chronic fatigue;

KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
PT New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 381; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.16e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x ADV42753 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 82
ADW97242
ID ADW97242 standard; DNA; 987 BP.
XX
AC ADW97242;
XX
DT 19-MAY-2005 (first entry)
XX
DE Human p40 gene that inhibits IL-23 immune response Seq 1a.
XX
KW immune inhibition; transplant rejection; immune disorder;
KW autoimmune disease; allergy; immunosuppressive; antiallergic; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a

/product= "P40 protein"

JP2005060313-A.

10-MAR-2005.

13-AUG-2003; 2003JP-00292937.

13-AUG-2003; 2003JP-00292937.

(CHIB-) CHIBA PREFECTURE.

WPI; 2005-200132/21.
P-PSDB; ADW97244.

Pharmaceutical formulation for inhibiting immune response generated by interleukin-23 (IL-23) and treating e.g. autoimmune diseases, comprises p40 molecules or gene encoding p40 molecules.

Claim 3; SEQ ID NO 1; 12pp; Japanese.

This invention relates to a novel pharmaceutical formulation used for inhibiting the immune response generated by interleukin-23 (IL-23). Specifically, it refers to a formulation comprising the p40 protein or the gene encoding this protein thereof. The present invention describes the p40 gene contained in the form of a viral or non-viral vector that is capable of expressing and secreting the p40 protein. This vector can be introduced into a cell such that it can in turn inhibit the immune response generated by the production of IL-23. Accordingly, this method is useful for suppressing organ transplant rejection or treating immunological disorders associated with abnormal immune response with regard to IL-23. Furthermore, it can be used to treat autoimmune diseases and allergy. As such, compositions exhibit immunosuppressive and antiallergic activities. This polynucleotide sequence is the human p40 gene of the invention.

Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

gnment Scores:

d. No.:	1.16e-25	Length:	987
re:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	10.7%	Indels:	0
	14	Gaps:	0

10-821-670A-56 (1-328) x ADW97242 (1-987)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

JLT 83
18822
AEB48822 standard; cDNA to mRNA; 987 BP.

AEB48822;

22-SEP-2005 (first entry)

Human interleukin-12 p40 domain coding sequence.

Interleukin-12; cytokine; lymphokine; cancer; tumor; glioblastoma; neoplasm; neurological disease; cytostatic; therapy; immunoconjugate; fusion protein; gene; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1. .987
FT /*tag= b
FT sig_peptide 1. .66
FT /*tag= a
FT mat_peptide 67. .984
FT /*tag= c
FT /product= "Mature interleukin-12 p40 subunit"
XX
PN WO2005066348-A2.
XX
PD 21-JUL-2005.
XX
PF 05-JAN-2005; 2005WO-GB000007.
XX
PR 05-JAN-2004; 2004US-0534307P.
XX
PA (EMDL-) EMD LEXIGEN RES CENT CORP.
PA (ANTI-) ANTISOMA PLC.
XX
PI Gillies S, Lo K, Lan Y, Verma R;
XX
DR WPI; 2005-512669/52.
XX
PT Novel compound comprising target specific portion having monoclonal
PT antibody having specificity for oncofetal fibronectin and effector
PT portion having interleukin-12, useful for treating cancer e.g.
PT glioblastoma.
XX
PS Claim 36; SEQ ID NO 10; 83pp; English.
XX
CC The invention provides a compound comprising a target specific portion
CC and an effector portion, in which the target specific portion comprises
CC or consists of a monoclonal antibody having specificity for oncofetal
CC fibronectin, or its fragment or variant which retains the antigen binding
CC specificity of the parent monoclonal antibody, and the effector portion
CC comprises or consists of interleukin-12, or its functional fragment or
CC variant. The monoclonal antibody binds to a region of oncofetal
CC fibronectin other than the extra-domain B region. Preferably, the
CC compound comprises a target specific portion that is capable of binding
CC to an amino acid sequence present in fibronectin expressed in both fetal
CC and normal adult tissue, especially the repeat 7 domain of fibronectin,
CC and is preferably specific for human oncofetal fibronectin. The
CC monoclonal antibody is preferably a BC1 antibody. The invention also
CC provides nucleic acids encoding the compounds of the invention and
CC methods of their use in the production of these compounds, as well as
CC methods of using the compounds in medicine, especially for the treatment
CC of cancer in a patient, where the patient is a mammal, preferably a
CC human, and the patient has a solid tumor. The cancer is a glioblastoma
CC (claimed) or ovarian, gastric, colorectal or pancreatic cancer. The
CC present sequence is the coding sequence of the p40 domain of human
CC interleukin-12. In a claimed compound, the effector portion consists of a
CC single chain interleukin-12 comprising or consisting of an interleukin-12
CC p40 domain conjugated to the interleukin-12 and p35 domain AEB48815 via a
CC disulfide bond. A further claimed compound comprises the p40 sequence
CC linked by disulfide bond to a fusion protein AEB48818 comprising the BC1
CC heavy chain fused to human interleukin-12 p35.
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.16e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x AEB48822 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705
```

```
      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          ||||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

LT 84
8585
 AAD18585 standard; DNA; 1007 BP.

 AAD18585;

 18-DEC-2001  (first entry)

 Human interleukin-12 (IL-12) p40 subunit DNA.

 Human; interleukin-12; IL-12; p40 subunit; cytostatic; virucide; AIDS;
 Acquired Immune Deficiency Syndrome; immunisation; hepatitis; malaria;
 tuberculosis; vaccine; gene therapy; cancer; influenza; ds.

 Homo sapiens.

 Key             Location/Qualifiers
 CDS             7. .993
                 /*tag=  a
                 /product= "Human IL-12p40 subunit protein"

 WO200168802-A2.

 20-SEP-2001.

 15-MAR-2001; 2001WO-KR000408.

 15-MAR-2000; 2000KR-00013133.
 13-MAR-2001; 2001KR-00012987.

 (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
 (PROG-) PROGEN CO LTD.

 Sung YC,  Lee SH,  Ha SJ,  Song MK,  Chang J;

 WPI; 2001-596904/67.
 P-PSDB; AAE11198.

 Novel human or mouse interleukin (IL)-12p40 subunit mutant genes, that
 inhibit secretion of IL-12p40, but normally secrete IL-12p70, useful as
 adjuvant for DNA vaccination and gene therapy to AIDS, cancer, malaria.

 Claim 1; Page 89-90; 103pp; English.

 The invention relates to mutant interleukin (IL)-12p40 subunit genes
 which produces highly active human or mouse IL-12p40 sequence. IL-12p40
 DNA is useful for DNA immunisation or gene therapy for treating diseases
 such as cancer, AIDS, hepatitis C, hepatitis B or influenza, malaria or
 tuberculosis, as an therapeutic or prophylactic adjuvant. IL-12p40 DNA
 induces immune response by increasing the hydrolysis activity of
 cytotoxic T lymphocytes when IL-12p40 subunit gene is injected with the
 DNA vaccine, or increasing secretion of interferon (IFN)-gamma from T
 helper cells or CD8+ T cells when IL-12p40 subunit gene is injected with
 DNA vaccine. IL-12p40 DNA is useful in gene therapy and as a DNA vaccine.
 The present sequence is a DNA encoding human Interleukin (IL)-12p40
 subunit protein

 Sequence 1007 BP; 270 A; 247 C; 265 G; 225 T; 0 U; 0 Other;

nment Scores:
. No.:              1.18e-25        Length:         1007
e:                  35.00           Matches:        35
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            10.7%           Indels:         0
                    5               Gaps:           0

0-821-670A-56 (1-328) x AAD18585 (1-1007)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756

RESULT 85
AAQ67879
ID   AAQ67879 standard; DNA; 1018 BP.
XX
AC   AAQ67879;
XX
DT   25-MAR-2003  (revised)
DT   23-MAR-1995  (first entry)
XX
DE   EPV 42 kD promoter/Human IL-12 p40 subunit expression cassette.
XX
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW   polymerase chain reaction; poxvirus; pSD542; immunological response;
KW   pathogen; human; interferon; IFN; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        1. .31
FT                   /*tag=  a
FT                   /note= "EPV 42 kD promoter"
FT   CDS             32. .1018
FT                   /*tag=  b
FT                   /product= "Human IL-12 p40"
XX
PN   WO9416716-A1.
XX
PD   04-AUG-1994.
XX
PF   21-JAN-1994;   94WO-US000888.
XX
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 1994-263767/32.
XX
PT   Attenuated recombinant virus used for cancer therapy - comprises DNA
PT   encoding cytokine and/or tumour associated antigen.
XX
PS   Example 27; Fig 33; 232pp; English.
XX
CC   The sequences given in AAQ67879-80 are expression cassettes which contain
CC   the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC   control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC   promoter, respectively. These sequences were used in the construction of
CC   an ALVAC-based recombinant virus containing the genes for the two
CC   subunits of human IL-12. The p40 subunit was amplified using primers
CC   JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC   42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC   using primers JP186 and JP201 and placed under the control of the
CC   vaccinia E3L promoter using primers JP218 and JP220. The expression
CC   cassette was isolated and ligated with pBSSK+ generating plasmid
CC   PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC   assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC   cassettes are orientated head-to-head relative to each other. The
CC   combination casette containing the poxvirus promoted genes for both IL-12
CC   subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC   plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC   and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
```

contains both the human IL-12 genes in the C6 locus. The resulting virus may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

gnment Scores:

i. No.:	1.2e-25	Length:	1018
re:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	10.7%	Indels:	0
	2	Gaps:	0

10-821-670A-56 (1-328) x AAQ67879 (1-1018)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781
```

JLT 86
)8510
AAZ08510 standard; DNA; 1018 BP.

AAZ08510;

19-OCT-1999 (first entry)

EPV 42 kDa/human IL-12 P40 expression cassette.

Attenuated recombinant virus; cytokine; tumour associated antigen; NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies; cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF; interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen; carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza; immunological response; immunotherapy; vaccine; Newcastle Disease; ss.

Synthetic.
pox virus.
Homo sapiens.
Unidentified.

US5942235-A.

24-AUG-1999.

02-JUN-1995; 95US-00458356.

24-DEC-1981; 81US-00334456.
08-DEC-1982; 82US-00446824.
19-JUN-1984; 84US-00622135.
27-AUG-1987; 87US-00090209.
28-AUG-1987; 87US-00090711.
20-OCT-1987; 87US-00110335.
25-APR-1988; 88US-00186054.
23-AUG-1988; 88US-00234390.
14-JUN-1990; 90US-00537882.
14-JUN-1990; 90US-00537890.
16-DEC-1991; 91US-00805567.
03-MAR-1992; 92US-00847977.
06-MAR-1992; 92US-00847951.
04-MAY-1992; 92US-00881995.
22-JUL-1992; 92US-00918278.
20-JAN-1993; 93US-00007115.
19-JAN-1994; 94US-00184009.
14-APR-1994; 94US-00228926.
13-SEP-1994; 94US-00306259.

PA (HEAL-) HEALTH RES INC.
XX
PI Paoletti E;
XX
DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 27; Fig 33; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC EPV 42 kDa/human IL-12 P40 expression cassette used in the
CC exemplification of the present invention
XX
SQ Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.2e-25	Length:	1018
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-56 (1-328) x AAZ08510 (1-1018)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781
```

RESULT 87
ADR21886
ID ADR21886 standard; DNA; 1018 BP.
XX
AC ADR21886;
XX
DT 04-NOV-2004 (first entry)
XX
DE EPV 42kDa/human IL-12 expression cassette.
XX
KW Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW cancer therapy; ds; human; IL-12; EPV 42kDa; expression cassette.
XX
OS Heliothis armigera entomopoxvirus.
OS Homo sapiens.
OS Synthetic.
XX
PN US6780407-B1.
XX
PD 24-AUG-2004.
XX

15-SEP-2000; 2000US-00663667.

08-MAR-1989; 89US-00320471.
14-FEB-1990; 90US-00478179.
07-JAN-1991; 91US-00638080.
07-MAR-1991; 91US-00666056.
11-JUN-1991; 91US-00713967.
16-DEC-1991; 91US-00805567.
03-MAR-1992; 92US-00847977.
06-MAR-1992; 92US-00847951.
21-JAN-1993; 93US-00007115.
19-JAN-1994; 94US-00184009.
30-AUG-1995; 95US-00521016.

(AVET) AVENTIS PASTEUR.

Paoletti E, Tartaglia J, Cox WI;

WPI; 2004-601998/58.

New recombinant poxvirus which is an attenuated avipox Virus that expresses an exogenous DNA encoding carcinoembryonic antigen and an exogenous DNA encoding B7 protein, useful for cancer therapy.

Example 27; SEQ ID NO 194; 181pp; English.

The invention describes a recombinant poxvirus containing exogenous DNA in a nonessential region of the poxvirus, where the poxvirus is an attenuated avipox Virus that expresses an exogenous DNA encoding carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also described are: a composition comprising a poxvirus above in admixture with a carrier; and expressing carcinoembryonic antigen and B7 protein in vivo comprising administering to a mammal the composition above. Disclosed are: making recombinant poxvirus defined above; recombinant poxvirus vaccine having an increased level of safety compared to known recombinant poxvirus vaccines; and a modified vector for expressing a gene product in a host. The recombinant poxvirus is useful for providing a recombinant poxvirus vaccine having an increased level of safety compared to known recombinant poxvirus vaccines. The recombinant poxvirus is useful for cancer therapy. This sequence represents a human IL-12 expression cassette used in the creation of NYVAC rescue virus and canarypox virus vector ALVAC comprising the human IL-12 gene.

Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

nment Scores:
. No.: 1.2e-25 Length: 1018
e: 35.00 Matches: 35
ent Similarity: 100.0% Conservative: 0
Local Similarity: 100.0% Mismatches: 0
y Match: 10.7% Indels: 0
13 Gaps: 0

0-821-670A-56 (1-328) x ADR21886 (1-1018)

217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

LT 88
8402
ADP88402 standard; cDNA; 1029 BP.

ADP88402;

09-SEP-2004 (first entry)

Human interleukin-12 beta chain coding sequence.

KW antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW antibacterial; protozoacide; gene therapy; expression vector;
KW interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004052929-A2.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2003; 2003WO-IB006404.
XX
PR 06-DEC-2002; 2002GB-00028465.
XX
PA (UYBE-) UNIV QUEENS BELFAST.
XX
PI Vandenbroeck K, Alloza I;
XX
DR WPI; 2004-487887/46.
XX
PT New expression vector comprising DNA encoding a subunit of a dimeric form
PT of interleukin under transcriptional control of an ecdysone-inducible
PT promoter, useful in preparing a composition for treating e.g.,
PT inflammatory disease.
XX
PS Disclosure; Page 86-87; 87pp; English.
XX
CC The present invention relates to an expression vector comprising DNA
CC encoding a subunit of a dimeric form of interleukin under transcriptional
CC control of an ecdysone-inducible promoter. The expression vector is
CC useful in preparing a composition for treating a disease having a
CC pathogenesis which includes endogenous production of cytokine IL-12, IL-
CC 23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
CC induced inflammation, epithelial airway inflammation such as asthma,
CC allergic disease, or autoimmune disease such as multiple sclerosis or
CC inflammatory bowel disease. The present sequence is the coding sequence
CC of the human interleukin-12 beta chain used in the exemplification of the
CC invention.
XX
SQ Sequence 1029 BP; 275 A; 261 C; 267 G; 226 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.21e-25 Length: 1029
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.7% Indels: 0
DB: 12 Gaps: 0

US-10-821-670A-56 (1-328) x ADP88402 (1-1029)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
Db 661 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 720

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
Db 721 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 765

RESULT 89
AAF76880
ID AAF76880 standard; DNA; 1389 BP.
XX
AC AAF76880;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human p40-IL-2 coding sequence.
XX
KW Human; p40-IL-2; interleukin-2; IL-2; antiviral; antibacterial;
KW antifungal; cytostatic; antiparasitic; vaccine; gene therapy;
KW fusion protein; protein complex; cytokine; immunoglobulin; cancer;

infection; ds.

Homo sapiens.
Synthetic.

WO200110912-A1.

15-FEB-2001.

09-AUG-2000; 2000WO-US021715.

09-AUG-1999; 99US-0147924P.

(LEXI-) LEXIGEN PHARM CORP.

Gillies SD, Lo KM;

WPI; 2001-191523/19.

Novel multifunctional fusion protein or protein complexes useful for treating cancer and viral infections, comprise two different cytokine molecules and a targeting group.

Example 1; Page 75-76; 90pp; English.

The present sequence is given in a specification relating to multifunctional fusion proteins and protein complexes comprising at least two different cytokine molecules and a targeting group such as an immunoglobulin. The fusion proteins and protein complexes are useful for treating cancers, and bacterial, viral, fungal and parasitic infections. They are also useful in gene therapy and as vaccines to prevent or treat various diseases

.Sequence 1389 BP; 413 A; 325 C; 327 G; 324 T; 0 U; 0 Other;

gnment Scores:
i. No.: 1.61e-25 Length: 1389
ce: 35.00 Matches: 35
cent Similarity: 100.0% Conservative: 0
: Local Similarity: 100.0% Mismatches: 0
ry Match: 10.7% Indels: 0
4 Gaps: 0

10-821-670A-56 (1-328) x AAF76880 (1-1389)

217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

JLT 90
77849
AAT77849 standard; DNA; 1397 BP.

AAT77849;

25-MAR-2003 (revised)
18-MAR-1998 (first entry)

40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.

Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit; interleukin-2; T-cell growth; antibody; lymphokine activated killer cell; CLMF bioactivity inhibition; affinity ligand; transplantation; cytotoxic T cell proliferation; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 41. .1027

FT /*tag= a
XX
PN EP790255-A2.
XX
PD 20-AUG-1997.
XX
PF 09-DEC-1990; 97EP-00104656.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 09-DEC-1990; 90EP-00123670.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE;
PI Podlanski FJ, Stern AS;
XX
DR WPI; 1997-404698/38.
DR P-PSDB; AAW24235.
XX
PT Antibodies to cytotoxic lymphocyte maturation factor protein - useful as affinity ligands, assay reagents and medicaments.
XX
PS Disclosure; Fig 25; 80pp; English.
XX
CC The present DNA sequence encodes the 40 kDa subunit of cytotoxic
CC lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC a 75 kDa heterodimer, where the 2 subunits (see AAT77850 for the 35 kDa
CC subunit) are bonded together via one or more disulphide bonds. CLMF
CC protein is produced by a human B lyphoblastoid cell line. CLMF
CC synergistically induces, in the presence of interleukin-2, the cytolytic
CC activity of lymphokine activated killer cells. CLMF is also capable of
CC stimulating T-cell growth. A novel antibody directed against an epitope
CC of CLMF protein (see AAW24237 for epitope) is capable of neutralising
CC and/or inhibiting CLMF bioactivity. This antibody may be used as an
CC affinity ligand for purifying the CLMF protein. The antibody can also be
CC used as an assay reagent for detecting the CLMF protein, and as a
CC medicament for selectively blocking the proliferation and activation of
CC cytotoxic T cells, e.g. in transplantation. (Updated on 25-MAR-2003 to
CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.62e-25 Length: 1397
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-56 (1-328) x AAT77849 (1-1397)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
Db 686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
Db 746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 91
AAT97969
ID AAT97969 standard; DNA; 1397 BP.
XX
AC AAT97969;
XX
DT 25-MAR-2003 (revised)
DT 18-MAR-1998 (first entry)
XX
DE 40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX

Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit; interleukin-2; T-cell growth; antibody; lymphokine activated killer cell; CLMF bioactivity inhibition; affinity ligand; transplantation; cytotoxic T cell proliferation; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	41. .1027
	/*tag= a

EP790308-A1.

20-AUG-1997.

09-DEC-1990; 97EP-00104682.

22-DEC-1989; 89US-00455708.
09-MAY-1990; 90US-00520935.
27-AUG-1990; 90US-00572284.
09-DEC-1990; 90EP-00123670.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE; Podlanski FJ, Stern AS;

WPI; 1997-404733/38.
P-PSDB; AAW36939.

Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for producing protein and as antitumour agent.

Disclosure; Fig 25; 83pp; English.

The present DNA sequence encodes a 40 kDa subunit of cytotoxic lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is a 75 kDa heterodimer, where the 2 subunits (see AAT97970 for the 35 kDa subunit) are bonded together via one or more disulphide bonds. CLMF protein is produced by a human B lyphoblastoid cell line. CLMF synergistically induces, in the presence of interleukin-2, the cytolytic activity of lymphokine activated killer cells. CLMF is also capable of stimulating T-cell growth. The subunits may be used for preparing the CLMF protein and for preparing medicants for antitumour therapy. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)

Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

nment Scores:			
. No.:	1.62e-25	Length:	1397
e:	35.00	Matches:	35
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	10.7%	Indels:	0
	2	Gaps:	0

0-821-670A-56 (1-328) x AAT97969 (1-1397)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

LT 92
0401
AAV00401 standard; DNA; 1397 BP.

AAV00401;

25-MAR-2003 (revised)

DT 18-MAR-1998 (first entry)
XX
DE 40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW CLMF bioactivity inhibition; affinity ligand; transplantation;
KW cytotoxic T cell proliferation; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	41. .1027
FT		/*tag= a

XX
PN EP790309-A1.
XX
PD 20-AUG-1997.
XX
PF 09-DEC-1990; 97EP-00104860.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 09-DEC-1990; 90EP-00123670.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Chizzonite RA, Gately MK, Gubler UA, Hulmes J, Pan YE;
PI Podlanski FJ, Stern AS, Witte H;
XX
DR WPI; 1997-404734/38.
DR P-PSDB; AAW36941.
XX
PT Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT producing CLMF protein and as an antitumour agent.
XX
PS Disclosure; Fig 25; 83pp; English.
XX
CC The present DNA sequence encodes a novel 40 kDa subunit of cytotoxic
CC lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC a 75 kDa heterodimer, where the 2 subunits (see AAV00402 for the 35 kDa
CC subunit) are bonded together via one or more disulphide bonds. CLMF
CC protein is produced by a human B lyphoblastoid cell line. CLMF
CC synergistically induces, in the presence of interleukin-2, the cytolytic
CC activity of lymphokine activated killer cells. CLMF is also capable of
CC stimulating T-cell growth. The subunits may be used for preparing the
CC CLMF protein and for preparing medicants for antitumour therapy. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1.62e-25	Length:	1397
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-56 (1-328) x AAV00401 (1-1397)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

RESULT 93
AAV37767

AAV37767 standard; cDNA; 1397 BP.

AAV37767;

17-SEP-1998 (first entry)

Cytotoxic lymphocyte maturation factor 40 kD subunit encoding cDNA.

Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize; interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying; proliferation; cytotoxic T cell; transplantation; antibody; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	41. .1027
	/*tag= a
	/product= "CLMF 40 kD subunit"

US5780597-A.

14-JUL-1998.

02-JUN-1995; 95US-00460061.

22-DEC-1989; 89US-00455708.
09-MAY-1990; 90US-00520935.
27-AUG-1990; 90US-00572284.
24-MAR-1992; 92US-00857023.
02-MAR-1994; 94US-00205011.

(HOFF) HOFFMANN LA ROCHE INC.

Podlaski FJ, Stern AS, Gately MK, Pan YE, Hulmes JD; Chizzonite RA, Gubler UA;

WPI; 1998-413150/35.
P-PSDB; AAW58725.

New antibodies to cytotoxic lymphocyte maturation factor - useful for detecting, purifying, and/or blocking proliferation and activation of cytotoxic T cells, such as in transplantation(s).

Example 10; Fig 25; 71pp; English.

An isolated antibody has been developed which binds specifically to cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF induced proliferation by more than 50% in a CLMF dependent T cell growth assay and/or inhibits binding of at least 60% of the factor to phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL) blasts as determined in a CLMF receptor binding assay. CLMF is a heterodimeric protein having a molecular weight band of 75 kD, determined by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) under non-reducing and/or reducing conditions, providing a first subunit having a molecular weight band of 40 kD and a second subunit having a molecular weight of 35 kD. The present sequence encodes the CLMF 40 kD subunit, from an example of the present invention. The antibody can be used for the purification and/or detection of CLMF. It is also used in therapeutic treatments which require selective blocking of proliferation and activation of cytotoxic T cells (CTLs) such as in transplantation

Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

ɔnment Scores:			
i. No.:	1.62e-25	Length:	1397
ːe:	35.00	Matches:	35
ːent Similarity:	100.0%	Conservative:	0
ː Local Similarity:	100.0%	Mismatches:	0
ːy Match:	10.7%	Indels:	0
	2	Gaps:	0

10-821-670A-56 (1-328) x AAV37767 (1-1397)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

RESULT 94
ADG39387
ID ADG39387 standard; DNA; 1397 BP.
XX
AC ADG39387;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human cytotoxic lymphocyte maturation factor, CLMF, 40 kDa subunit DNA.
XX
KW ds; gene; human; cytotoxic lymphocyte maturation factor; CLMF;
KW activated T-cell stimulator; natural killer cell stimulator;
KW immunoenhancer; antitumour; tumour; cancer.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	41. .1027
FT		/*tag= a
FT		/product= "CLMF 40 kDa subunit"

XX
PN US2003204059-A1.
XX
PD 30-OCT-2003.
XX
PF 08-OCT-2002; 2002US-00267565.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 24-MAR-1992; 92US-00857023.
PR 02-MAR-1994; 94US-00205011.
PR 02-JUN-1995; 95US-00459151.
PR 22-SEP-1999; 99US-00401839.
XX
PA (HOFF) HOFFMANN LA ROCHE & CIE SA F.
XX
PI Gately MK, Gubler UA, Hulmes JD, Podlaski FJ, Stern AS;
PI Chizzonite RA, Pan YE;
XX
DR WPI; 2004-010534/01.
DR P-PSDB; ADG39388.
XX
PT Novel protein comprising cytotoxic lymphocyte maturation factor in
PT substantially pure form or protein which exhibits cytotoxic lymphocyte
PT maturation factor activity, useful as antitumor and immunoenhancing
PT agent.
XX
PS Disclosure; Fig 25; 74pp; English.
XX
CC The invention relates to a protein which comprises a cytotoxic lymphocyte
CC maturation factor (CLMF). The protein is useful for stimulating activated
CC T-cells which involves treating T-cells with the protein. The method
CC further involves treating the activated T-cells with IL2 or its
CC biologically active fragment. The protein is useful for stimulating
CC natural killer cells which involves treating the natural killer cells
CC with the protein. The protein has immunoenhancing and antitumour effects
CC when used as single therapeutic agent in vivo. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1.62e-25	Length:	1397
Score:	35.00	Matches:	35

```
ent Similarity:     100.0%          Conservative:  0
 Local Similarity:  100.0%          Mismatches:    0
y Match:            10.7%           Indels:        0
                    12              Gaps:          0

0-821-670A-56 (1-328) x ADG39387 (1-1397)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||||
      746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

LT 95
3758
 ADO03758 standard; cDNA; 1397 BP.

 ADO03758;

 01-JUL-2004  (first entry)

 Human CLMF 40kDa subunit cDNA.

 pharmaceutical composition; T cell growth factor assay; cytokine;
 cytokine lymphocyte maturation factor; CLMF; interleukin-12; IL-12;
 NC-37 B lymphoblastoid cell; T-cell growth stimulator; human; gene; ss;
 40 kDa subunit.

 Homo sapiens.

 Key             Location/Qualifiers
 CDS             41. .1027
                 /*tag= b
                 /product= "CLMF 40 kDa subunit"
                 /note= "Cytotoxic Lymphocyte Maturation Factor"
 sig_peptide     41. .106
                 /*tag= a
 mat_peptide     107. .1024
                 /*tag= c
                 /note= "Mature CLMF 40 kDa subunit"

 US6683046-B1.

 27-JAN-2004.

 02-JUN-1995;   95US-00459151.

 22-DEC-1989;   89US-00455708.
 09-MAY-1990;   90US-00520935.
 27-AUG-1990;   90US-00572284.
 24-MAR-1992;   92US-00857023.
 02-MAR-1994;   94US-00205011.

 (HOFF ) HOFFMANN LA ROCHE INC.

 Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
 Chizzonite RA,  Pan YE;

 WPI; 2004-118577/12.
 P-PSDB; ADO03759, ADO03795.

 Pharmaceutical composition useful for activating T cell growth factors in
 assays comprises heterodimeric protein comprising first and second
 subunits and carrier.

 Disclosure; Fig 25; 72pp; English.

 The invention describes a pharmaceutical composition active in a T cell
 growth factor assay. The pharmaceutical composition comprises a
 heterodimeric protein having a molecular weight of 75 kDa as determined
 by Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)
 CC   under non-reducing conditions, and under reducing conditions, providing a
 CC   first subunit having a molecular weight of 40 kDa as determined by (SDS-
 CC   PAGE), and having a fully defined sequence of 306 amino acids as given in
 CC   the specification, and second subunit having a molecular weight of 35 kDa
 CC   as determined by (SDS-PAGE). Also described are: a novel cytokine protein
 CC   called Cytokine lymphocyte maturation factor (CLMF) or interleukin-12 (IL
 CC   -12) synthesised by mammalian cells, particularly human NC-37 B
 CC   lymphoblastoid cells, and capable of stimulating T-cell growth; and
 CC   monoclonal antibodies directed against (CLMF). (I) is useful as a
 CC   pharmaceutical composition which is active in a T cell growth factor
 CC   assay. This sequence encodes human cytotoxic lymphocyte maturation factor
 CC   (CLMF) 40 kDa subunit.
 XX
 SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

 Alignment Scores:
 Pred. No.:              1.62e-25        Length:         1397
 Score:                  35.00           Matches:        35
 Percent Similarity:     100.0%          Conservative:   0
 Best Local Similarity:  100.0%          Mismatches:     0
 Query Match:            10.7%           Indels:         0
 DB:                     12              Gaps:           0

 US-10-821-670A-56 (1-328) x ADO03758 (1-1397)

 Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

 Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||||
 Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

 RESULT 96
 AAZ40021
 ID   AAZ40021 standard; DNA; 1399 BP.
 XX
 AC   AAZ40021;
 XX
 DT   14-FEB-2000  (first entry)
 XX
 DE   Human p40 coding sequence.
 XX
 KW   Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
 KW   IL-12 p40 subunit; gene therapy; tumour; leukaemia; ss.
 XX
 OS   Homo sapiens.
 XX
 PN   US5994104-A.
 XX
 PD   30-NOV-1999.
 XX
 PF   08-NOV-1996;   96US-00751767.
 XX
 PR   08-NOV-1996;   96US-00751767.
 XX
 PA   (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
 XX
 PI   Anderson RJ,  Prentice HG,  Macdonald ID;
 XX
 DR   WPI; 2000-038261/03.
 DR   P-PSDB; AAY54919.
 XX
 PT   Nucleic acid constructs encoding interleukin-12 fusion proteins useful
 PT   for treating leukemia and other cancers.
 XX
 PS   Example; Fig 9; 73pp; English.
 XX
 CC   This sequence encodes the human p40 protein sequence. The invention
 CC   relates to an isolated nucleic acid construct (I) comprising a region
 CC   encoding an interleukin-12 (IL-12) fusion protein (comprising an IL-12
 CC   p35 subunit, an IL-12 p40 subunit and a linker peptide (joining the
 CC   subunits)) and a region encoding a B7 protein. (I) may be used to produce
```

IL-12 fusion proteins according to standard recombinant DNA methodologies. The fusion proteins may be produced either in vitro in a fermentation culture or in vivo as part of a gene therapy protocol (in this case (I) is used to transform a patients cells, which then secrete the functional polypeptide to supplement the patients own production of IL-12 or to rectify mutations which lead to the expression of inactive polypeptides). The fusion proteins produced in this way may be used to treat any disease which responds to IL-12 such as tumours (both solid and dispersed of the kidney, breast, colon, ovarian and cervical tumours and melanomas) and in particular, tumours of the blood such as leukaemia. Alternatively, the polypeptides may be used as antigens in the production of antibodies to IL-12 and to assay for agonists and antagonists of its activity. The antibodies and antagonists may be used to inhibit the activity of IL-12. (I) may also be used diagnostically as a probe which hybridizes to sequences encoding IL-12 and the antibodies may be used to detect the presence of IL-12 polypeptides in samples. They may be used diagnostically to quantitate the expression of the polypeptide by patients and hence which subjects may be in need of restorative therapy

Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

ɜnment Scores:			
i. No.:	1.62e-25	Length:	1399
ɛe:	35.00	Matches:	35
ɛent Similarity:	100.0%	Conservative:	0
ɛ Local Similarity:	100.0%	Mismatches:	0
ɛy Match:	10.7%	Indels:	0
	3	Gaps:	0

L0-821-670A-56 (1-328) x AAZ40021 (1-1399)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

JLT 97
36632
ADY86632 standard; DNA; 1399 BP.

ADY86632;

02-JUN-2005 (first entry)

Human interleukin-12 40 kDa (IL-12 p40) subunit gene.

Gene expression; screening; multiple sclerosis; neuroprotective; immune disorder; neurological disease; DNA microarray; gene; ds; interleukin-12; lymphokine; cytokine.

Homo sapiens.

US2005064483-A1.

24-MAR-2005.

30-AUG-2004; 2004US-00929182.

28-AUG-2003; 2003US-0498731P.

(BAYU) BAYLOR COLLEGE MEDICINE.

Zang JZ, Hong J;

WPI; 2005-252668/26.
GENBANK; M65272.

Monitoring multiple sclerosis patient taking beta-interferon or glatiramer acetate to predict treatment response by determining expression profile of inflammatory nucleic acids using RNA of patient and comparing to control.

PT
XX
PS Claim 1; SEQ ID NO 22; 73pp; English.
XX
CC The present invention relates to gene expression profiling technology to
CC quantatively measure the expression profiles of genes selected based on
CC their role in inflammation and their susceptibility to regulation by
CC current multiple sclerosis (MS) treatment agents by isolating RNA from
CC peripheral blood mononuclear cells (PBMC) of patient. The invention is
CC particularly useful for monitoring a multiple sclerosis patient taking
CC interferon-beta (IFN-beta) or glatiramer acetate (GA) in order to predict
CC treatment response. The present sequence is human interleukin-12 40 kDa
CC (IL-12 p40) subunit gene. This gene is used to illustrate the evaluation
CC of PBMC responses to in Vitro treatment with IFN-beta or GA agents by
CC gene expression profiling technology.
XX
SQ Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1.62e-25	Length:	1399
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x ADY86632 (1-1399)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

RESULT 98
AAA92406
ID AAA92406 standard; cDNA; 2300 BP.
XX
AC AAA92406;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human interleukin 2 encoding p35 and p40 proteins.
XX
KW Human; interleukin 2; IL-2; p35; p40; immune response; tumour;
KW infectious disease; bacteria; virus; parasite; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	19. .678
FT		/*tag= a
FT		/product= "p35"
FT	CDS	1304. .2290
FT		/*tag= b
FT		/product= "p40"

XX
PN CN1258740-A.
XX
PD 05-JUL-2000.
XX
PF 31-DEC-1998; 98CN-00126748.
XX
PR 31-DEC-1998; 98CN-00126748.
XX
PA (HUAC-) HUACHEN BIOLOGICAL TECHNOLOGY INST SHANG.
XX
PI Cao X, Zhang W, Ju D;
XX
DR WPI; 2000-558956/52.
DR P-PSDB; AAB23795, AAB23796.

Recombinant adenovirus expressing human interleukin-12 and its preparation and use.

Example 3; Fig 4; 27pp; Chinese.

The present invention describes a recombinant adenovirus and its preparation and use, as well as medicine composite containing the recombinant adenovirus. The recombinant adenovirus is used clinically, has the advantages of low cost, easy use and high efficiency and is especially suitable for immune treatment of tumour and infectious diseases caused by bacteria, virus and parasite. The present sequence represents human interleukin 2 (IL-2) cDNA which encodes the p35 and p40 proteins, which is used in an example from the present invention

Sequence 2300 BP; 598 A; 591 C; 571 G; 540 T; 0 U; 0 Other;

nment Scores:

. No.:	2.62e-25	Length:	2300
e:	35.00	Matches:	35
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	10.7%	Indels:	0
	3	Gaps:	0

0-821-670A-56 (1-328) x AAA92406 (1-2300)

```
      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1949 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 2008

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
     2009 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 2053
```

LT 99
3207
AEE03207 standard; DNA; 2336 BP.

AEE03207;

26-JAN-2006 (first entry)

Human interleukin-12 DNA, SEQ ID 13.

Cytostatic; gene therapy; tumor; immune stimulation; cancer; vector; ds.

Homo sapiens.

WO2005112541-A2.

01-DEC-2005.

18-MAY-2005; 2005WO-ES000277.

20-MAY-2004; 2004ES-00001219.

(PROY-) PROYECTO BIOMEDICINA CIMA SL.

Qian C, Guan M, Smerdou Picazo C, Prieto Valtuena J;

WPI; 2005-812033/82.

Hybrid adenoviral gene expression vector for treating cancer, comprises adenovirus liberation system, alpha virus derived vector and specific tumoral promoter.

Disclosure; SEQ ID NO 13; 149pp; Spanish.

The invention relates to a novel adenovirus/alphavirus hybrid vector used in the expression of therapeutic genes in tumor cells. The vector comprises: a first chain of adenoviral origin containing a first inverted terminal repeated sequence and a signal sequence for packing the

CC adenovirus; a first non-coding filler sequence; a sequence corresponding
CC to a specific tissue promoter; an alpha virus-derived cDNA chain, the
CC sequence of which is in part complementary to an alpha viral RNA,
CC comprising at least one sequence coding for at least one exogenous gene
CC of interest, a polyadenylation sequence and a second adenoviral ITR
CC sequence. The invention further includes pharmaceutical compositions
CC containing the vector. The novel vector is used to transfer genetic
CC material to a cell, preferably a tumoral cell, especially one which
CC expresses an alfa fetoprotein (AFP). The vector is used to prepare drugs
CC for treating tumors. The vector or pharmaceutical compositions containing
CC them can be used to induce an immune response against foreign antigens.
CC This gene therapy method can be used to treat cancer. This polynucleotide
CC represents a human interleukin-12 DNA sequence used in the construction
CC of a novel vector of the invention.
XX
SQ Sequence 2336 BP; 612 A; 602 C; 577 G; 545 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.66e-25	Length:	2336
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x AEE03207 (1-2336)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1964 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 2023

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db       2024 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 2068
```

RESULT 100
ACF57534
ID ACF57534 standard; DNA; 2347 BP.
XX
AC ACF57534;
XX
DT 22-APR-2004 (first entry)
XX
DE Human IL12B DNA SEQ ID NO: 35.
XX
KW Protein targeting; angiogenesis inhibitor; fusion gene; cancer; gene; ds;
KW antiangiogenic; cytostatic; ophthalmological; antiarthritic;
KW antirheumatic; antiinflammatory; dermatological; immunosuppressive;
KW antipsoriatic; antidiabetic; neuroprotective; vasotropic; anorectic.
XX
OS Homo sapiens.
XX
PN WO2003093303-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-US014243.
XX
PR 06-MAY-2002; 2002US-0380063P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Hung M, Lan K, Ou-Yang F, Liu J, Lan K;
XX
DR WPI; 2004-053038/05.
XX
PT New polypeptide comprising an antiangiogenesis polypeptide region linked
PT to a therapeutic protein or a diagnostic protein, useful for diagnosing
PT or treating angiogenesis-dependent diseases e.g. cancer, lupus or
PT restenosis.
XX
PS Disclosure; Page 111-112; 0pp; English.
XX

The present invention relates to a polypeptide comprising an antiangiogenesis polypeptide region linked to a therapeutic protein or polypeptide region, or a diagnostic protein or polypeptide region. The polypeptide comprising an antiangiogenesis polypeptide region or the nucleic acid encoding the polypeptide comprising the antiangiogenesis polypeptide is useful for diagnosing or treating angiogenesis-dependent diseases or cancer. Angiogenesis-dependent diseases include age-related macular degeneration, artherosclerosis, angiofibroma, neovascular glaucoma, arteriovenous malformations, nonunion fractures, arthritis, rheumatoid arthritis, lupus, connective tissue disorders, Osler-Weber syndrome, psoriasis, corneal graft neovascularisation, pyogenic granuloma, delayed wound healing, retrolental fibroplasia, diabetic retinopathy, scleroderma, granulations, haemangioma, trachoma, haemophilic joints, vascular adhesions, hypertrophic scars, multiple sclerosis, restenosis or obesity. The present sequence is a coding sequence shown in the exemplification of the invention

Sequence 2347 BP; 695 A; 486 C; 543 G; 623 T; 0 U; 0 Other;

gnment Scores:

d. No.:	2.67e-25	Length:	2347
re:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	10.7%	Indels:	0
	12	Gaps:	0

10-821-670A-56 (1-328) x ACF57534 (1-2347)

```
       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

ch completed: June 10, 2006, 02:29:45
time : 833.721 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

on: June 10, 2006, 01:35:52 ; Search time 4544.78 Seconds
(without alignments)
6053.601 Million cell updates/sec

le: US-10-821-670A-56
fect score: 328
uence: 1 MHPQQLVIAWFSLVLLAPPL.....VQARDRYYSSSWSNWASVSC 328

ring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

rched: 48236798 seqs, 27959665780 residues

l size: 1

al number of hits satisfying chosen parameters: 96471816

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Listing first 200 summaries

mand line parameters:
DEL=frame+_p2n.model -DEV=xlp
/abss/ABSSWEB_spool/US10821670/runat_07062006_110453_27580/app_query.fasta_1
=EST -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rst -MINMATCH=0.1 -LOOPCL=0
OPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
ST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL
TFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
ER=US10821670_@CGN_1_1_22222_@runat_07062006_110453_27580 -NCPU=6 -ICPU=3
MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
N_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
APOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

abase : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	% Query Match	Length	DB	ID	Description
1	35	10.7	725	5	CD559454	CD559454 AGENCOURT
2	35	10.7	736	5	CD559453	CD559453 AGENCOURT
3	35	10.7	762	5	CD559451	CD559451 AGENCOURT
4	35	10.7	766	5	CD559449	CD559449 AGENCOURT
c 5	35	10.7	772	5	CD559450	CD559450 AGENCOURT
c 6	35	10.7	785	5	CD559448	CD559448 AGENCOURT
7	31	9.5	700	12	CE093997	CE093997 tigr-gss-
8	24	7.3	735	5	CD559605	CD559605 AGENCOURT
9	23	7.0	745	5	CD559602	CD559602 AGENCOURT
10	23	7.0	747	5	CD559607	CD559607 AGENCOURT
c 11	23	7.0	754	5	CD559452	CD559452 AGENCOURT
12	23	7.0	756	5	CK130264	CK130264 AGENCOURT
13	23	7.0	772	5	CD559604	CD559604 AGENCOURT
14	20	6.1	252	10	DV799576	DV799576 est_t_tru
15	20	6.1	724	5	CD559603	CD559603 AGENCOURT
16	20	6.1	1042	5	CD559606	CD559606 AGENCOURT
17	18	5.5	704	13	CZ422673	CZ422673 1018376 R
18	17	5.2	1839	6	AK162981	AK162981 Mus muscu
19	17	5.2	2908	6	AK155593	AK155593 Mus muscu
c 20	16	4.9	581	11	AQ394113	AQ394113 CITBI-E1-
21	13	4.0	346	4	BY164658	BY164658 BY164658
22	13	4.0	355	4	BY221814	BY221814 BY221814
23	13	4.0	375	4	BY222535	BY222535 BY222535
24	13	4.0	387	4	BY167742	BY167742 BY167742
25	13	4.0	417	8	CO949904	CO949904 UMC-pd12c
26	13	4.0	423	4	BY218447	BY218447 BY218447
27	13	4.0	432	4	BY154173	BY154173 BY154173
28	13	4.0	475	7	BF704417	BF704417 MI-P-E6-a
c 29	13	4.0	569	11	AZ853726	AZ853726 2M0157M01
30	13	4.0	649	5	CJ134671	CJ134671 CJ134671
31	13	4.0	666	4	BY749553	BY749553 BY749553
c 32	13	4.0	668	14	AG079702	AG079702 Pan trogl
33	12	3.7	535	11	AZ441303	AZ441303 1M0232M24
c 34	10	3.0	385	1	AA879565	AA879565 vx37c03.r
c 35	10	3.0	414	13	CW885638	CW885638 RPCI42_10
c 36	9	2.7	115	14	ATH521069	AJ521069 Arabidops
37	9	2.7	263	3	BQ356685	BQ356685 PM0-HT033
38	9	2.7	353	4	BY024612	BY024612 BY024612
39	9	2.7	354	4	BY024263	BY024263 BY024263
40	9	2.7	355	4	BY013557	BY013557 BY013557
41	9	2.7	361	10	W00972	W00972 za55d07.r1
42	9	2.7	382	4	BY204279	BY204279 BY204279
43	9	2.7	409	4	BY183786	BY183786 BY183786
c 44	9	2.7	415	11	AQ305003	AQ305003 HS_2012_A
c 45	9	2.7	423	7	AW382621	AW382621 PM0-HT033
c 46	9	2.7	435	7	BE153120	BE153120 PM0-HT033
c 47	9	2.7	442	5	CI330861	CI330861 CI330861
c 48	9	2.7	442	7	BE677126	BE677126 7d80f03.x
c 49	9	2.7	463	1	AU143811	AU143811 AU143811
c 50	9	2.7	477	1	AI754066	AI754066 cr19c06.x
51	9	2.7	479	1	AI683279	AI683279 tw50a03.x
52	9	2.7	479	4	CA699592	CA699592 wlk8.pk00
c 53	9	2.7	494	2	BI325004	BI325004 ic21a08.x
54	9	2.7	500	11	AQ300559	AQ300559 HS_3175_B
c 55	9	2.7	504	2	BM090808	BM090808 ig15e03.x
56	9	2.7	507	7	AW367597	AW367597 MR0-HT016
c 57	9	2.7	510	1	AI554405	AI554405 tq11a12.x
c 58	9	2.7	516	1	AV706519	AV706519 AV706519
c 59	9	2.7	546	9	DA098991	DA098991 DA098991
c 60	9	2.7	548	7	BE143328	BE143328 MR0-HT016
c 61	9	2.7	553	9	DB284546	DB284546 DB284546
c 62	9	2.7	561	9	DA102042	DA102042 DA102042
63	9	2.7	563	13	CW054731	CW054731 104_295_1
64	9	2.7	566	9	DB349096	DB349096 DB349096
65	9	2.7	572	3	BM907722	BM907722 AGENCOURT
c 66	9	2.7	593	5	CK818181	CK818181 ic21a08.y
c 67	9	2.7	624	13	CW136151	CW136151 104_521_1
c 68	9	2.7	631	3	BU813156	BU813156 N006A02 P
69	9	2.7	638	13	CW136150	CW136150 104_521_1
70	9	2.7	645	13	CL344654	CL344654 RPCI44_27
c 71	9	2.7	648	10	DT874689	DT874689 AGENCOURT
c 72	9	2.7	649	13	CW374083	CW374083 fsbb001f0
73	9	2.7	650	2	BG696339	BG696339 602658709
74	9	2.7	657	13	CL344592	CL344592 RPCI44_27
c 75	9	2.7	661	3	BU773963	BU773963 SJEGBC03
76	9	2.7	677	7	AW956339	AW956339 EST368409
77	9	2.7	683	10	DR724059	DR724059 AGENCOURT

78	9	2.7	688	4	CA413781	CA413781 UI-H-EZ0-
79	9	2.7	692	13	CW470377	CW470377 fsbb001f2
80	9	2.7	697	7	BE387304	BE387304 601275594
81	9	2.7	700	3	BQ009739	BQ009739 UI-H-ED0-
82	9	2.7	707	8	CN279085	CN279085 170004247
83	9	2.7	722	8	CN412356	CN412356 170005325
84	9	2.7	746	9	DN494937	DN494937 N006A02.5
85	9	2.7	757	3	BU633670	BU633670 UI-H-FL1-
86	9	2.7	763	3	BP446084	BP446084 BP446084
87	9	2.7	780	3	BU375548	BU375548 603807808
88	9	2.7	796	11	BZ056171	BZ056171 11b95f10.
89	9	2.7	798	11	BZ020584	BZ020584 oeg90c01.
90	9	2.7	798	14	CT202661	CT202661 Sus scrof
91	9	2.7	802	9	DN518405	DN518405 1259097 M
92	9	2.7	819	2	BG332928	BG332928 602430781
93	9	2.7	819	9	DN521145	DN521145 1263973 M
94	9	2.7	829	7	BF616281	BF616281 HVSMEc000
95	9	2.7	841	2	BG582789	BG582789 EST484535
96	9	2.7	864	8	CR551254	CR551254 CR551254
97	9	2.7	876	11	AQ895672	AQ895672 HS_4861_B
98	9	2.7	893	8	CX115638	CX115638 EI100A06
99	9	2.7	894	2	BI258748	BI258748 602970329
100	9	2.7	895	2	BI088766	BI088766 602851556
101	9	2.7	913	5	CF409178	CF409178 CH3#059_B
102	9	2.7	923	9	DN565372	DN565372 90930534
103	9	2.7	937	9	DN786150	DN786150 94044776
104	9	2.7	938	5	CF406341	CF406341 CH3#041_F
105	9	2.7	943	13	DU365640	DU365640 109831307
106	9	2.7	960	2	BG035474	BG035474 602325507
107	9	2.7	986	2	BG027599	BG027599 602294475
108	9	2.7	1029	13	CL493139	CL493139 SAIL_574_
109	9	2.7	1030	2	BG539271	BG539271 602567868
110	9	2.7	1037	1	AL539211	AL539211 AL539211
111	9	2.7	1183	2	BG853175	BG853175 1024036D0
112	9	2.7	1315	14	AG430040	AG430040 Mus muscu
113	9	2.7	1340	14	AG448476	AG448476 Mus muscu
114	9	2.7	1447	10	DV783213	DV783213 HW_LIVER_
115	9	2.7	2562	6	CR592197	CR592197 full-leng
116	8	2.4	88	1	AA727638	AA727638 vv02c12.r
117	8	2.4	113	4	C00679	C00679 HUMGS000823
118	8	2.4	113	11	AQ282443	AQ282443 RPCI11-79
119	8	2.4	117	7	AW478729	AW478729 21097 MAR
120	8	2.4	123	7	BE721839	BE721839 189673 MA
121	8	2.4	141	1	AU260162	AU260162 AU260162
122	8	2.4	142	7	BE812604	BE812604 RC3-AN004
123	8	2.4	167	14	AG475481	AG475481 Mus muscu
124	8	2.4	168	11	B28469	B28469 F25I18TR IG
125	8	2.4	168	12	CE024998	CE024998 tigr-gss-
126	8	2.4	195	2	BG953233	BG953233 CM4-CT063
127	8	2.4	201	7	BE843494	BE843494 CM3-TN006
128	8	2.4	202	1	AI450727	AI450727 ms78g05.x
129	8	2.4	209	4	CD087249	CD087249 MC1-0036T
130	8	2.4	215	1	AA863462	AA863462 oh43c02.s
131	8	2.4	215	12	BZ949925	BZ949925 CH240_38B
132	8	2.4	217	5	CJ097946	CJ097946 CJ097946
133	8	2.4	221	2	BF950279	BF950279 CM3-NN021
134	8	2.4	223	13	CZ024046	CZ024046 CH240_184
135	8	2.4	232	2	BF767515	BF767515 CM4-CN009
136	8	2.4	235	1	AI639761	AI639761 ms78g05.y
137	8	2.4	235	1	AA174908	AA174908 ms78g05.r
138	8	2.4	235	3	BP888606	BP888606 BP888606
139	8	2.4	238	7	AW893763	AW893763 RC4-NN002
140	8	2.4	240	5	CK886537	CK886537 SGP166980
141	8	2.4	242	2	BJ656057	BJ656057 BJ656057
142	8	2.4	242	7	BE204318	BE204318 EST396994
143	8	2.4	243	14	TA90A03P	AL465275 T. brucei
144	8	2.4	244	12	CE767861	CE767861 tigr-gss-
145	8	2.4	249	7	BB481174	BB481174 BB481174
146	8	2.4	250	12	CE820902	CE820902 tigr-gss-
147	8	2.4	252	1	AI152063	AI152063 ud19c07.r
148	8	2.4	252	5	CD240364	CD240364 AREL5P2LH
149	8	2.4	258	4	BW840228	BW840228 BW840228
150	8	2.4	258	10	R95251	R95251 SWOvL3CA136
151	8	2.4	259	1	AI077000	AI077000 BSBmMFSZ1
c 152	8	2.4	264	8	CN801148	CN801148 DI8P00356
c 153	8	2.4	270	9	CX357606	CX357606 ssalrgb51
c 154	8	2.4	271	8	CN297233	CN297233 170005326
155	8	2.4	272	7	AW660342	AW660342 98331 MAR
c 156	8	2.4	275	10	DW181457	DW181457 SGP307413
157	8	2.4	276	7	AW383445	AW383445 PM0-HT034
c 158	8	2.4	277	8	CN635347	CN635347 114G02_54
c 159	8	2.4	279	10	DY126470	DY126470 001017BEM
c 160	8	2.4	285	14	FR0014280	AL005523 F.rubripe
c 161	8	2.4	290	7	BF053671	BF053671 EST438901
c 162	8	2.4	291	11	AQ422723	AQ422723 RPCI-11-1
c 163	8	2.4	293	7	BF283817	BF283817 EST448408
164	8	2.4	296	1	AA459674	AA459674 zx49c07.s
165	8	2.4	296	7	BB231764	BB231764 BB231764
166	8	2.4	297	2	BM002849	BM002849 1031107A0
c 167	8	2.4	298	1	AV144660	AV144660 AV144660
c 168	8	2.4	300	1	AA766328	AA766328 oa31b01.s
c 169	8	2.4	301	2	BI504009	BI504009 BB170026B
c 170	8	2.4	301	2	BI508512	BI508512 BB170008B
171	8	2.4	302	8	CV068923	CV068923 f2_new_ch
c 172	8	2.4	302	10	DY061950	DY061950 000308BSP
c 173	8	2.4	302	10	DY126242	DY126242 000910BEM
174	8	2.4	303	1	AJ670502	AJ670502 AJ670502
c 175	8	2.4	309	8	CX215577	CX215577 MNS25532
c 176	8	2.4	320	7	BB830723	BB830723 BB830723
177	8	2.4	321	12	CC988275	CC988275 ZUAFC89TV
c 178	8	2.4	324	11	AQ981401	AQ981401 RPCI-23-3
c 179	8	2.4	326	13	CZ811335	CZ811335 OC_Ba018
180	8	2.4	327	7	AW613780	AW613780 hh81b08.x
181	8	2.4	337	8	CO884451	CO884451 BovGen_12
c 182	8	2.4	338	3	BQ374466	BQ374466 RC0-TT000
183	8	2.4	340	3	BQ081130	BQ081130 san20b06.
184	8	2.4	342	12	CC507444	CC507444 CH240_349
185	8	2.4	346	1	AA894731	AA894731 oj28d02.s
c 186	8	2.4	346	7	AW388577	AW388577 MR2-ST012
c 187	8	2.4	346	8	CN999170	CN999170 UMC-bend_
188	8	2.4	347	4	BX638688	BX638688 BX638688
189	8	2.4	351	1	AA970176	AA970176 op60g06.s
190	8	2.4	351	1	AL385304	AL385304 MtBC27F11
c 191	8	2.4	353	7	BF515693	BF515693 UI-H-BW1-
c 192	8	2.4	355	11	BH257866	BH257866 CH230-283
c 193	8	2.4	355	13	CZ241047	CZ241047 AIAA-aah1
194	8	2.4	357	12	BZ934589	BZ934589 CH240_90J
c 195	8	2.4	358	14	CR300210	CR300210 mte1-18O1
c 196	8	2.4	361	7	BE109169	BE109169 UI-R-BS1-
c 197	8	2.4	369	2	BG788723	BG788723 SEAUMC008
198	8	2.4	369	2	BI191084	BI191084 j3b09fs.r
c 199	8	2.4	371	4	BY164446	BY164446 BY164446
c 200	8	2.4	374	4	BW924716	BW924716 BW924716

ALIGNMENTS

RESULT 1
CD559454/c
LOCUS CD559454 725 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971868 5', mRNA sequence.
ACCESSION CD559454
VERSION CD559454.2 GI:38453478
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585522.
Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 11
High quality sequence start: 13
High quality sequence stop: 573.

TURES Location/Qualifiers
source 1. .725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971868"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

GIN

gnment Scores:

d. No.:	6.03e-24	Length:	725
re:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	10.7%	Indels:	0
	5	Gaps:	0

10-821-670A-56 (1-328) x CD559454 (1-725)

```
217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
441 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 382

237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
    |||||||||||||||||||||||||||||||||||||||||||||
381 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 337
```

ULT 2
59453/c

US	CD559453	736 bp	mRNA	linear	EST 19-NOV-2003

INITION AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
ESSION CD559453
SION CD559453.2 GI:38453475
WORDS EST.
RCE Homo sapiens (human)
RGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 736)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585521.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 683.

FEATURES Location/Qualifiers
source 1. .736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	6.11e-24	Length:	736
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-56 (1-328) x CD559453 (1-736)

```
Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      416 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 357

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      356 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 312
```

RESULT 3
CD559451/c

LOCUS	CD559451	762 bp	mRNA	linear	EST 19-NOV-2003

DEFINITION AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CD559451
VERSION CD559451.2 GI:38453471
KEYWORDS EST.

```
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 762)
THORS    NIH-MGC http://mgc.nci.nih.gov/.
TLE      National Institutes of Health, Mammalian Gene Collection (MGC)
URNAL    Unpublished (1999)
ENT      On Jun 10, 2003 this sequence version replaced gi:31585519.
         Contact: Daniela S. Gerhard, Ph.D.
         Office of Cancer Genomics
         National Cancer Institute / NIH
         Bldg. 31 Rm10A07 Bethesda, MD 20892
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Narayan Bhat
          cDNA Library Preparation: Bhat Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: IRBK2  row: h  column: 02
         High quality sequence start: 38
         High quality sequence stop: 761.
URES             Location/Qualifiers
  source         1. .762
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:6971871"
                 /tissue_type="mixed"
                 /lab_host="DH5A (T1 phage-resistant)"
                 /clone_lib="NIH_MGC_195"
                 /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                 loxP-HindIII; Clones from this library have been
                 PCR-amplified using gene-specific primers to contain the
                 complete open reading frame (based on known gene sequences
                 available from NCBI's RefSeq). Template for PCR is cDNA
                 derived from either pooled cytoplasmic polyA RNA from 30
                 cells lines or pooled total RNA from 10 different tissues
                 (from BD Biosciences/Clontech and Washington University).
                 PCR products are directionally cloned into the loxP sites
                 of the pDNR-Dual vector. Library constructed by Dr.
                 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                 Expression Laboratory, Research Technology Program, SAIC
                 Frederick, NCI-Frederick, Frederick, MD 21702). For
                 information on which gene each clone represents, please
                 visit our anonymous ftp site at
                 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                 a Note: this is a NIH_MGC Library."
IN

nment Scores:
i. No.:              6.3e-24        Length:         762
e:                   35.00          Matches:        35
ent Similarity:      100.0%         Conservative:   0
 Local Similarity:   100.0%         Mismatches:     0
y Match:             10.7%          Indels:         0
                     5              Gaps:           0

.0-821-670A-56 (1-328) x CD559451 (1-762)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       437 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 378

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       377 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 333

LT 4
9449/c
```

```
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
     source          1. .766
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              6.33e-24        Length:         766
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-56 (1-328) x CD559449 (1-766)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 370

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||
       369 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 325

ULT 5
59450/c
US        CD559450                 772 bp    mRNA    linear   EST 19-NOV-2003
INITION   AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
          IMAGE:6971872 5', mRNA sequence.
ESSION    CD559450
SION      CD559450.2  GI:38453469
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 772)
UTHORS    NIH-MGC http://mgc.nci.nih.gov/.
ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL    Unpublished (1999)
MENT      On Jun 10, 2003 this sequence version replaced gi:31585518.
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: h  column: 03
          High quality sequence start: 2
          High quality sequence stop: 753.
TURES               Location/Qualifiers
   source           1. .772
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971872"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
GIN

gnment Scores:
d. No.:              6.38e-24       Length:         772
re:                  35.00          Matches:        35
cent Similarity:     100.0%         Conservative:   0
 Local Similarity:   100.0%         Mismatches:     0
ry Match:            10.7%          Indels:         0
                     5              Gaps:           0

10-821-670A-56 (1-328) x CD559450 (1-772)
```

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 381

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        380 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 336

RESULT 6
CD559448/c
LOCUS       CD559448                 785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES              Location/Qualifiers
     source           1. .785
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971874"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              6.47e-24       Length:         785
Score:                  35.00          Matches:        35
Percent Similarity:     100.0%         Conservative:   0
```

```
. Local Similarity:  100.0%        Mismatches:    0
y Match:             10.7%         Indels:        0
                     5             Gaps:          0

.0-821-670A-56 (1-328) x CD559448 (1-785)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       431 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 372

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           ||||||||||||||||||||||||||||||||||||||||||||||||
       371 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 327

LT 7
3997
S        CE093997                 700 bp    DNA     linear   GSS 24-SEP-2003
NITION   tigr-gss-dog-17000359883851 Dog Library Canis familiaris genomic,
         genomic survey sequence.
SSION    CE093997
ION      CE093997.1  GI:35160844
WORDS    GSS.
RCE      Canis familiaris (dog)
RGANISM  Canis familiaris
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
         Canis.
ERENCE   1  (bases 1 to 700)
THORS    Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
         Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
         Venter,J.C.
TLE      The dog genome: survey sequencing and comparative analysis
URNAL    Science 301 (5641), 1898-1903 (2003)
PUBMED   14512627
ENT      Contact: Kirkness EF
         The Institute for Genomic Research
         Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
         Rockville, MD 20850, USA
         Tel: 301-838-0200
         Fax: 301-838-0208
         Email: ekirknes@tigr.org
         Class: shotgun.
URES             Location/Qualifiers
  source         1. .700
                 /organism="Canis familiaris"
                 /mol_type="genomic DNA"
                 /strain="Standard Poodle"
                 /db_xref="taxon:9615"
                 /clone_lib="Dog Library"
                 /note="Site_1: BstXI; Libraries were prepared from
                 peripheral blood"
IN

nment Scores:
l. No.:              5.65e-20       Length:        700
e:                   31.00          Matches:       31
ent Similarity:      100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
y Match:             9.5%           Indels:        0
                     12             Gaps:          0

.0-821-670A-56 (1-328) x CE093997 (1-700)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       430 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 489

       223 AsnTyrThrSerSerPhePheIleArgAspIle 233
           |||||||||||||||||||||||||||||||||
       490 AACTACACCAGCAGCTTCTTCATCAGAGACATC 522

LT 8
9605
```

```
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              5.56e-13       Length:        735
Score:                  24.00          Matches:       24
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            7.3%           Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-56 (1-328) x CD559605 (1-735)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 721

Qy        237 AspProProLys 240
```

```
              ||||||||||||
       722 GACCCACCCAAG 733

JLT 9
59602
US       CD559602                 745 bp    mRNA    linear   EST 26-NOV-2003
INITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
         IMAGE:6971874 5', mRNA sequence.
SSION    CD559602
SION     CD559602.2  GI:38558930
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 745)
UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL   Unpublished (1999)
MENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
         Contact: Daniela S. Gerhard, Ph.D.
         Office of Cancer Genomics
         National Cancer Institute / NIH
         Bldg. 31 Rm10A07 Bethesda, MD 20892
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Narayan Bhat
          cDNA Library Preparation: Bhat Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: IRBK2  row: h  column: 05
         High quality sequence start: 2
         High quality sequence stop: 644.
TURES             Location/Qualifiers
   source         1. .745
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:6971874"
                  /tissue_type="mixed"
                  /lab_host="DH5A (T1 phage-resistant)"
                  /clone_lib="NIH_MGC_195"
                  /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                  loxP-HindIII; Clones from this library have been
                  PCR-amplified using gene-specific primers to contain the
                  complete open reading frame (based on known gene sequences
                  available from NCBI's RefSeq). Template for PCR is cDNA
                  derived from either pooled cytoplasmic polyA RNA from 30
                  cells lines or pooled total RNA from 10 different tissues
                  (from BD Biosciences/Clontech and Washington University).
                  PCR products are directionally cloned into the loxP sites
                  of the pDNR-Dual vector. Library constructed by Dr.
                  Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                  Expression Laboratory, Research Technology Program, SAIC
                  Frederick, NCI-Frederick, Frederick, MD 21702). For
                  information on which gene each clone represents, please
                  visit our anonymous ftp site at
                  ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                  a Note: this is a NIH_MGC Library."
GIN

gnment Scores:
d. No.:              5.57e-12       Length:         745
re:                  23.00          Matches:        23
cent Similarity:     100.0%         Conservative:   0
t Local Similarity:  100.0%         Mismatches:     0
ry Match:            7.0%           Indels:         0
                     5              Gaps:           0

10-821-670A-56 (1-328) x CD559602 (1-745)
```

```
Qy       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       471 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 530

Qy       176 SerAlaGlu 178
             |||||||||
Db       531 TCTGCAGAG 539

RESULT 10
CD559607
LOCUS       CD559607                 747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES              Location/Qualifiers
     source           1. .747
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971868"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:           5.59e-12       Length:         747
Score:               23.00          Matches:        23
```

```
:ent Similarity:     100.0%          Conservative:  0
': Local Similarity: 100.0%          Mismatches:    0
:y Match:            7.0%            Indels:        0
                     5               Gaps:          0

10-821-670A-56 (1-328) x CD559607 (1-747)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       494 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 553

       176 SerAlaGlu 178
           |||||||||
       554 TCTGCAGAG 562

:LT 11
;9452/c
)S        CD559452                 754 bp    mRNA    linear   EST 19-NOV-2003
:NITION   AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
          IMAGE:6971870 5', mRNA sequence.
:SSION    CD559452
:ION      CD559452.2  GI:38453473
'ORDS     EST.
:CE       Homo sapiens (human)
'GANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
'RENCE    1  (bases 1 to 754)
'THORS    NIH-MGC http://mgc.nci.nih.gov/.
.TLE      National Institutes of Health, Mammalian Gene Collection (MGC)
'URNAL    Unpublished (1999)
'ENT      On Jun 10, 2003 this sequence version replaced gi:31585520.
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: h  column: 01
          High quality sequence start: 130
          High quality sequence stop: 572.
'URES                Location/Qualifiers
  source             1. .754
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:           5.63e-12        Length:        754
Score:               23.00           Matches:       23
Percent Similarity:  100.0%          Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:         7.0%            Indels:        0
DB:                  5               Gaps:          0

US-10-821-670A-56 (1-328) x CD559452 (1-754)

Qy        228 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TTTTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 344

Qy        248 LysAsnSer 250
              ||||||||
Db        343 AAGAATTCT 335

RESULT 12
CK130264
LOCUS       CK130264                 756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES              Location/Qualifiers
     source           1. .756
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971871"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
```

Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

GIN

gnment Scores:

d. No.:	5.65e-12	Length:	756
re:	23.00	Matches:	23
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	7.0%	Indels:	0
	5	Gaps:	0

10-821-670A-56 (1-328) x CK130264 (1-756)

```
156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
499 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 558

176 SerAlaGlu 178
    |||||||||
559 TCTGCAGAG 567
```

JLT 13
59604
JS CD559604 772 bp mRNA linear EST 26-NOV-2003
INITION AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971872 5', mRNA sequence.
ESSION CD559604
SION CD559604.2 GI:38558934
WORDS EST.
RCE Homo sapiens (human)
RGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
ERENCE 1 (bases 1 to 772)
UTHORS NIH-MGC http://mgc.nci.nih.gov/.
ITLE National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL Unpublished (1999)
MENT On Jun 10, 2003 this sequence version replaced gi:31585672.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 03
High quality sequence start: 13
High quality sequence stop: 750.

TURES Location/Qualifiers
source 1. .772
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971872"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	5.75e-12	Length:	772
Score:	23.00	Matches:	23
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.0%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-56 (1-328) x CD559604 (1-772)

```
Qy      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      503 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 562

Qy      176 SerAlaGlu 178
            |||||||||
Db      563 TCTGCAGAG 571
```

RESULT 14
DV799576
LOCUS DV799576 252 bp mRNA linear EST 23-NOV-2005
DEFINITION est_t_truncatus2262 HML_TuTr_IL-2_PBL Tursiops truncatus cDNA, mRNA sequence.
ACCESSION DV799576
VERSION DV799576.1 GI:82652485
KEYWORDS EST.
SOURCE Tursiops truncatus (bottlenosed dolphin)
ORGANISM Tursiops truncatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Tursiops.
REFERENCE 1 (bases 1 to 252)
AUTHORS Mancia,A., Gefroh,H.A., Lundqvist,M.L., Romano,T.A., Almeida,J.S., Chen,Y., McKillen,D.J., Trent,H.F., Wu,S. and Warr,G.W.
TITLE Construction and validation of T. truncatus immunospecific cDNA microarray at marinegenomics.org
JOURNAL Unpublished (2005)
COMMENT Contact: Annalaura Mancia
Hollings Marine Lab
Medical University of South Carolina
Hollings Marine Lab, 331 Ft. Johnson Rd., Charleston, SC 29412, USA
Tel: (843) 762 8962
Fax: (843) 762 8737
Email: mancia@musc.edu.
FEATURES Location/Qualifiers
source 1. .252
/organism="Tursiops truncatus"
/mol_type="mRNA"
/db_xref="taxon:9739"
/tissue_type="PBL"
/cell_type="PBL"
/clone_lib="HML_TuTr_IL-2_PBL"
/note="Vector: pCR2.1TOPO; Site_1: GAATTC"

ORIGIN

Alignment Scores:

Pred. No.:	2.07e-09	Length:	252
Score:	20.00	Matches:	20
Percent Similarity:	100.0%	Conservative:	0

: Local Similarity: 100.0% Mismatches: 0
:y Match: 6.1% Indels: 0
10 Gaps: 0

.0-821-670A-56 (1-328) x DV799576 (1-252)

194 CysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValVal 213
143 TGTCAGGAGGGCAGCGCCTGCCCAGCCGCCGAGGAGAGCCTGCCCATTGAGGTCGTGGTG 202

LT 15
9603
'S CD559603 724 bp mRNA linear EST 26-NOV-2003
NITION AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971873 5', mRNA sequence.
:SSION CD559603
:ION CD559603.2 GI:38558932
VORDS EST.
:CE Homo sapiens (human)
:RGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
:ERENCE 1 (bases 1 to 724)
:UTHORS NIH-MGC http://mgc.nci.nih.gov/.
:TLE National Institutes of Health, Mammalian Gene Collection (MGC)
)URNAL Unpublished (1999)
:ENT On Jun 10, 2003 this sequence version replaced gi:31585671.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 04
High quality sequence stop: 525.
'URES Location/Qualifiers
source 1. .724
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971873"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
:IN

;nment Scores:
i. No.: 5.3e-09 Length: 724
:e: 20.00 Matches: 20

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 6.1% Indels: 0
DB: 5 Gaps: 0

US-10-821-670A-56 (1-328) x CD559603 (1-724)

Qy 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
Db 200 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 259

RESULT 16
CD559606
LOCUS CD559606 1042 bp mRNA linear EST 11-JUN-2003
DEFINITION AGENCOURT_14497125 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
ACCESSION CD559606
VERSION CD559606.1 GI:31585674
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1042)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 386.
FEATURES Location/Qualifiers
source 1. .1042
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.: 7.33e-09 Length: 1042
Score: 20.00 Matches: 20

cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 6.1% Indels: 0
5 Gaps: 0

10-821-670A-56 (1-328) x CD559606 (1-1042)

63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
190 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 249

JLT 17
22673
US CZ422673 704 bp DNA linear GSS 06-APR-2005
INITION 1018376 RP42 Bos taurus genomic clone RP42-49A21, genomic survey sequence.
ESSION CZ422673
SION CZ422673.1 GI:62309882
WORDS GSS.
RCE Bos taurus (cattle)
RGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
ERENCE 1 (bases 1 to 704)
UTHORS Sonstegard,T.S., Van Tassell,C.P., Capuco,A.V., de Jong,P., Matukumalli,L.K., Shade,L.S., Bosak,S., Rubenfield,M. and Gasbarre,L.C.
ITLE Bovine BAC End Sequences from Library RPCI-42
OURNAL Unpublished (2005)
MENT Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Clones are derived from the bovine BAC library RPCI-42 (http://bacpac.chori.org/mbovine42.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by USDA-ARS-BFGL.
Plate: 49 row: A column: 21
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends.
TURES Location/Qualifiers
source 1. .704
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="RP42-49A21"
/sex="male"
/cell_type="Blood"
/clone_lib="RP42"
/note="Vector: pBACe3.6; Site_1: MboI; Site_2: MboI; RPCI-42 Bovine BAC library (Male Holstein) produced by Pieter de Jong"
GIN

gnment Scores:
d. No.: 5.08e-07 Length: 704
re: 18.00 Matches: 18
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 5.5% Indels: 0
13 Gaps: 0

10-821-670A-56 (1-328) x CZ422673 (1-704)

257 TrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPhe 274

Db 4 TGGGAGTACCCTGACACGTGGAGCACCCCGCATTCCTACTTCTCCCTGACGTTT 57

RESULT 18
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,

Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

:NSRTM FANTOM Consortium
:TLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
:URNAL Nature 420 (6915), 563-573 (2002)
:UBMED 12466851
:RENCE 6
:THORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

:NSRTM FANTOM Consortium
:TLE The transcriptional landscape of the mammalian genome
:URNAL Science 309 (5740), 1559-1563 (2005)
:UBMED 16141072
:RENCE 7
:THORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 1839)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers
source 1. .1839
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A430014H12"
/db_xref="taxon:10090"
/clone="A430014H12"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
CDS 58. .1065
/note="unnamed protein product; interleukin 12b (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%, match=1816)
putative"
/codon_start=1
/protein_id="BAE37146.1"
/db_xref="GI:74188062"
/translation="MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGE
TVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHL
LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
S"

ORIGIN

Alignment Scores:

Pred. No.:	1.18e-05	Length:	1839
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x AK162981 (1-1839)

Qy 227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 727 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 777

RESULT 19

55593
US AK155593 2908 bp mRNA linear HTC 21-SEP-2005
INITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730005O03 product:interleukin 12b, full insert sequence.
ESSION AK155593
SION AK155593.1 GI:74212721
WORDS HTC; CAP trapper.
RCE Mus musculus (house mouse)
RGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE 1
UTHORS Carninci,P. and Hayashizaki,Y.
ITLE High-efficiency full-length cDNA cloning
OURNAL Meth. Enzymol. 303, 19-44 (1999)
UBMED 10349636
ERENCE 2
UTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
ITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
OURNAL Genome Res. 10 (10), 1617-1630 (2000)
UBMED 11042159
ERENCE 3
UTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
ITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
OURNAL Genome Res. 10 (11), 1757-1771 (2000)
UBMED 11076861
ERENCE 4
UTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
ONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
ITLE Functional annotation of a full-length mouse cDNA collection
OURNAL Nature 409 (6821), 685-690 (2001)
UBMED 11217851
ERENCE 5
UTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group

```
TLE     Antisense transcription in the mammalian transcriptome
URNAL   Science 309 (5740), 1564-1566 (2005)
UBMED   16141073
RENCE   8  (bases 1 to 2908)
THORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
        Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
        Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
        Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
        Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
        Muramatsu,M. and Hayashizaki,Y.
 TLE    Direct Submission
 URNAL  Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
        Physical and Chemical Research (RIKEN), Laboratory for Genome
        Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
        RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
        Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
        URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
        Fax:81-45-503-9216)
MENT    cDNA library was prepared and sequenced in Mouse Genome
        Encyclopedia Project of Genome Exploration Research Group in Riken
        Genomic Sciences Center and Genome Science Laboratory in RIKEN.
        Division of Experimental Animal Research in Riken contributed to
        prepare mouse tissues.
        Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
        Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
        Trust/MRC building Addenbrookes Hospital Cambridge) whose
        assistance we gratefully acknowledge.
        Please visit our web site for further details.
        URL:http://genome.gsc.riken.jp/
        URL:http://fantom.gsc.riken.jp/.
TURES             Location/Qualifiers
  source          1. .2908
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="FANTOM_DB:F730005O03"
                  /db_xref="taxon:10090"
                  /clone="F730005O03"
                  /cell_type="B6-derived CD11 +ve dendritic cells"
                  /clone_lib="RIKEN full-length enriched mouse cDNA library"
  misc_feature    1. .2908
                  /note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence:
                  BLASTN, 99%, match=1807)
                  putative"
IN

nment Scores:
. No.:              1.78e-05        Length:         2908
e:                  17.00           Matches:        17
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            5.2%            Indels:         0
                    6               Gaps:           0

 0-821-670A-56 (1-328) x AK155593 (1-2908)

      227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
     1131 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1181

JLT 20
94113/c
JS      AQ394113                581 bp    DNA     linear   GSS 06-MAR-1999
NITION  CITBI-E1-2542F7.TF CITBI-E1 Homo sapiens genomic clone 2542F7,
        genomic survey sequence.
SSION   AQ394113
SION    AQ394113.1  GI:4365136
WORDS   GSS.
RCE     Homo sapiens (human)
RGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.

REFERENCE   1  (bases 1 to 581)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2542F7.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .581
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /clone="2542F7"
                      /sex="male"
                      /cell_type="sperm"
                      /clone_lib="CITBI-E1"
                      /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                      CalTech Human BAC Library D"
ORIGIN

Alignment Scores:
Pred. No.:              4.21e-05        Length:         581
Score:                  16.00           Matches:        16
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.9%            Indels:         0
DB:                     11              Gaps:           0

US-10-821-670A-56 (1-328) x AQ394113 (1-581)

Qy        235 LysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 AAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCG 1

RESULT 21
BY164658
LOCUS       BY164658                346 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY164658 RIKEN full-length enriched, bone marrow macrophage Mus
            musculus cDNA clone I830052P21 5', mRNA sequence.
ACCESSION   BY164658
VERSION     BY164658.1  GI:26301304
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
```

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

OURNAL Nature 420, 563-573 (2002)

UBMED 12466851

MENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

TURES Location/Qualifiers

source 1. .346
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I830052P21"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"

GIN

gnment Scores:

d. No.:	0.0258	Length:	346
re:	13.00	Matches:	13
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.0%	Indels:	0

DB: 4 Gaps: 0

US-10-821-670A-56 (1-328) x BY164658 (1-346)

```
Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
              ||||||||||||||||||||||||||||||||||||||||
Db        211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249
```

RESULT 22
BY221814
LOCUS BY221814 355 bp mRNA linear EST 10-DEC-2002
DEFINITION BY221814 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830223O08 5', mRNA sequence.
ACCESSION BY221814
VERSION BY221814.1 GI:26402917
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 355)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
URES             Location/Qualifiers
  source         1. .355
                 /organism="Mus musculus"
                 /mol_type="mRNA"
                 /strain="NOD"
                 /db_xref="taxon:10090"
                 /clone="F830223O08"
                 /tissue_type="activated spleen"
                 /clone_lib="RIKEN full-length enriched, activated spleen"
IN

nment Scores:
.. No.:              0.0264          Length:         355
e:                   13.00           Matches:        13
ent Similarity:      100.0%          Conservative:   0
 Local Similarity:   100.0%          Mismatches:     0
y Match:             4.0%            Indels:         0
                     4               Gaps:           0

0-821-670A-56 (1-328) x BY221814 (1-355)

       52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
          ||||||||||||||||||||||||||||||||||||||||
      210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248

LT 23
22535
S        BY222535                  375 bp    mRNA    linear   EST 10-DEC-2002
NITION   BY222535 RIKEN full-length enriched, activated spleen Mus musculus
         cDNA clone F830228K06 5', mRNA sequence.
SSION    BY222535
ION      BY222535.1  GI:26403638
ORDS     EST.
CE       Mus musculus (house mouse)
GANISM   Mus musculus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
         Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE   1  (bases 1 to 375)
THORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
         Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
         Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
         Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
         Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
         Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
         Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
         Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
         Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
         Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
         Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
         Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
         Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
         Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
         Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
         Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
         Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
         Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
         Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
         Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
         Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
         Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
         Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
         Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
         Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
         Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
         Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE    Analysis of the mouse transcriptome based on functional annotation
         of 60,770 full-length cDNAs
JOURNAL  Nature 420, 563-573 (2002)
PUBMED   12466851
COMMENT  Contact: Yoshihide Hayashizaki
         Laboratory for Genome Exploration Research Group, RIKEN Genomic
         Sciences Center(GSC), Yokohama Institute
         The Institute of Physical and Chemical Research (RIKEN)
         1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
         Tel: 81-45-503-9222
         Fax: 81-45-503-9216
         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
         Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
         Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
         Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
         Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
         Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
         Hayashizaki,Y. Direct Submission
         Computational Analysis of Full-Length Mouse cDNAs Compared with
         Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
         Normalization and subtraction of cap-trapper-selected cDNAs to
         prepare full-length cDNA libraries for rapid discovery of new
         genes. Genome Res. 10 (10), 1617-1630 (2000)
         RIKEN integrated sequence analysis (RISA) system--384-format
         sequencing pipeline with 384 multicapillary sequencer. Genome Res.
         10 (11), 1757-1771 (2000)
         Computer-based methods for the mouse full-length cDNA
         encyclopedia: real-time sequence clustering for construction of a
         nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
         cDNA library was prepared and sequenced in Mouse Genome
         Encyclopedia Project of Genome Exploration Research Group in Riken
         Genomic Sciences Center and Genome Science Laboratory in RIKEN.
         Division of Experimental Animal Research in Riken contributed to
         prepare mouse tissues.
         Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
         Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
         Trust/MRC building Addenbrookes Hospital Cambridge) whose
         assistance we gratefully acknowledge.
         Please visit our web site (http://genome.gsc.riken.go.jp) for
         further details.
FEATURES         Location/Qualifiers
     source      1. .375
                 /organism="Mus musculus"
                 /mol_type="mRNA"
                 /strain="NOD"
                 /db_xref="taxon:10090"
                 /clone="F830228K06"
                 /tissue_type="activated spleen"
                 /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

Alignment Scores:
Pred. No.:              0.0277          Length:         375
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.0%            Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-56 (1-328) x BY222535 (1-375)

Qy          52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
               ||||||||||||||||||||||||||||||||||||||||
Db         210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248
```

ULT 24
57742
US BY167742 387 bp mRNA linear EST 10-DEC-2002
INITION BY167742 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830068I17 5', mRNA sequence.
ESSION BY167742
SION BY167742.1 GI:26304388
WORDS EST.
RCE Mus musculus (house mouse)
RGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE 1 (bases 1 to 387)
UTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
ITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
OURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
MENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
     source          1. .387
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="I830068I17"
                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched, bone marrow
                     macrophage"
ORIGIN

Alignment Scores:
Pred. No.:              0.0285          Length:         387
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.0%            Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-56 (1-328) x BY167742 (1-387)

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
              ||||||||||||||||||||||||||||||||||||||||
Db        211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

RESULT 25
CO949904
LOCUS       CO949904                417 bp    mRNA    linear   EST 09-SEP-2004
DEFINITION  UMC-pd12cl-003-b07 Day 12 Corpus Luteum pd12cl Sus scrofa cDNA 3',
            mRNA sequence.
ACCESSION   CO949904
VERSION     CO949904.1  GI:51326849
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 417)
  AUTHORS   Jiang,H., Whitworth,K.M., Bivens,N.J., Ries,J.E., Woods,R.J.,
            Forrester,L.J., Springer,G.K., Mathialagan,N., Agca,C.,
            Prather,R.S. and Lucy,M.C.
  TITLE     Large-scale Generation and Analysis of Expressed Sequence Tags from
            Porcine Ovary
  JOURNAL   Unpublished (2004)
COMMENT     Contact: DNA Core Facility (Swine Project)
            Animal Science - RS Prather
            University of Missouri-Columbia
            M616 Medical Sciences Bldg., Columbia, MO 65212, USA
            Tel: (573)882-0428
            Fax: (573)884-5552
            Email: porcine@rnet.missouri.edu
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .417
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /dev_stage="Day 12 Corpus Luteum"
                     /clone_lib="pd12cl"
                     /note="Vector: T3T7PAC; Funding: A grant from the Monsanto
                     Company to the University of Missouri. Genetic Source:
```

Ovarian tissue (whole ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea; Day 12 corpora lutea and Day 12 follicles. More information regarding the methods can be found at:
http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mg of poly(A)+ RNA will be annealed at 37 degrees Celsius with 10mg of NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs was ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pSPORT1 vector (Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. 2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.

TAG_TISSUE=Day 12 Corpus Luteum
TAG_SEQ=Not found"
ORIGIN

Alignment Scores:

Pred. No.:	0.0305	Length:	417
Score:	13.00	Matches:	13
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.0%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-56 (1-328) x CO949904 (1-417)

```
Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
              |||||||||||||||||||||||||||||||||||||||
Db        198 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 236
```

RESULT 26
BY218447
LOCUS BY218447 423 bp mRNA linear EST 10-DEC-2002
DEFINITION BY218447 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830107N16 5', mRNA sequence.
ACCESSION BY218447
VERSION BY218447.1 GI:26399344
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,

Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

TURES Location/Qualifiers
source 1. .423
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830107N16"
/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"

GIN

gnment Scores:

i. No.:	0.0309	Length:	423
ce:	13.00	Matches:	13
cent Similarity:	100.0%	Conservative:	0
c Local Similarity:	100.0%	Mismatches:	0
cy Match:	4.0%	Indels:	0
	4	Gaps:	0

10-821-670A-56 (1-328) x BY218447 (1-423)

```
        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
       210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248
```

ULT 27
54173
US BY154173 432 bp mRNA linear EST 10-DEC-2002
INITION BY154173 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone G530005B20 5', mRNA sequence.
ESSION BY154173
SION BY154173.1 GI:26290747
WORDS EST.
URCE Mus musculus (house mouse)
RGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE 1 (bases 1 to 432)
UTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .432
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G530005B20"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"
ORIGIN

Alignment Scores:

```
i. No.:              0.0315          Length:         432
:e:                  13.00           Matches:        13
:ent Similarity:     100.0%          Conservative:   0
': Local Similarity: 100.0%          Mismatches:     0
:y Match:            4.0%            Indels:         0
                     4               Gaps:           0

.0-821-670A-56 (1-328) x BY154173 (1-432)

       52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
          ||||||||||||||||||||||||||||||||||||||||
      211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

:LT 28
:4417
:S       BF704417                 475 bp    mRNA    linear   EST 22-DEC-2000
:NITION  MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
         MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
:SSION   BF704417
:ION     BF704417.1  GI:11989825
:ORDS    EST.
:CE      Sus scrofa (pig)
:RGANISM Sus scrofa
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
         Sus.
:RENCE   1  (bases 1 to 475)
 THORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TLE     Normalization and subtraction: two approaches to facilitate gene
         discovery
 URNAL   Genome Res. 6 (9), 791-806 (1996)
 UBMED   8889548
:ENT     Contact: Tuggle CK
         Molecular Genetics Laboratory, Department of Animal Science
         Iowa State University
         201 Kildee Hall, Ames, IA 50011-3150, USA
         Tel: 5152944252
         Fax: 5152942401
         Email: cktuggle@iastate.edu
         Oligo-dT track not found, Not I site shown in beginning of sequence
         is likely internal to the message. cDNA Library Preparation: RJ
         Woods, JA Green, RS Prather S142 Animal Science Research Center,
         Department of Animal Science, University of Missouri-Columbia,
         65211 Clone distribution: clones will be available through Research
         Genetics (www.resgen.com)
         Seq primer: M13 Forward
         POLYA=No.
:URES              Location/Qualifiers
  source           1. .475
                   /organism="Sus scrofa"
                   /mol_type="mRNA"
                   /strain="crossbreed"
                   /db_xref="taxon:9823"
                   /clone="MI-P-E6-acc-g-09-1-UM"
                   /lab_host="DH10B (Life Technologies)"
                   /clone_lib="MI-P-E6"
                   /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: EcoRI;
                   The MI-P-E6 library is derived from fetus at gestational
                   day 20.  For a detailed description of the  library from
                   which this clone was derived, please visit our web site at
                   http://pigest.genome.iastate.edu/.
                   TAG_SEQ=None found"
:IN

:nment Scores:
 . No.:              0.0343          Length:         475
 e:                  13.00           Matches:        13
 ent Similarity:     100.0%          Conservative:   0
  Local Similarity:  100.0%          Mismatches:     0
 y Match:            4.0%            Indels:         0
                     7               Gaps:           0

 0-821-670A-56 (1-328) x BF704417 (1-475)
```

```
Qy        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
             ||||||||||||||||||||||||||||||||||||||||
Db       199 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 237

RESULT 29
AZ853726/c
LOCUS       AZ853726                 569 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157M01 F, genomic survey sequence.
ACCESSION   AZ853726
VERSION     AZ853726.1  GI:13042136
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: M  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157M01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Alignment Scores:
Pred. No.:           0.0402          Length:         569
Score:               13.00           Matches:        13
```

```
:ent Similarity:     100.0%          Conservative:  0
: Local Similarity:  100.0%          Mismatches:    0
:y Match:            4.0%            Indels:        0
                     11              Gaps:          0

10-821-670A-56 (1-328) x AZ853726 (1-569)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
       217 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 179

JLT 30
34671
JS        CJ134671                 649 bp    mRNA    linear   EST 23-SEP-2005
INITION   CJ134671 RIKEN full-length enriched mouse cDNA library, C57BL/6J
          bone marrow macrophage Mus musculus cDNA clone G530135F14 5', mRNA
          sequence.
3SSION    CJ134671
3ION      CJ134671.1  GI:76234999
WORDS     EST.
RCE       Mus musculus (house mouse)
RGANISM   Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
3RENCE    1  (bases 1 to 649)
JTHORS    The FANTOM Consortium and RIKEN Genome Exploration Research Group
          and Genome Science Group (Genome Network Project Core Group).
ITLE      The transcriptional landscape of the mammalian genome
)URNAL    Science 309 (5740), 1559-1563 (2005)
PUBMED    16141072
MENT      Contact: Yoshihide Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center(GSC), Yokohama Institute
          The Institute of Physical and Chemical Research (RIKEN)
          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel: 81-45-503-9222
          Fax: 81-45-503-9216
          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
          cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues. Tissues were provided by David A. Hume (
          Depts. of Biochemistry and Microbiology/Parasitology Institute for
          Molecular Bioscience University of Queensland Brisbane,Q 4072
          Australia ) whose assistance we gratefully acknowledge.
          Please visit our web site for further details.
          URL:http://genome.gsc.riken.jp/.
TURES                Location/Qualifiers
  source             1. .649
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G530135F14"
                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J bone marrow macrophage"
3IN

gnment Scores:
i. No.:              0.0452          Length:        649
:e:                  13.00           Matches:       13
:ent Similarity:     100.0%          Conservative:  0
: Local Similarity:  100.0%          Mismatches:    0
:y Match:            4.0%            Indels:        0
                     5               Gaps:          0

10-821-670A-56 (1-328) x CJ134671 (1-649)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
```

```
           ||||||||||||||||||||||||||||||||||||||||
Db     211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

RESULT 31
BY749553
LOCUS       BY749553                 666 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY749553 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730005O03 5', mRNA sequence.
ACCESSION   BY749553
VERSION     BY749553.1  GI:27179008
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
```

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
:URES             Location/Qualifiers
  source          1. .666
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="F730005O03"
                  /cell_type="B6-derived CD11 +ve dendritic cells"
                  /clone_lib="RIKEN full-length enriched, B6-derived CD11
                  +ve dendritic cells"
:IN

;nment Scores:
i. No.:               0.0463          Length:         666
:e:                   13.00           Matches:        13
:ent Similarity:      100.0%          Conservative:   0
t Local Similarity:   100.0%          Mismatches:     0
:y Match:             4.0%            Indels:         0
                      4               Gaps:           0

 0-821-670A-56 (1-328) x BY749553 (1-666)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
       611 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 649

:LT 32
:9702/c
 S        AG079702                  668 bp    DNA     linear   GSS 03-NOV-2001
 .NITION  Pan troglodytes DNA, clone: PTB-075I07.R, genomic survey sequence.
 SSION    AG079702
 'ION     AG079702.1  GI:16631504
 .ORDS    GSS.
 'CE      Pan troglodytes (chimpanzee)
 :GANISM  Pan troglodytes
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Pan.
:ERENCE  1
.UTHORS  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Totoki,Y., Watanabe,H. and Sakaki,Y.
:TLE     BAC end sequences of Library PTB
)URNAL   Unpublished
:RENCE   2  (bases 1 to 668)
:THORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Totoki,Y., Watanabe,H. and Sakaki,Y.
:TLE     Direct Submission
)URNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
          Tel:81-45-503-9111, Fax:81-45-503-9170)
:ENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
          was generated during the R&D process and may have higher chance of
          clone tracking errors.
           PRIMERS
               Sequencing: M13Rev
           LIBRARY
               Vector    : pKS145
               R.Site 1  : SacI
               R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .668
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-075I07.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

Alignment Scores:
Pred. No.:               0.0464          Length:         668
Score:                   13.00           Matches:        13
Percent Similarity:      100.0%          Conservative:   0
Best Local Similarity:   100.0%          Mismatches:     0
Query Match:             4.0%            Indels:         0
DB:                      14              Gaps:           0

US-10-821-670A-56 (1-328) x AG079702 (1-668)

Qy        134 LysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThr 146
              ||||||||||||||||||||||||||||||||||||||||
Db        506 AAGAATTATTCAGGACGTTTCACCTGCTGGTGGCTGACG 468

RESULT 33
AZ441303
LOCUS       AZ441303                  535 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0232M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0232M24 R, genomic survey sequence.
ACCESSION   AZ441303
VERSION     AZ441303.1  GI:10565316
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0232M24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

GIN

gnment Scores:

i. No.:	0.378	Length:	535
re:	12.00	Matches:	12
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.7%	Indels:	0
	11	Gaps:	0

10-821-670A-56 (1-328) x AZ441303 (1-535)

```
        84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGlu 95
           ||||||||||||||||||||||||||||||||||||
       249 GATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAG 284
```

JLT 34
79565/c

JS	AA879565 385 bp mRNA linear EST 26-MAR-1998
INITION	vx37c03.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1277380 5' similar to TR:Q24331 Q24331 TUMOROUS IMAGINAL DISCS. ;, mRNA sequence.
SSION	AA879565
SION	AA879565.1 GI:2990270
WORDS	EST.
RCE	Mus musculus (house mouse)
RGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE	1 (bases 1 to 385)
JTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
ITLE	The WashU-HHMI Mouse EST Project
OURNAL	Unpublished (1996)
MENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:669180 Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 292.

TURES	Location/Qualifiers
source	1. .385 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6 x CBA" /db_xref="taxon:10090" /clone="IMAGE:1277380"

/sex="female"
/tissue_type="lung"
/dev_stage="6-8 month old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse lung 937302"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"

ORIGIN

Alignment Scores:

Pred. No.:	27.7	Length:	385
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	1	Gaps:	0

US-10-821-670A-56 (1-328) x AA879565 (1-385)

```
Qy          94 GlyGluValLeuSerHisSerPheLeuLeu 103
               |||||||||||||||||||||||||||||||
Db         346 GGAGAAGTGTTGTCACATAGTTTTCTGTTG 317
```

RESULT 35
CW885638/c

LOCUS	CW885638 414 bp DNA linear GSS 08-DEC-2004
DEFINITION	RPCI42_102G16.TV RPCI-42 Bos taurus genomic clone RPCI42_102G16, genomic survey sequence.
ACCESSION	CW885638
VERSION	CW885638.1 GI:56424578
KEYWORDS	GSS.
SOURCE	Bos taurus (cattle)
ORGANISM	Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE	1 (bases 1 to 414)
AUTHORS	Larkin,D.M., Donthu,K., LeDuc,R., Ryan,K., Liu,L., de Jong,P.J. and Lewin,H.A.
TITLE	End sequencing of Holstein BAC library RPCI-42
JOURNAL	Unpublished (2004)
COMMENT	Contact: Harris Lewin Department of Animal Sciences University of Illinois at Urbana Champaign 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 217 333 5998 Fax: 217 244 5617 Email: h-lewin@uiuc.edu Clones are derived from the bovine BAC library RPCI-42 (http://bacpac.chori.org/mbovine42.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). Funding was provided in part by grant no. AG2004-34480-14417 from USDA-CSREES (Livestock Genome Sequencing Initiative) and AG58-5438-2-313 from USDA-ARS Plate: 102 row: G column: 16 Seq primer: T7 Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .414 /organism="Bos taurus" /mol_type="genomic DNA" /strain="Holstein" /db_xref="taxon:9913" /clone="RPCI42_102G16" /sex="male" /cell_type="blood" /clone_lib="RPCI-42"

```
                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                RPCI-42 Bovine BAC library (Male) produced by Pieter de
                Jong"
IN

nment Scores:
. No.:              29.5          Length:        414
e:                  10.00         Matches:       10
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            3.0%          Indels:        0
                    13            Gaps:          0

0-821-670A-56 (1-328) x CW885638 (1-414)

      235 LysProAspProProLysAsnLeuGlnLeu 244
          |||||||||||||||||||||||||||||
       30 AAACCAGACCCACCCAAGAACCTGCAACTG 1

LT 36
21069/c
S       ATH521069               115 bp    DNA     linear   GSS 08-FEB-2006
NITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
        052B02, genomic survey sequence.
SSION   AJ521069
ION     AJ521069.1  GI:26789305
ORDS    GSS; left border; T-DNA flanking sequence.
CE      Arabidopsis thaliana (thale cress)
GANISM  Arabidopsis thaliana
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
RENCE   1
THORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
        Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
        Lepiniec,L., Caboche,M. and Lecharny,A.
TLE     T-DNA integration into the Arabidopsis genome depends on sequences
        of pre-insertion sites
URNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
UBMED   12446565
RENCE   2  (bases 1 to 115)
THORS   Balzergue,S.
TLE     Direct Submission
URNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
        Gaston Cremieux, 91057 Evry cedex, FRANCE
MENT    PCR was performed on DNA from transformants of Arabidopsis thaliana
        plants from INRA (Versailles). The DNA fragment(s) resulting from
        the PCR were directly sequenced from the left or the right border
        to determine the genomic sequence flanking the insertion. T-DNA
        derived sequences were removed. Information to order the
        corresponding mutant line and a link to a database providing a
        graphical display of the insertion site are available at
        http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
        been generated in the framework of the French plant genomics
        program 'Genoplante' (http://www.genoplante.com and
        http://genoplante-info.infobiogen.fr).
URES            Location/Qualifiers
  source        1. .115
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /cultivar="Wassillewskija"
                /db_xref="taxon:3702"
                /clone="052B02"
                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                /ecotype="Wassilewskija"
  misc_feature  1. .115
                /note="T-DNA flanking sequence
                left border"
IN

nment Scores:
. No.:              93.5          Length:        115
e:                  9.00          Matches:       9
```

```
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     14            Gaps:          0

US-10-821-670A-56 (1-328) x ATH521069 (1-115)

Qy        239 ProLysAsnLeuGlnLeuLysProLeu 247
              |||||||||||||||||||||||||||
Db         59 CCCAAAAATTTACAATTAAAACCCTTA 33

RESULT 37
BQ356685
LOCUS       BQ356685                263 bp    mRNA    linear   EST 20-MAY-2002
DEFINITION  PM0-HT0335-050400-007-G05 HT0335 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ356685
VERSION     BQ356685.1  GI:21021850
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 263)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  PUBMED    10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-HT0335-
            050400-007-G05&t3=2000-04-05&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 31
            High quality sequence stop: 69.
FEATURES            Location/Qualifiers
     source         1. .263
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /dev_stage="Adult"
                    /clone_lib="HT0335"
                    /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                    Site_2: SmaI; A mini-library was made by cloning products
                    derived from  ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 -  Ludwig Institute for Cancer Research)
                    profiles into  the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              195           Length:        263
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     3             Gaps:          0
```

```
10-821-670A-56 (1-328) x BQ356685 (1-263)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       160 TTTTTACTGATTCACAAAAAGGAAGAC 186

ULT 38
24612
US        BY024612                  353 bp    mRNA    linear   EST 06-DEC-2002
INITION   BY024612 RIKEN full-length enriched, mammary gland RCB-0527
          Jyg-MC(B) cDNA Mus musculus cDNA clone G930023O12 5', mRNA
          sequence.
SSION     BY024612
SION      BY024612.1  GI:26130055
WORDS     EST.
RCE       Mus musculus (house mouse)
RGANISM   Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE    1  (bases 1 to 353)
UTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
          Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
          Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
          Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
          Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
          Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
          Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
          Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
          Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
          Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
          Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
          Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
          Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
          Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
          Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
          Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
          Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
          Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
          Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
          Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
          Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
          Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
          Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
          Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
          Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
          Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
          Rogers,J., Birney,E. and Hayashizaki,Y.
ITLE      Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
OURNAL    Nature 420, 563-573 (2002)
UBMED     12466851
MENT      Contact: Yoshihide Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center(GSC), Yokohama Institute
          The Institute of Physical and Chemical Research (RIKEN)
          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel: 81-45-503-9222
          Fax: 81-45-503-9216
          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
          Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
          Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
          Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
          Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
          Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
          Hayashizaki,Y. Direct Submission
           Computational Analysis of Full-Length Mouse cDNAs Compared with
          Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
           Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new
          genes. Genome Res. 10 (10), 1617-1630 (2000)
           RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer. Genome Res.
          10 (11), 1757-1771 (2000)
           Computer-based methods for the mouse full-length cDNA
          encyclopedia: real-time sequence clustering for construction of a
          nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
           cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
           Please visit our web site (http://genome.gsc.riken.go.jp) for
          further details.
FEATURES             Location/Qualifiers
     source          1. .353
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="G930023O12"
                     /tissue_type="mammary gland"
                     /cell_line="RCB-0527 Jyg-MC(B)"
                     /clone_lib="RIKEN full-length enriched, mammary gland
                     RCB-0527 Jyg-MC(B) cDNA"
ORIGIN

Alignment Scores:
Pred. No.:                 254          Length:          353
Score:                     9.00         Matches:         9
Percent Similarity:        100.0%       Conservative:    0
Best Local Similarity:     100.0%       Mismatches:      0
Query Match:               2.7%         Indels:          0
DB:                        4            Gaps:            0

US-10-821-670A-56 (1-328) x BY024612 (1-353)

Qy        265 ThrProHisSerTyrPheSerLeuThr 273
              |||||||||||||||||||||||||||
Db         83 ACCCCTCATTCCTACTTCTCCCTCACC 109

RESULT 39
BY024263
LOCUS       BY024263                  354 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  BY024263 RIKEN full-length enriched, mammary gland RCB-0527
            Jyg-MC(B) cDNA Mus musculus cDNA clone G930022C19 5', mRNA
            sequence.
ACCESSION   BY024263
VERSION     BY024263.1  GI:26129706
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
```

Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

URNAL Nature 420, 563-573 (2002)

UBMED 12466851

ENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

URES Location/Qualifiers

source 1. .354
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="G930022C19"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
/clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"

IN

nment Scores:

.. No.:	255	Length:	354
e:	9.00	Matches:	9
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	2.7%	Indels:	0
	4	Gaps:	0

0-821-670A-56 (1-328) x BY024263 (1-354)

```
      265 ThrProHisSerTyrPheSerLeuThr 273
          |||||||||||||||||||||||||||
       83 ACCCCTCATTCCTACTTCTCCCTCACC 109
```

LT 40

3557

S BY013557 355 bp mRNA linear EST 06-DEC-2002

NITION BY013557 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus musculus cDNA clone G730040C02 5', mRNA sequence.

ACCESSION BY013557

VERSION BY013557.1 GI:26073806

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 355)

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers

```
  source          1. .355
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /db_xref="taxon:10090"
                  /clone="G730040C02"
                  /tissue_type="lung"
                  /cell_line="RCB-0558 LLC"
                  /clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
                  cDNA"
GIN

gnment Scores:
1. No.:               255           Length:        355
ce:                   9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
: Local Similarity:   100.0%        Mismatches:    0
ry Match:             2.7%          Indels:        0
                      4             Gaps:          0

10-821-670A-56 (1-328) x BY013557 (1-355)

       265 ThrProHisSerTyrPheSerLeuThr 273
           ||||||||||||||||||||||||||||
        82 ACCCCTCATTCCTACTTCTCCCTCACC 108

JLT 41
972
JS        W00972                    361 bp    mRNA    linear   EST 18-APR-1996
INITION   za55d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
          IMAGE:296461 5' similar to contains element L1 repetitive element
          ;, mRNA sequence.
ESSION    W00972
SION      W00972.1  GI:1272951
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 361)
JTHORS    Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
          Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
          Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
          Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
          Wilson,R.
ITLE      The WashU-Merck EST Project
OURNAL    Unpublished (1995)
MENT      Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Seq primer: mob.REGA+ET
          High quality sequence stop: 217.
TURES             Location/Qualifiers
  source          1. .361
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="GDB:1241382"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:296461"
                  /sex="male"
                  /dev_stage="20 week-post conception fetus"
                  /lab_host="DH10B (ampicillin resistant)"
                  /clone_lib="Soares fetal liver spleen 1NFLS"
                  /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                  with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                  1st strand cDNA was primed with a Pac I - oligo(dT) primer
                  [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                  double-stranded cDNA was ligated to Eco RI adaptors
                  (Pharmacia), digested with Pac I and cloned into the Pac I
                  and Eco RI sites of the modified pT7T3 vector.  Library
                  went through one round of normalization. Library
                  constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:              259           Length:        361
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     10            Gaps:          0

US-10-821-670A-56 (1-328) x W00972 (1-361)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        118 TTTTTACTGATTCACAAAAAGGAAGAC 144

RESULT 42
BY204279
LOCUS       BY204279                  382 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY204279 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730212J07 5', mRNA sequence.
ACCESSION   BY204279
VERSION     BY204279.1  GI:26384080
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 382)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
```

Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

URES Location/Qualifiers
source 1. .382
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F730212J07"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells"

IN

nment Scores:

. No.:	273	Length:	382
e:	9.00	Matches:	9
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	2.7%	Indels:	0
	4	Gaps:	0

0-821-670A-56 (1-328) x BY204279 (1-382)

265 ThrProHisSerTyrPheSerLeuThr 273
||||||||||||||||||||||||||
76 ACCCCTCATTCCTACTTCTCCCTCACC 102

LT 43
3786
S BY183786 409 bp mRNA linear EST 10-DEC-2002
NITION BY183786 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630110G11 5', mRNA sequence.
SSION BY183786
ION BY183786.1 GI:26320432
ORDS EST.
CE Mus musculus (house mouse)
GANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
RENCE 1 (bases 1 to 409)
THORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .409
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630110G11"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells"

```
GIN

gnment Scores:
i. No.:                290             Length:         409
ce:                    9.00            Matches:        9
cent Similarity:       100.0%          Conservative:   0
c Local Similarity:    100.0%          Mismatches:     0
cy Match:              2.7%            Indels:         0
                       4               Gaps:           0

10-821-670A-56 (1-328) x BY183786 (1-409)

       265 ThrProHisSerTyrPheSerLeuThr 273
           |||||||||||||||||||||||||||
        82 ACCCCTCATTCCTACTTCTCCCTCACC 108

JLT 44
05003/c
JS        AQ305003                415 bp    DNA     linear   GSS 16-DEC-1998
INITION   HS_2012_A1_E07_T7 CIT Approved Human Genomic Sperm Library D Homo
          sapiens genomic clone Plate=2012 Col=13 Row=I, genomic survey
          sequence.
SSION     AQ305003
SION      AQ305003.1  GI:4024789
WORDS     GSS.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 415)
UTHORS    Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
          Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
          Hood,L.
ITLE      Sequence-tagged connectors: A sequence approach to mapping and
          scanning the human genome
OURNAL    Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED    10449764
MENT      Contact: Mahairas GG, Wallace JC, Hood L
          High Throughput Sequencing Center
          University of Washington
          401 Queen Anne Avenue North, Seattle, WA 98109, USA
          Tel: (206) 616-3618
          Fax: (206) 616-3887
          Email: jwallace@u.washington.edu
          Sequence Tagged Connector
          Plate: 2012  row: I  column: 13
          Class: BAC ends
          High quality sequence stop: 415.
TURES               Location/Qualifiers
  source            1. .415
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /clone="Plate=2012 Col=13 Row=I"
                    /sex="male"
                    /clone_lib="CIT Approved Human Genomic Sperm Library D"
                    /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                    E-Coli DH10B"
GIN

gnment Scores:
i. No.:                293             Length:         415
ce:                    9.00            Matches:        9
cent Similarity:       100.0%          Conservative:   0
c Local Similarity:    100.0%          Mismatches:     0
cy Match:              2.7%            Indels:         0
                       11              Gaps:           0

10-821-670A-56 (1-328) x AQ305003 (1-415)

       109 AspGlyIleTrpSerThrAspIleLeu 117
           |||||||||||||||||||||||||||
```

```
Db        249 GACGGTATTTGGTCAACCGATATTCTT 223

RESULT 45
AW382621/c
LOCUS       AW382621                423 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  PM0-HT0335-171199-002-f07 HT0335 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW382621
VERSION     AW382621.1  GI:6887280
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 423)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-HT0335-
            171199-002-f07&t3=1999-11-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 151.
FEATURES              Location/Qualifiers
     source           1. .423
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /dev_stage="Adult"
                      /clone_lib="HT0335"
                      /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                      Site_2: SmaI; A mini-library was made by cloning products
                      derived from  ORESTES PCR (U.S. Letters Patent application
                      No. 196,716 -  Ludwig Institute for Cancer Research)
                      profiles into  the pUC 18 vector. Reverse transcription of
                      tissue mRNA and cDNA amplification were performed under
                      low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:             299             Length:         423
Score:                 9.00            Matches:        9
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           2.7%            Indels:         0
DB:                    7               Gaps:           0

US-10-821-670A-56 (1-328) x AW382621 (1-423)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        271 TTTTTACTGATTCACAAAAAGGAAGAC 245

RESULT 46
BE153120/c
LOCUS       BE153120                435 bp    mRNA    linear   EST 21-JUN-2000
DEFINITION  PM0-HT0335-060300-006-h01 HT0335 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE153120
VERSION     BE153120.1  GI:8615841
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
RENCE 1 (bases 1 to 435)
THORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
URNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
UBMED 10737800
ENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM0-HT0335-060300-006-h01&t3=2000-03-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence stop: 435.

URES Location/Qualifiers
source 1. .435
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0335"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

IN

nment Scores:
. No.: 306 Length: 435
e: 9.00 Matches: 9
ent Similarity: 100.0% Conservative: 0
Local Similarity: 100.0% Mismatches: 0
y Match: 2.7% Indels: 0
7 Gaps: 0

0-821-670A-56 (1-328) x BE153120 (1-435)

101 PheLeuLeuIleHisLysLysGluAsp 109
||||||||||||||||||||||||||
283 TTTTTACTGATTCACAAAAAGGAAGAC 257

LT 47
0861/c
S CI330861 442 bp mRNA linear EST 07-FEB-2006
NITION CI330861 Oryza sativa (japonica cultivar-group) shoot Oryza sativa (japonica cultivar-group) cDNA clone J01B3122J01M3 3', mRNA sequence.
SSION CI330861
ION CI330861.1 GI:86865330
ORDS EST.
CE Oryza sativa (japonica cultivar-group)
GANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
RENCE 1 (bases 1 to 442)
AUTHORS Kikuchi,S.
TITLE Collection and mapping of over 30,000 transcription units by the rice full- length cDNA project from japonica rice
JOURNAL Unpublished (2006)
COMMENT Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA Project
URL:http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES Location/Qualifiers
source 1. .442
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J01B3122J01M3"
/tissue_type="shoot"
/clone_lib="Oryza sativa (japonica cultivar-group) shoot"

ORIGIN

Alignment Scores:
Pred. No.: 310 Length: 442
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 5 Gaps: 0

US-10-821-670A-56 (1-328) x CI330861 (1-442)

Qy 284 ArgGluLysLysAspArgLeuSerVal 292
||||||||||||||||||||||||||
Db 166 AGAGAAAAGAAGGATCGCCTGTCAGTG 140

RESULT 48
BE677126/c
LOCUS BE677126 442 bp mRNA linear EST 08-SEP-2000
DEFINITION 7d80f03.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279293 3' similar to contains Alu repetitive element;contains element MER14 repetitive element ;, mRNA sequence.
ACCESSION BE677126
VERSION BE677126.1 GI:10037667
KEYWORDS EST.

RCE Homo sapiens (human)
RGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
ERENCE 1 (bases 1 to 442)
UTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
ITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
OURNAL Unpublished (1997)
MENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lupski
cDNA Library Preparation: Lupski Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 410.

TURES Location/Qualifiers
source 1. .442
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3279293"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

IN

gnment Scores:

i. No.:	310	Length:	442
re:	9.00	Matches:	9
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	2.7%	Indels:	0
	7	Gaps:	0

10-821-670A-56 (1-328) x BE677126 (1-442)

```
101 PheLeuLeuIleHisLysLysGluAsp 109
    |||||||||||||||||||||||||||
405 TTTTTACTGATTCACAAAAAGGAAGAC 379
```

ULT 49
13811/c
US AU143811 463 bp mRNA linear EST 05-AUG-2002
INITION AU143811 HEMBA1 Homo sapiens cDNA clone HEMBA1000076 3', mRNA sequence.
ESSION AU143811
SION AU143811.1 GI:11005332
WORDS EST.
RCE Homo sapiens (human)
RGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
ERENCE 1 (bases 1 to 463)
UTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES Location/Qualifiers
source 1. .463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1000076"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBA1"
/note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:

Pred. No.:	324	Length:	463
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	1	Gaps:	0

US-10-821-670A-56 (1-328) x AU143811 (1-463)

```
Qy      101 PheLeuLeuIleHisLysLysGluAsp 109
            |||||||||||||||||||||||||||
Db      400 TTTTTACTGATTCACAAAAAGGAAGAC 374
```

RESULT 50
AI754066/c
LOCUS AI754066 477 bp mRNA linear EST 20-JUN-2002
DEFINITION cr19c06.x1 Human bone marrow stromal cells Homo sapiens cDNA clone HBMSC_cr19c06 3', mRNA sequence.
ACCESSION AI754066
VERSION AI754066.1 GI:5132330
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 477)
AUTHORS Jia,L., Young,M.F., Powell,J., Yang,L., Ho,N.C., Hotchkiss,R., Robey,P.G. and Francomano,C.A.
TITLE Gene expression profile of human bone marrow stromal cells: high-throughput expressed sequence tag sequencing analysis
JOURNAL Genomics 79 (1), 7-17 (2002)
PUBMED 11827452
COMMENT Contact: Libin Jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157

```
        Email: libin@helix.nih.gov
        DNA Sequencing and analyses by National Institutes of Health
        Intramural Sequencing Center (NISC).
        Plate: 19  row: c  column: 06
        Seq primer: -21M13 forward primer (ABI).
URES            Location/Qualifiers
 source         1. .477
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="HBMSC_cr19c06"
                /sex="mixed"
                /tissue_type="bone marrow stroma"
                /dev_stage="mixed"
                /lab_host="XL1-Blue MRF'/SOLR"
                /clone_lib="Human bone marrow stromal cells"
                /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI;
                mRNA made from human bone marrow stroma, cDNA made by
                oligo-dT priming. Directionally cloned. Size-selected for
                average insert size >0.5 kb. Library constructed by Dr.
                Marian Young and Dr. Pamela Gehron Robey (NIDCR). Library
                supplied by Dr. Libin Jia (NHGRI)"
IN

nment Scores:
. No.:              332             Length:         477
e:                  9.00            Matches:        9
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            2.7%            Indels:         0
                    1               Gaps:           0

0-821-670A-56 (1-328) x AI754066 (1-477)

      101 PheLeuLeuIleHisLysLysGluAsp 109
          |||||||||||||||||||||||||||
      418 TTTTTACTGATTCACAAAAAGGAAGAC 392

LT 51
3279
S       AI683279                479 bp    mRNA    linear   EST 26-MAY-1999
NITION  tw50a03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2263084 3',
        mRNA sequence.
SSION   AI683279
ION     AI683279.1  GI:4893461
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 479)
THORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
        Tumor Gene Index
URNAL   Unpublished (1997)
ENT     Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
        Emmert-Buck, M.D., Ph.D.
         cDNA Library Preparation: Life Technologies, Inc.
         cDNA Library Arrayed by: Greg Lennon, Ph.D.
         DNA Sequencing by: Washington University Genome Sequencing Center
         Clone distribution: NCI-CGAP clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        www-bio.llnl.gov/bbrp/image/image.html
        Seq primer: -40UP from Gibco
        High quality sequence stop: 415.
URES            Location/Qualifiers
 source         1. .479
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2263084"
                /tissue_type="well-differentiated endometrial
                adenocarcinoma, 7 pooled tumors"
                /lab_host="DH10B"
                /clone_lib="NCI_CGAP_Ut1"
                /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                Average insert size 1.75 kb. Life Technologies catalog #:
                11538-014"
ORIGIN

Alignment Scores:
Pred. No.:              333             Length:         479
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     1               Gaps:           0

US-10-821-670A-56 (1-328) x AI683279 (1-479)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        451 TTTTTACTGATTCACAAAAAGGAAGAC 477

RESULT 52
CA699592
LOCUS       CA699592                479 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  wlk8.pk0021.d7 wlk8 Triticum aestivum cDNA clone wlk8.pk0021.d7 5'
            end, mRNA sequence.
ACCESSION   CA699592
VERSION     CA699592.1  GI:25421385
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 479)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES            Location/Qualifiers
     source         1. .479
                    /organism="Triticum aestivum"
                    /mol_type="mRNA"
                    /cultivar="Stephens"
                    /db_xref="taxon:4565"
                    /clone="wlk8.pk0021.d7"
                    /tissue_type="leaf"
                    /clone_lib="wlk8"
                    /note="Vector: pGEM-7; Site_1: EcoRI; Site_2: XhoI; Wheat
                    (Triticum aestivum L.) seedlings 8 hr after treatment with
                    6-iodo-3-propyl-2-propyloxy-4(3H)-quinazolinone"
ORIGIN

Alignment Scores:
Pred. No.:              333             Length:         479
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     4               Gaps:           0
```

10-821-670A-56 (1-328) x CA699592 (1-479)

```
       239 ProLysAsnLeuGlnLeuLysProLeu 247
           |||||||||||||||||||||||||||
       394 CCCAAGAATCTTCAACTCAAGCCGTTA 420
```

ULT 53
25004/c

```
US        BI325004                  494 bp    mRNA    linear   EST 30-JUL-2001
INITION   ic21a08.x2 HR85 islet Homo sapiens cDNA 3', mRNA sequence.
SSION     BI325004
SION      BI325004.1  GI:15004190
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 494)
UTHORS    Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
          Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
          Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
          Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
          Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
          Williams,T., Jackson,Y. and Bowers,Y.
ITLE      Endocrine Pancreas Consortium
OURNAL    Unpublished (2000)
MENT      Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
          Endocrine Pancreas Consortium
          Harvard University, Howard Hughes Medical Institute
          Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
          MA 02138
          Tel: 617-495-1812
          Fax: 617-495-8557
          Email: dmelton@biohp.harvard.edu
          Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
          Washington University Genome Sequencing Center For information on
          obtaining a clone please contact: Dr. Hiroshi Inoue
          (hinoue@im.wustl.edu)
          Seq primer: -40UP from Gibco
          High quality sequence stop: 455.
TURES               Location/Qualifiers
  source            1. .494
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /tissue_type="Purified pancreatic islet"
                    /lab_host="DH10B"
                    /clone_lib="HR85 islet"
                    /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                    NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                    Size-selected on agarose gel. Average insert size ~1kb. 5'
                    XhoI site was destroyed after directional cloning.
                    Amplified once. Contact information: Hiroshi Inoue, MD,
                    Metabolism Div. (Alan Permutt Lab), Washington University
                    School of Medicine, Box 8127, 660 South Euclid Ave., St.
                    Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                    314-362-1916, Fax: 314-747-2692."
IN
```

gnment Scores:

i. No.:	343	Length:	494
ce:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
cy Match:	2.7%	Indels:	0
	2	Gaps:	0

10-821-670A-56 (1-328) x BI325004 (1-494)

```
       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       400 TTTTTACTGATTCACAAAAAGGAAGAC 374
```

RESULT 54
AQ300559

```
LOCUS       AQ300559                500 bp    DNA     linear   GSS 16-DEC-1998
DEFINITION  HS_3175_B1_B09_T7 CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3175 Col=17 Row=D, genomic survey
            sequence.
ACCESSION   AQ300559
VERSION     AQ300559.1  GI:4020236
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 500)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  PUBMED    10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3175  row: D  column: 17
            Class: BAC ends
            High quality sequence stop: 500.
FEATURES              Location/Qualifiers
     source           1. .500
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /clone="Plate=3175 Col=17 Row=D"
                      /sex="male"
                      /clone_lib="CIT Approved Human Genomic Sperm Library D"
                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                      E-Coli DH10B"
ORIGIN
```

Alignment Scores:

Pred. No.:	346	Length:	500
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	11	Gaps:	0

US-10-821-670A-56 (1-328) x AQ300559 (1-500)

```
Qy          94 GlyGluValLeuSerHisSerPheLeu 102
               |||||||||||||||||||||||||||
Db         278 GGGGAGGTCCTGAGTCACTCCTTCTTA 304
```

RESULT 55
BM090808/c

```
LOCUS       BM090808                504 bp    mRNA    linear   EST 20-NOV-2001
DEFINITION  ig15e03.x1 Human Fetal Pancreas 1A Homo sapiens cDNA 3', mRNA
            sequence.
ACCESSION   BM090808
VERSION     BM090808.1  GI:17019774
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```

```
RENCE   1  (bases 1 to 504)
THORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
        Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
        Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
        Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
        Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
        Williams,T., Jackson,Y. and Bowers,Y.
TLE     Endocrine Pancreas Consortium
URNAL   Unpublished (2000)
ENT     Other_ESTs: ig15e03.y1
        Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
        Endocrine Pancreas Consortium
        Harvard University, Howard Hughes Medical Institute
        Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
        MA 02138
        Tel: 617-495-1812
        Fax: 617-495-8557
        Email: dmelton@biohp.harvard.edu
        Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
        Washington University Genome Sequencing Center For information on
        obtaining a clone please contact: Dr. Hiroshi Inoue
        (hinoue@imgate.wustl.edu)
        High quality sequence stop: 447.
URES            Location/Qualifiers
 source         1. .504
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="Fetal Pancreas (4 Pooled Donors, 18 - 20
                weeks, Stratagene #738023)"
                /dev_stage="Fetal Pancreas"
                /clone_lib="Human Fetal Pancreas 1A"
                /note="Vector: pBluescript SK(-); Site_1: NotI; Site_2:
                XhoI; cDNA made by oligo-dT priming. Size-selected by
                CHROMA SPIN-1000  (Clontech). Average insert size ~1kb. 5'
                XhoI site was destroyed after directional cloning.
                Amplified once.  Contact information: Hiroshi Inoue, MD,
                Metabolism Div. (Alan Permutt Lab),  Washington University
                School of Medicine, Box 8127, 660 South Euclid Ave., St.
                Louis, MO 63110 E-mail: hinoue@imgate.wustl.edu Tel:
                314-362-1916, Fax:314-747-2692."
IN

nment Scores:
. No.:              349             Length:         504
e:                  9.00            Matches:        9
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            2.7%            Indels:         0
                    2               Gaps:           0

0-821-670A-56 (1-328) x BM090808 (1-504)

      101 PheLeuLeuIleHisLysLysGluAsp 109
          |||||||||||||||||||||||||||
      400 TTTTTACTGATTCACAAAAAGGAAGAC 374

LT 56
7597
S       AW367597                507 bp    mRNA    linear   EST 04-FEB-2000
NITION  MR0-HT0164-151299-012-b02 HT0164 Homo sapiens cDNA, mRNA sequence.
SSION   AW367597
ION     AW367597.1  GI:6872247
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 507)
THORS   HCGP http://www.ludwig.org.br/ORESTES.
TLE     The FAPESP/LICR Human Cancer Genome Project
URNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-HT0164-
            151299-012-b02&t3=1999-12-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 13
            High quality sequence stop: 95.
FEATURES            Location/Qualifiers
     source         1. .507
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /dev_stage="Adult"
                    /clone_lib="HT0164"
                    /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                    Site_2: SmaI; A mini-library was made by cloning products
                    derived from  ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 -  Ludwig Institute for Cancer Research)
                    profiles into  the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              351             Length:         507
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-56 (1-328) x AW367597 (1-507)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        106 TTTTTACTGATTCACAAAAAGGAAGAC 132

RESULT 57
AI554405/c
LOCUS       AI554405                510 bp    mRNA    linear   EST 13-MAY-1999
DEFINITION  tq11a12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2208478 3'
            similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION   AI554405
VERSION     AI554405.1  GI:4486768
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
```

```
        Insert Length: 2025   Std Error: 0.00
        Seq primer: -40UP from Gibco
        High quality sequence stop: 404
        POLYA=No.
TURES             Location/Qualifiers
  source          1. .510
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:2208478"
                  /tissue_type="poorly-differentiated endometrial
                  adenocarcinoma, 2 pooled tumors"
                  /lab_host="DH10B"
                  /clone_lib="NCI_CGAP_Ut3"
                  /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                  Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                  Average insert size 1.45 kb. Life Technologies catalog #:
                  11541-018"
GIN

gnment Scores:
d. No.:              353            Length:        510
ce:                  9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
cy Match:            2.7%           Indels:        0
                     1              Gaps:          0

10-821-670A-56 (1-328) x AI554405 (1-510)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       403 TTTTTACTGATTCACAAAAAGGAAGAC 377

JLT 58
06519/c
JS        AV706519                  516 bp    mRNA    linear   EST 09-OCT-2000
INITION   AV706519 ADB Homo sapiens cDNA clone ADBAVE10 5', mRNA sequence.
SSION     AV706519
SION      AV706519.1  GI:10723798
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 516)
THORS     Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G.,
          Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z.,
          Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S.,
          Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
ITLE      Homo sapiens cDNA ADB clones
URNAL     Unpublished (2000)
MENT      Contact: Zeguang Han
          Chinese National Human Genome Center at Shanghai
          351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
          201203, P. R. China
          Tel: 86-21-50801919(ex.45)
          Fax: 86-21-50801922
          Email: hanzg@chgc.sh.cn
          This clone is available at CHGC in Shanghai.
TURES             Location/Qualifiers
  source          1. .516
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="ADBAVE10"
                  /tissue_type="Adrenal gland"
                  /dev_stage="Adult"
                  /lab_host="SOLR"
                  /clone_lib="ADB"
                  /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                  XhoI"
ORIGIN

Alignment Scores:
Pred. No.:              356            Length:        516
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            2.7%           Indels:        0
DB:                     1              Gaps:          0

US-10-821-670A-56 (1-328) x AV706519 (1-516)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        143 TTTTTACTGATTCACAAAAAGGAAGAC 117

RESULT 59
DA098991/c
LOCUS       DA098991                  546 bp    mRNA    linear   EST 02-NOV-2005
DEFINITION  DA098991 BRACE3 Homo sapiens cDNA clone BRACE3010218 5', mRNA
            sequence.
ACCESSION   DA098991
VERSION     DA098991.1  GI:78757572
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 546)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
  PUBMED    16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES            Location/Qualifiers
     source         1. .546
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="BRACE3010218"
                    /tissue_type="cerebellum"
                    /clone_lib="BRACE3"
                    /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              375            Length:        546
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            2.7%           Indels:        0
DB:                     9              Gaps:          0
```

```
0-821-670A-56 (1-328) x DA098991 (1-546)

      101 PheLeuLeuIleHisLysLysGluAsp 109
          |||||||||||||||||||||||||||
       98 TTTTTACTGATTCACAAAAAGGAAGAC 72

LT 60
3328/c
S       BE143328                548 bp    mRNA    linear   EST 21-JUN-2000
NITION  MR0-HT0162-191099-002-b03 HT0162 Homo sapiens cDNA, mRNA sequence.
SSION   BE143328
ION     BE143328.1  GI:8606049
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 548)
THORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
        Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
        Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
        Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
        O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
        Simpson,A.J.
TLE     Shotgun sequencing of the human transcriptome with ORF expressed
        sequence tags
URNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
UBMED   10737800
ENT     Contact: Simpson A.J.G.
        Laboratory of Cancer Genetics
        Ludwig Institute for Cancer Research
        Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
        Brazil
        Tel: +55-11-2704922
        Fax: +55-11-2707001
        Email: asimpson@ludwig.org.br
        This sequence was derived from the FAPESP/LICR Human Cancer Genome
        Project. This entry can be seen in the following URL
        (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR0-HT0162-191
        099-002-b03&t3=1999-10-19&t4=1)
        Seq primer: puc 18 forward
        High quality sequence start: 9
        High quality sequence stop: 528.
URES            Location/Qualifiers
 source         1. .548
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /dev_stage="Adult"
                /clone_lib="HT0162"
                /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                Site_2: SmaI; A mini-library was made by cloning products
                derived from  ORESTES PCR (U.S. Letters Patent application
                No. 196,716 -  Ludwig Institute for Cancer Research)
                profiles into  the pUC 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
IN

nment Scores:
. No.:              376           Length:        548
e:                  9.00          Matches:       9
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            2.7%          Indels:        0
                    7             Gaps:          0

0-821-670A-56 (1-328) x BE143328 (1-548)

       15 LeuLeuAlaProProLeuMetAlaIle 23
          |||||||||||||||||||||||||||
      439 CTACTTGCCCCACCCCTAATGGCCATA 413
```

```
RESULT 61
DB284546/c
LOCUS       DB284546                553 bp    mRNA    linear   EST 10-DEC-2005
DEFINITION  DB284546 UTERU3 Homo sapiens cDNA clone UTERU3012510 5', mRNA
            sequence.
ACCESSION   DB284546
VERSION     DB284546.1  GI:83439601
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 553)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES            Location/Qualifiers
     source         1. .553
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UTERU3012510"
                    /tissue_type="uterus"
                    /clone_lib="UTERU3"
                    /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              379           Length:        553
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     9             Gaps:          0

US-10-821-670A-56 (1-328) x DB284546 (1-553)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        483 TTTTTACTGATTCACAAAAAGGAAGAC 457

RESULT 62
DA102042/c
LOCUS       DA102042                561 bp    mRNA    linear   EST 01-NOV-2005
DEFINITION  DA102042 BRACE3 Homo sapiens cDNA clone BRACE3014468 5', mRNA
            sequence.
ACCESSION   DA102042
VERSION     DA102042.1  GI:78562825
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
```

```
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 561)
UTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
         Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
         Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
         Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
         Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
         Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
ITLE     Diversification of Transcriptional Modulation: Large-scale
         Identification and Characterization of Putative Alternative
         Promoters of Human Genes
URNAL    Genome Res. 16 (1), 55-65 (2006)
UBMED    16344560
IENT     Contact: Takao Isogai
         FLJ Project (HRI Team)
         Helix Research Institute
         2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
         Tel: 81-438-52-3975
         Fax: 81-438-52-3986
         Email: flj-cdna@nifty.com
         NEDO human cDNA project (New Energy and Industrial Technology
         Development Organization, Japan); cDNA library construction:
         Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
         Research Association for Biotechnology (RAB) and Biotechnology
         Center, National Institute of Technology and Evaluation; 3'-end one
         pass sequencing: RAB.
TURES                Location/Qualifiers
  source             1. .561
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="BRACE3014468"
                     /tissue_type="cerebellum"
                     /clone_lib="BRACE3"
                     /note="Vector: pME18SFL3"
IN

gnment Scores:
i. No.:                384            Length:          561
ce:                    9.00           Matches:         9
cent Similarity:       100.0%         Conservative:    0
 Local Similarity:     100.0%         Mismatches:      0
y Match:               2.7%           Indels:          0
                       9              Gaps:            0

10-821-670A-56 (1-328) x DA102042 (1-561)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       459 TTTTTACTGATTCACAAAAAGGAAGAC 433

JLT 63
54731
JS       CW054731                  563 bp    DNA     linear   GSS 28-OCT-2004
INITION  104_295_10516691_115_30176 Sorghum methylation filtered library
         (LibID: 104) Sorghum bicolor genomic clone 10516691, genomic survey
         sequence.
SSION    CW054731
SION     CW054731.1  GI:54731461
WORDS    GSS.
RCE      Sorghum bicolor (sorghum)
RGANISM  Sorghum bicolor
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
         clade; Panicoideae; Andropogoneae; Sorghum.
ERENCE   1  (bases 1 to 563)
UTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
         Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
         McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
         Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
         Martienssen,R.A.
  TITLE      Sorghum genome sequencing by methylation filtration
  JOURNAL    PLoS Biol. 3 (1), e13 (2005)
  PUBMED     15660154
COMMENT      Contact: Bedell JA
             Orion Genomics, LLC
             4041 Forest Park Ave, St. Louis, MO 63108, USA
             Tel: 314 615 6979
             Fax: 314 615 5975
             Email: jbedell@oriongenomics.com
             Plate: 295  row: k  column: 09
             Seq primer: M13/pUC Reverse
             Class: methylation filtered
             High quality sequence stop: 563.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10516691"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:                385            Length:          563
Score:                    9.00           Matches:         9
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              2.7%           Indels:          0
DB:                       13             Gaps:            0

US-10-821-670A-56 (1-328) x CW054731 (1-563)

Qy         121 LysGluSerLysAsnLysIlePheLeu 129
               |||||||||||||||||||||||||||
Db         533 AAAGAATCAAAGAACAAGATCTTCTTA 559

RESULT 64
DB349096
LOCUS       DB349096                  566 bp    mRNA    linear   EST 04-DEC-2005
DEFINITION  DB349096 TRACH3 Homo sapiens cDNA clone TRACH3005200 3', mRNA
            sequence.
ACCESSION   DB349096
VERSION     DB349096.1  GI:83258035
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 566)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
  PUBMED    16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
```

```
       2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
       Tel: 81-438-52-3975
       Fax: 81-438-52-3986
       Email: flj-cdna@nifty.com
       NEDO human cDNA project (New Energy and Industrial Technology
       Developmental Organization, Japan); cDNA library construction:
       Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
       Research Association for Biotechnology (RAB) and Biotechnology
       Center, National Institute of Technology and Evaluation; 3'-end one
       pass sequencing: RAB.
URES             Location/Qualifiers
 source          1. .566
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="TRACH3005200"
                 /tissue_type="trachea"
                 /clone_lib="TRACH3"
                 /note="Vector: pME18SFL3"
IN

nment Scores:
. No.:              387          Length:        566
e:                  9.00         Matches:       9
ent Similarity:     100.0%       Conservative:  0
 Local Similarity:  100.0%       Mismatches:    0
y Match:            2.7%         Indels:        0
                    9            Gaps:          0

0-821-670A-56 (1-328) x DB349096 (1-566)

      101 PheLeuLeuIleHisLysLysGluAsp 109
          |||||||||||||||||||||||||||
      393 TTTTTACTGATTCACAAAAAGGAAGAC 419

LT 65
7722
S       BM907722                572 bp    mRNA    linear   EST 12-MAR-2002
NITION  AGENCOURT_6618905 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5736102
        5', mRNA sequence.
SSION   BM907722
ION     BM907722.1  GI:19358101
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 572)
THORS   NIH-MGC http://mgc.nci.nih.gov/.
TLE     National Institutes of Health, Mammalian Gene Collection (MGC)
URNAL   Unpublished (1999)
ENT     Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: DCTD/DTP/Gazdar
         cDNA Library Preparation: Life Technologies, Inc.
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Agencourt Bioscience Corporation
         Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: LLAM12744  row: b  column: 07
        High quality sequence stop: 572.
URES             Location/Qualifiers
 source          1. .572
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:5736102"
                 /tissue_type="large cell carcinoma"
                 /lab_host="DH10B (phage-resistant)"
                 /clone_lib="NIH_MGC_68"
                 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                 Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                 Average insert size 1.8 kb.   Library constructed by Life
                 Technologies. "
ORIGIN

Alignment Scores:
Pred. No.:              391          Length:        572
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.7%         Indels:        0
DB:                     3            Gaps:          0

US-10-821-670A-56 (1-328) x BM907722 (1-572)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        156 TTTTTACTGATTCACAAAAAGGAAGAC 182

RESULT 66
CK818181/c
LOCUS       CK818181                593 bp    mRNA    linear   EST 11-MAR-2004
DEFINITION  ic21a08.y5 HR85 islet Homo sapiens cDNA clone IMAGE: 5', mRNA
            sequence.
ACCESSION   CK818181
VERSION     CK818181.1  GI:44835106
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 593)
  AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
            Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
            Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
            McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
            Bowers,Y.
  TITLE     WashU-Harvard Pancreas EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            This read is a 5' RESEQUENCE of a previously sequenced pancreas
            clone
            Good hit to opposite strand read. . .wrong orientation BUT PASSED FOR
            MOUSE-PANCREAS VERIFICATION
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .593
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN
```

```
gnment Scores:
d. No.:                 403             Length:         593
re:                     9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
: Local Similarity:     100.0%          Mismatches:     0
cy Match:               2.7%            Indels:         0
                        5               Gaps:           0

10-821-670A-56 (1-328) x CK818181 (1-593)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       408 TTTTTACTGATTCACAAAAAGGAAGAC 382

JLT 67
36151/c
JS        CW136151                  624 bp    DNA     linear   GSS 29-OCT-2004
INITION   104_521_11118228_148_34843_048 Sorghum methylation filtered library
          (LibID: 104) Sorghum bicolor genomic clone 11118228, genomic survey
          sequence.
SSION     CW136151
SION      CW136151.1  GI:54828698
WORDS     GSS.
RCE       Sorghum bicolor (sorghum)
RGANISM   Sorghum bicolor
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Sorghum.
ERENCE    1  (bases 1 to 624)
UTHORS    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
          Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
          McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
          Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
          Martienssen,R.A.
ITLE      Sorghum genome sequencing by methylation filtration
OURNAL    PLoS Biol. 3 (1), e13 (2005)
UBMED     15660154
MENT      Contact: Bedell JA
          Orion Genomics, LLC
          4041 Forest Park Ave, St. Louis, MO 63108, USA
          Tel: 314 615 6979
          Fax: 314 615 5975
          Email: jbedell@oriongenomics.com
          Plate: 521  row: b  column: 12
          Seq primer: SWfor Forward
          Class: methylation filtered
          High quality sequence stop: 624.
TURES               Location/Qualifiers
  source            1. .624
                    /organism="Sorghum bicolor"
                    /mol_type="genomic DNA"
                    /cultivar="ATx623"
                    /db_xref="taxon:4558"
                    /clone="11118228"
                    /clone_lib="Sorghum methylation filtered library (LibID:
                    104)"
                    /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                    prepared from purified nuclei was randomly sheared,
                    end-repaired, size fractionated to enrich for the 0.5 to 5
                    kb fraction, ligated into HincII-digested pBCSK(-) vector
                    and electroporated into E. coli cells. This is a
                    methylation filtered library."
IN

gnment Scores:
d. No.:                 422             Length:         624
re:                     9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
: Local Similarity:     100.0%          Mismatches:     0
cy Match:               2.7%            Indels:         0
                        13              Gaps:           0

10-821-670A-56 (1-328) x CW136151 (1-624)

Qy        121 LysGluSerLysAsnLysIlePheLeu 129
              |||||||||||||||||||||||||||
Db        324 AAAGAATCAAAGAACAAGATCTTCTTA 298

RESULT 68
BU813156/c
LOCUS       BU813156                  631 bp    mRNA    linear   EST 15-OCT-2002
DEFINITION  N006A02 Populus bark cDNA library Populus tremula x Populus
            tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION   BU813156
VERSION     BU813156.1  GI:23968892
KEYWORDS    EST.
SOURCE      Populus tremula x Populus tremuloides
  ORGANISM  Populus tremula x Populus tremuloides
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
  TITLE     The poplar tree transcriptome: Analysis of expressed sequence tags
            from multiple libraries
  JOURNAL   Unpublished (2002)
COMMENT     Contact: BHALERAO RUPALI R.
            Umea Plant Science Center
            Department of Plant Physiology
            University of Umea, 901 87 Umea, Sweden
            Tel: +46 90 786 5279
            Fax: +46 90 786 6676
            Email: rupali.bhalerao@plantphys.umu.se.
FEATURES              Location/Qualifiers
     source           1. .631
                      /organism="Populus tremula x Populus tremuloides"
                      /mol_type="mRNA"
                      /db_xref="taxon:47664"
                      /tissue_type="bark"
                      /clone_lib="Populus bark cDNA library"
ORIGIN

Alignment Scores:
Pred. No.:              426             Length:         631
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x BU813156 (1-631)

Qy         11 PheSerLeuValLeuLeuAlaProPro 19
              |||||||||||||||||||||||||||
Db        190 TTCTCTCTTGTCCTGCTCGCTCCCCCT 164

RESULT 69
CW136150
LOCUS       CW136150                  638 bp    DNA     linear   GSS 29-OCT-2004
DEFINITION  104_521_11118228_116_34847_048 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 11118228, genomic survey
            sequence.
ACCESSION   CW136150
VERSION     CW136150.1  GI:54828697
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 638)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
```

```
TLE     Sorghum genome sequencing by methylation filtration
URNAL   PLoS Biol. 3 (1), e13 (2005)
UBMED   15660154
ENT     Contact: Bedell JA
        Orion Genomics, LLC
        4041 Forest Park Ave, St. Louis, MO 63108, USA
        Tel: 314 615 6979
        Fax: 314 615 5975
        Email: jbedell@oriongenomics.com
        Plate: 521  row: b  column: 12
        Seq primer: T3 Reverse
        Class: methylation filtered
        High quality sequence stop: 638.
URES            Location/Qualifiers
 source         1. .638
                /organism="Sorghum bicolor"
                /mol_type="genomic DNA"
                /cultivar="ATx623"
                /db_xref="taxon:4558"
                /clone="11118228"
                /clone_lib="Sorghum methylation filtered library (LibID:
                104)"
                /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                prepared from purified nuclei was randomly sheared,
                end-repaired, size fractionated to enrich for the 0.5 to 5
                kb fraction, ligated into HincII-digested pBCSK(-) vector
                and electroporated into E. coli cells. This is a
                methylation filtered library."
IN

nment Scores:
. No.:              431           Length:        638
e:                  9.00          Matches:       9
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            2.7%          Indels:        0
                    13            Gaps:          0

0-821-670A-56 (1-328) x CW136150 (1-638)

      121 LysGluSerLysAsnLysIlePheLeu 129
          |||||||||||||||||||||||||||
      525 AAAGAATCAAAGAACAAGATCTTCTTA 551

LT 70
4654
S       CL344654                645 bp    DNA     linear   GSS 19-AUG-2004
NITION  RPCI44_278P18.r RPCI-44 Sus scrofa genomic clone RPCI44_278P18,
        genomic survey sequence.
SSION   CL344654
ION     CL344654.1  GI:51396622
ORDS    GSS.
CE      Sus scrofa (pig)
GANISM  Sus scrofa
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
       .Sus.
RENCE   1  (bases 1 to 645)
THORS   Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
        Beever,J.E. and Schook,L.B.
TLE     Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
        Through Comparative Genomics
URNAL   Unpublished (2004)
ENT     Other_GSSs: RPCI44_278P18.f
        Contact: Lawrence B. Schook
        Department of Animal Sciences
        University of Illinois at Urbana Champaign
        1201 W. Gregory Dr., Urbana, IL 61801, USA
        Tel: 217 265 5326
        Fax: 217 244 5617
        Email: schook@uiuc.edu
        Clones are derived from the porcine BAC library RPCI-44
        (http://www.bacpac.chori.org/porcine242.htm). For BAC library
        availability, please contact Pieter de Jong (pdejong@chori.org).
        Clones may be purchased from BACPAC Resources
        (http://BACPACorders.chori.org). This work was undertaken as part
        of the International Swine Genome Sequencing Consortium by
        University of Illinois at Urbana Champaign, USA with funds provided
        by grant No. AG2002-34480-11828 from USDA-CSREES and
        AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
        Initiative)
        Plate: 278  row: P  column: 18
        Seq primer: SP6
        Class: BAC ends.
FEATURES        Location/Qualifiers
     source     1. .645
                /organism="Sus scrofa"
                /mol_type="genomic DNA"
                /strain="four pigs (breed: 37.5% Yorks Landrace and 25%
                Meishan)"
                /db_xref="taxon:9823"
                /clone="RPCI44_278P18"
                /sex="male"
                /cell_type="blood"
                /clone_lib="RPCI-44"
                /note="Vector: pTARBAC2; Site_1: EcoRI; Site_2: EcoRI;
                porcine male BAC library produced by Pieter de Jong"
ORIGIN

Alignment Scores:
Pred. No.:              435           Length:        645
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     13            Gaps:          0

US-10-821-670A-56 (1-328) x CL344654 (1-645)

Qy        274 PheGlyValGlnValGlnGlyLysAsn 282
              |||||||||||||||||||||||||||
Db         29 TTTGGTGTTCAGGTTCAGGGCAAGAAC 55

RESULT 71
DT874689/c
LOCUS       DT874689                 648 bp    mRNA    linear   EST 18-SEP-2005
DEFINITION  AGENCOURT_58684019 NIH_ZGC_5 Danio rerio cDNA clone IMAGE:8101578
            5', mRNA sequence.
ACCESSION   DT874689
VERSION     DT874689.1  GI:75844429
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 648)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: John Postlethwait, University of Oregon
             cDNA Library Preparation: Dr. Sumio Sugano
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM17510  row: o  column: 16
            High quality sequence start: 8
            High quality sequence stop: 559.
FEATURES        Location/Qualifiers
```

```
  source          1. .648
                  /organism="Danio rerio"
                  /mol_type="mRNA"
                  /db_xref="taxon:7955"
                  /clone="IMAGE:8101578"
                  /tissue_type="contains eggs from one female, from all
                  stages of development as well as support cells"
                  /lab_host="DH10B TonA"
                  /clone_lib="NIH_ZGC_5"
                  /note="Organ: ovary; Vector: pME18S-FL3; Site_1: DraIII;
                  Site_2: DraIII; 1st strand cDNA was primed with an
                  oligo(dT) primer
                  [GCGGCTGAAGACGGCCTATGTGGCCTTTTTTTTTTTTTTTT];
                  double-stranded cDNA was ligated to a DraIII adaptor
                  [GGCCUACUGG], digested and directionally cloned into
                  distinct DraIII sites of the pME18S-FL3. Library was size
                  selected for 1.0 kb, with a average insert size of ~1.2kb.
                  Library constructed by Yutaka Suzuki (University of Tokyo
                  Institute of Medical Science). Custom primers recommended
                  for sequencing: 5' end primer 5'-GGATGTTGCCTTTACTTCTA-3'
                  and 3' end primer 5'-CGACCTGCAGCTCGAGCACA-3'. Note: This
                  is a Zebrafish Gene Collection (ZGC) library"
ORIGIN

Alignment Scores:
Pred. No.:                437             Length:         648
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              2.7%            Indels:         0
DB:                       10              Gaps:           0

US-10-821-670A-56 (1-328) x DT874689 (1-648)

Qy        225 ThrSerSerPhePheIleArgAspIle 233
                ||||||||||||||||||||||||||
Db         29 ACGTCCTCTTTCTTCATTCGCGACATC 3

RESULT 72
DT874689/c
LOCUS       CW374083                649 bp    DNA     linear   GSS 01-NOV-2004
DEFINITION  fsbb001f050m06k0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f050m06, genomic survey
            sequence.
ACCESSION   CW374083
VERSION     CW374083.1  GI:55092527
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
  PUBMED    15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f050  row: m  column: 06
            Seq primer: k Reverse
            Class: methylation filtered
            High quality sequence stop: 649.
FEATURES             Location/Qualifiers
  source             1. .649
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="fsbb001f050m06"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:                437             Length:         649
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              2.7%            Indels:         0
DB:                       13              Gaps:           0

US-10-821-670A-56 (1-328) x CW374083 (1-649)

Qy        121 LysGluSerLysAsnLysIlePheLeu 129
                ||||||||||||||||||||||||||
Db        323 AAAGAATCAAAGAACAAGATCTTCTTA 297

RESULT 73
BG696339
LOCUS       BG696339                650 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602658709F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4801803 5',
            mRNA sequence.
ACCESSION   BG696339
VERSION     BG696339.1  GI:13961382
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 650)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10695  row: a  column: 04
            High quality sequence stop: 650.
FEATURES             Location/Qualifiers
     source          1. .650
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4801803"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

Alignment Scores:
Pred. No.:                438             Length:         650
```

```
e:                  9.00          Matches:       9
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            2.7%          Indels:        0
                    2             Gaps:          0

0-821-670A-56 (1-328) x BG696339 (1-650)

      101 PheLeuLeuIleHisLysLysGluAsp 109
          |||||||||||||||||||||||||||
      372 TTTTTACTGATTCACAAAAAGGAAGAC 398

LT 74
4592
S       CL344592                657 bp    DNA     linear   GSS 19-AUG-2004
NITION  RPCI44_278D6.r RPCI-44 Sus scrofa genomic clone RPCI44_278D6,
        genomic survey sequence.
SSION   CL344592
ION     CL344592.1  GI:51396560
ORDS    GSS.
CE      Sus scrofa (pig)
GANISM  Sus scrofa
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
        Sus.
RENCE   1  (bases 1 to 657)
THORS   Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
        Beever,J.E. and Schook,L.B.
TLE     Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
        Through Comparative Genomics
URNAL   Unpublished (2004)
ENT     Other_GSSs: RPCI44_278D6.f
        Contact: Lawrence B. Schook
        Department of Animal Sciences
        University of Illinois at Urbana Champaign
        1201 W. Gregory Dr., Urbana, IL 61801, USA
        Tel: 217 265 5326
        Fax: 217 244 5617
        Email: schook@uiuc.edu
        Clones are derived from the porcine BAC library RPCI-44
        (http://www.bacpac.chori.org/porcine242.htm). For BAC library
        availability, please contact Pieter de Jong (pdejong@chori.org).
        Clones may be purchased from BACPAC Resources
        (http://BACPACorders.chori.org). This work was undertaken as part
        of the International Swine Genome Sequencing Consortium by
        University of Illinois at Urbana Champaign, USA with funds provided
        by grant No. AG2002-34480-11828 from USDA-CSREES and
        AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
        Initiative)
        Plate: 278  row: D  column: 6
        Seq primer: SP6
        Class: BAC ends.
URES            Location/Qualifiers
 source         1. .657
                /organism="Sus scrofa"
                /mol_type="genomic DNA"
                /strain="four pigs (breed: 37.5% Yorks Landrace and 25%
                Meishan)"
                /db_xref="taxon:9823"
                /clone="RPCI44_278D6"
                /sex="male"
                /cell_type="blood"
                /clone_lib="RPCI-44"
                /note="Vector: pTARBAC2; Site_1: EcoRI; Site_2: EcoRI;
                porcine male BAC library produced by Pieter de Jong"
IN

nment Scores:
. No.:              442           Length:        657
e:                  9.00          Matches:       9
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            2.7%          Indels:        0
DB:                 13            Gaps:          0

US-10-821-670A-56 (1-328) x CL344592 (1-657)

Qy      274 PheGlyValGlnValGlnGlyLysAsn 282
            |||||||||||||||||||||||||||
Db       27 TTTGGTGTTCAGGTTCAGGGCAAGAAC 53

RESULT 75
BU773963/c
LOCUS       BU773963                661 bp    mRNA    linear   EST 23-OCT-2003
DEFINITION  SJEGBC03 SJE Schistosoma japonicum cDNA similar to
            gi|639869|dbj|BAA07127.1| (D37885) choline kinase R2 [Rattus
            norvegicus], mRNA sequence.
ACCESSION   BU773963
VERSION     BU773963.1  GI:28341279
KEYWORDS    EST.
SOURCE      Schistosoma japonicum
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 661)
  AUTHORS   Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
            Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
            Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
            McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
  TITLE     Evolutionary and biomedical implications of a Schistosoma japonicum
            complementary DNA resource
  JOURNAL   Nat. Genet. 35 (2), 139-147 (2003)
   PUBMED   12973349
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn.
FEATURES            Location/Qualifiers
     source         1. .661
                    /organism="Schistosoma japonicum"
                    /mol_type="mRNA"
                    /db_xref="taxon:6182"
                    /tissue_type="Whole egg"
                    /dev_stage="egg"
                    /lab_host="rabbits"
                    /clone_lib="SJE"
ORIGIN

Alignment Scores:
Pred. No.:          444           Length:        661
Score:              9.00          Matches:       9
Percent Similarity: 100.0%        Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:        2.7%          Indels:        0
DB:                 3             Gaps:          0

US-10-821-670A-56 (1-328) x BU773963 (1-661)

Qy      223 AsnTyrThrSerSerPhePheIleArg 231
            |||||||||||||||||||||||||||
Db      306 AACTACACTTCTAGTTTCTTCATAAGA 280

RESULT 76
AW956339
LOCUS       AW956339                677 bp    mRNA    linear   EST 01-JUN-2000
DEFINITION  EST368409 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW956339
VERSION     AW956339.1  GI:8146022
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

```
        Hominidae; Homo.
ERENCE  1  (bases 1 to 677)
UTHORS  Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
        Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
        Quackenbush,J.
ITLE    Assessment of gene expression patterns in a model of colon tumor
        metastasis using a 19,200 element cDNA microarray
OURNAL  Unpublished (2000)
MENT    Contact: John Quackenbush
        The Institute for Genomic Research
        9712 Medical Center Dr., Rockville, MD 20850, USA
        Tel: 301 838 3528
        Fax: 301 838 0208
        Email: johnq@tigr.org
        Plate: 90
        Seq primer: Reverse.
TURES           Location/Qualifiers
  source        1. .677
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="MAGE resequences, MAGD"
                /note="Vector: pBluescriptSKm"
IN

gnment Scores:
i. No.:              454          Length:        677
ce:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
 Local Similarity:   100.0%       Mismatches:    0
cy Match:            2.7%         Indels:        0
                     7            Gaps:          0

10-821-670A-56 (1-328) x AW956339 (1-677)

      101 PheLeuLeuIleHisLysLysGluAsp 109
          |||||||||||||||||||||||||||
      330 TTTTTACTGATTCACAAAAAGGAAGAC 356

JLT 77
24059
JS      DR724059                683 bp    mRNA    linear   EST 15-JUL-2005
INITION AGENCOURT_55148409 NICHD_XGC_Emb9 Xenopus laevis cDNA clone
        IMAGE:7973954 3', mRNA sequence.
SSION   DR724059
ION     DR724059.1  GI:70898171
WORDS   EST.
RCE     Xenopus laevis (African clawed frog)
RGANISM Xenopus laevis
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
        Xenopodinae; Xenopus; Xenopus.
ERENCE  1  (bases 1 to 683)
UTHORS  NIH-MGC http://mgc.nci.nih.gov/.
ITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL  Unpublished (1999)
MENT    Contact: Daniela S. Gerhard, Ph.D.
        Office of Cancer Genomics
        National Cancer Institute / NIH
        Bldg. 31 Rm10A07 Bethesda, MD 20892
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: Dr. Igor Dawid
         cDNA Library Preparation: Express Genomics
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Agencourt Bioscience Corporation
         Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: LLAM17094  row: i  column: 24
        High quality sequence start: 170
        High quality sequence stop: 404.
TURES           Location/Qualifiers
  source        1. .683
                /organism="Xenopus laevis"
                /mol_type="mRNA"
                /db_xref="taxon:8355"
                /clone="IMAGE:7973954"
                /tissue_type="Embryonic stage 17/19"
                /lab_host="DH10B TonA"
                /clone_lib="NICHD_XGC_Emb9"
                /note="Organ: embryo; Vector: pExpress-1; Site_1: EcoRV;
                Site_2: NotI; cDNA was primed using oligo-dT primer:
                5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                the EcoRV/NotI sites of pExpress-1. Size-selection 1.4kb
                resulted in an average insert size of 2.1kb. This is a
                non-normalized primary library (normalized library is
                NICHD_XGC_Emb10) and was constructed by Express Genomics
                (Frederick, MD). Note: this is a Xenopus Gene Collection
                (http://xgc.nci.nih.gov/) library."
ORIGIN

Alignment Scores:
Pred. No.:              458          Length:        683
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.7%         Indels:        0
DB:                     10           Gaps:          0

US-10-821-670A-56 (1-328) x DR724059 (1-683)

Qy          96 ValLeuSerHisSerPheLeuLeuIle 104
               |||||||||||||||||||||||||||
Db         457 GTTTTAAGTCACTCTTTTCTTCTTATT 483

RESULT 78
CA413781
LOCUS       CA413781                688 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-EZ0-bat-p-08-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens cDNA clone
            UI-H-EZ0-bat-p-08-0-UI 3', mRNA sequence.
ACCESSION   CA413781
VERSION     CA413781.1  GI:24776432
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthoapedics
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 313-608, >ALU
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES            Location/Qualifiers
     source         1. .688
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UI-H-EZ0-bat-p-08-0-UI"
                    /tissue_type="Chondrosarcoma Grade II"
                    /dev_stage="Adult"
                    /lab_host="DH10B (Life Technologies)"
                    /clone_lib="NCI_CGAP_Ch1"
```

```
                /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                NCI_CGAP_Ch1 is a cDNA library containing the following
                tissue(s): Chondrosarcoma Grade II. The library was
                constructed according to Bonaldo, Lennon and Soares,
                Genome Research, 6:791-806, 1996. First strand cDNA
                synthesis was primed with an oligo-dT primer containing a
                Not I site. Double stranded cDNA was ligated to an EcoR I
                adaptor, digested with Not I, and cloned directionally
                into pT7T3-Pac vector. The oligonucleotide used to prime
                the synthesis of first-strand cDNA contains a library tag
                sequence that is located between the Not I site and the
                (dT)18 tail. The sequence tag for this library is
                TGATCACGCT.
                TAG_TISSUE=grade-2-chondrosarcoma
                TAG_LIB=UI-H-EZ0
                TAG_SEQ=ATCTAATATG"
IN

nment Scores:
. No.:              461             Length:         688
e:                  9.00            Matches:        9
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            2.7%            Indels:         0
                    4               Gaps:           0

0-821-670A-56 (1-328) x CA413781 (1-688)

      101 PheLeuLeuIleHisLysLysGluAsp 109
          |||||||||||||||||||||||||||
      201 TTTTTACTGATTCACAAAAAGGAAGAC 227

LT 79
0377
S       CW470377                692 bp    DNA     linear   GSS 02-NOV-2004
NITION  fsbb001f223i17k0 Sorghum methylation filtered library (LibID: 104)
        Sorghum bicolor genomic clone fsbb001f223i17, genomic survey
        sequence.
SSION   CW470377
ION     CW470377.1  GI:55218338
ORDS    GSS.
CE      Sorghum bicolor (sorghum)
GANISM  Sorghum bicolor
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
        clade; Panicoideae; Andropogoneae; Sorghum.
RENCE   1  (bases 1 to 692)
THORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
        Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
        McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
        Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
        Martienssen,R.A.
TLE     Sorghum genome sequencing by methylation filtration
URNAL   PLoS Biol. 3 (1), e13 (2005)
UBMED   15660154
ENT     Contact: Bedell JA
        Orion Genomics, LLC
        4041 Forest Park Ave, St. Louis, MO 63108, USA
        Tel: 314 615 6979
        Fax: 314 615 5975
        Email: jbedell@oriongenomics.com
        Plate: fsbb001f223  row: i  column: 17
        Seq primer: k Reverse
        Class: methylation filtered
        High quality sequence stop: 692.
URES            Location/Qualifiers
 source         1. .692
                /organism="Sorghum bicolor"
                /mol_type="genomic DNA"
                /cultivar="ATx623"
                /db_xref="taxon:4558"
                /clone="fsbb001f223i17"
                /clone_lib="Sorghum methylation filtered library (LibID:
                104)"
                /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                prepared from purified nuclei was randomly sheared,
                end-repaired, size fractionated to enrich for the 0.5 to 5
                kb fraction, ligated into HincII-digested pBCSK(-) vector
                and electroporated into E. coli cells. This is a
                methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              463             Length:         692
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     13              Gaps:           0

US-10-821-670A-56 (1-328) x CW470377 (1-692)

Qy        121 LysGluSerLysAsnLysIlePheLeu 129
              |||||||||||||||||||||||||||
Db         37 AAAGAATCAAAGAACAAGATCTTCTTA 63

RESULT 80
BE387304
LOCUS       BE387304                697 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  601275594F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616655 5',
            mRNA sequence.
ACCESSION   BE387304
VERSION     BE387304.1  GI:9332669
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM282  row: k  column: 24
            High quality sequence start: 82
            High quality sequence stop: 534.
FEATURES            Location/Qualifiers
     source         1. .697
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:3616655"
                    /tissue_type="melanotic melanoma"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_20"
                    /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming.  Directionally
                    cloned into EcoRI/XhoI sites using the following 5'
                    adaptor: GGCACGAG(G).  Size-selected >500bp for average
                    insert size 1.8kb.  Library constructed by Ling Hong in
                    the laboratory of Gerald M. Rubin (University of
                    California, Berkeley) using  ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Alignment Scores:
Pred. No.:              466             Length:         697
```

```
ce:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
: Local Similarity:  100.0%        Mismatches:    0
cy Match:            2.7%          Indels:        0
                     7             Gaps:          0

10-821-670A-56 (1-328) x BE387304 (1-697)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       117 TTTTTACTGATTCACAAAAAGGAAGAC 143

JLT 81
)9739/c
JS        BQ009739                 700 bp    mRNA    linear   EST 26-MAR-2002
INITION   UI-H-ED0-aya-h-21-0-UI.s1 NCI_CGAP_ED0 Homo sapiens cDNA clone
          IMAGE:5836100 3', mRNA sequence.
ESSION    BQ009739
SION      BQ009739.1  GI:19734640
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 700)
UTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
ITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
OURNAL    Unpublished (1997)
MENT      Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Jose Mercuende
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           The following repetitive elements were found in this cDNA
          sequence: 11-306, >ALU (matched compliment)
          Seq primer: M13 FORWARD
          POLYA=Yes.
TURES               Location/Qualifiers
  source            1. .700
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5836100"
                    /tissue_type="Chondrosarcoma"
                    /dev_stage="Adult"
                    /lab_host="DH10B (Life Technologies)"
                    /clone_lib="NCI_CGAP_ED0"
                    /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                    (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                    Site_2: Not I; NCI_CGAP_ED0 is a cDNA library containing
                    the following tissue(s): Chondrosarcoma cell line CS5. The
                    library was constructed according to Bonaldo, Lennon and
                    Soares, Genome Research, 6:791-806, 1996. First strand
                    cDNA synthesis was primed with an oligo-dT primer
                    containing a Not I site. Double stranded cDNA was ligated
                    to an EcoR I adaptor, digested with Not I, and cloned
                    directionally into pT7T3-Pac vector. The oligonucleotide
                    used to prime the synthesis of first-strand cDNA contains
                    a library tag sequence that is located between the Not I
                    site and the (dT)18 tail. The sequence tag for this
                    library is GCTCAAGGCT.
                    TAG_TISSUE=chondrosarcoma
                    TAG_LIB=UI-H-ED0
                    TAG_SEQ=CGTCAAGGCT"
IN

gnment Scores:
d. No.:              468           Length:        700
```

```
Score:               9.00          Matches:       9
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         2.7%          Indels:        0
DB:                  3             Gaps:          0

US-10-821-670A-56 (1-328) x BQ009739 (1-700)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        418 TTTTTACTGATTCACAAAAAGGAAGAC 392

RESULT 82
CN279085/c
LOCUS       CN279085                 707 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000424715748 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN279085
VERSION     CN279085.1  GI:47295499
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 707)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 707   Std Error: 0.00.
FEATURES              Location/Qualifiers
     source           1. .707
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="embryonic stem cells, cell lines H1, H7, and
                      H9"
                      /clone_lib="GRN_ES"
                      /note="oligo dT primed, full-length enriched cDNA library
                      from undifferentiated hES cell lines H1 (p32), H7 (p29),
                      and H9 (p26) maintained in feeder-free conditions"
ORIGIN

Alignment Scores:
Pred. No.:           472           Length:        707
Score:               9.00          Matches:       9
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         2.7%          Indels:        0
DB:                  8             Gaps:          0

US-10-821-670A-56 (1-328) x CN279085 (1-707)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        235 TTTTTACTGATTCACAAAAAGGAAGAC 209

RESULT 83
CN412356
LOCUS       CN412356                 722 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000532543092 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN412356
VERSION     CN412356.1  GI:47399950
```

```
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 722)
THORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
        Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
        Lebkowski,J and Stanton,L.W.
TLE     Transcriptome characterization elucidates signaling networks that
        control human ES cell growth and differentiation
URNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
UBMED   15146197
ENT     Contact: Brandenberger R
        Regenerative Medicine
        Geron Corporation
        230 Constitution Drive, Menlo Park, CA 94025, USA
        Tel: 650 473 8658
        Fax: 650 473 7760
        Email: rbrandenberger@geron.com
        Insert Length: 722   Std Error: 0.00.
URES            Location/Qualifiers
 source         1. .722
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="embryonic stem cells, cell lines H1, H7, and
                H9"
                /clone_lib="GRN_ES"
                /note="oligo dT primed, full-length enriched cDNA library
                from undifferentiated hES cell lines H1 (p32), H7 (p29),
                and H9 (p26) maintained in feeder-free conditions"
IN

nment Scores:
. No.:              481             Length:         722
e:                  9.00            Matches:        9
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            2.7%            Indels:         0
                    8               Gaps:           0

0-821-670A-56 (1-328) x CN412356 (1-722)

      101 PheLeuLeuIleHisLysLysGluAsp 109
          |||||||||||||||||||||||||||
      395 TTTTTACTGATTCACAAAAAGGAAGAC 421

LT 84
4937/c
S       DN494937                746 bp    mRNA    linear   EST 10-MAR-2005
NITION  N006A02.5pR Populus bark cDNA library Populus tremula x Populus
        tremuloides cDNA clone N006A02 5', mRNA sequence.
SSION   DN494937
ION     DN494937.1  GI:60705127
ORDS    EST.
CE      Populus tremula x Populus tremuloides
GANISM  Populus tremula x Populus tremuloides
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
RENCE   1  (bases 1 to 746)
THORS   Sterky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,
        Brunner,A.M., Charbonnel-Campaa,L., Lindvall,J.J., Tandre,K.,
        Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P.,
        Nilsson,O., Sandberg,G., Karlsson,J., Lundeberg,J. and Jansson,S.
TLE     A Populus EST resource for plant functional genomics
URNAL   Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
UBMED   15353603
ENT     Other_ESTs: N006A02
        Contact: Bo Segerman
        Umea Plant Science Center, Department of Plant Physiology
        Umea University
        901 87 Umea, Sweden
        Tel: +46 90 786 5279
        Fax: +46 90 786 6676
        Email: bo.segerman@plantphys.umu.se.
FEATURES        Location/Qualifiers
     source     1. .746
                /organism="Populus tremula x Populus tremuloides"
                /mol_type="mRNA"
                /db_xref="taxon:47664"
                /clone="N006A02"
                /tissue_type="bark"
                /clone_lib="Populus bark cDNA library"
ORIGIN

Alignment Scores:
Pred. No.:              495             Length:         746
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-56 (1-328) x DN494937 (1-746)

Qy          11 PheSerLeuValLeuLeuAlaProPro 19
               |||||||||||||||||||||||||||
Db         152 TTCTCTCTTGTCCTGCTCGCTCCCCCT 126

RESULT 85
BU633670/c
LOCUS       BU633670                757 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FL1-bgv-k-06-0-UI.s1 NCI_CGAP_FL1 Homo sapiens cDNA clone
            UI-H-FL1-bgv-k-06-0-UI 3', mRNA sequence.
ACCESSION   BU633670
VERSION     BU633670.1  GI:23300919
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 21-151, >MER20#DNA/MER1_type 302-597, >ALU (matched
            compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES            Location/Qualifiers
     source         1. .757
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UI-H-FL1-bgv-k-06-0-UI"
                    /tissue_type="Cell lines"
                    /dev_stage="Adult"
                    /lab_host="DH10B (Life Technologies)"
                    /clone_lib="NCI_CGAP_FL1"
                    /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                    (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                    Site_2: Not I; NCI_CGAP_FL1 is a normalized cDNA library
```

derived from a pool of mRNA obtained from 4 cell lines
from grade III chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GAGGTCGGTG. The cell lines were provided by Dr. James
Martin from the University of Iowa.
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_LIB=UI-H-FL1
TAG_SEQ=GAGGTCGGTG"

```
GIN

gnment Scores:
d. No.:                 501             Length:         757
re:                     9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               2.7%            Indels:         0
                        3               Gaps:           0

10-821-670A-56 (1-328) x BU633670 (1-757)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       709 TTTTTACTGATTCACAAAAAGGAAGAC 683

ULT 86
46084/c
US        BP446084                763 bp    mRNA    linear   EST 30-DEC-2003
INITION   BP446084 full-length enriched swine cDNA library, adult liver Sus
          scrofa cDNA clone LVR010002F10 5', mRNA sequence.
ESSION    BP446084
SION      BP446084.1  GI:40436151
WORDS     EST.
RCE       Sus scrofa (pig)
RGANISM   Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
          Sus.
ERENCE    1  (bases 1 to 763)
UTHORS    Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
          Okumura,N., Hamasima,N. and Awata,T.
ITLE      PEDE (Pig EST Data Explorer): construction of a database for ESTs
          derived from porcine full-length cDNA libraries
OURNAL    Nucleic Acids Res. 32 (1), D484-D488 (2004)
UBMED     14681463
MENT      Contact: Hirohide Uenishi
          Animal Genome Laboratory, Genome Research Department
          National Institute of Agrobiological Sciences
          2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
          Tel: +81-29-838-8627
          Fax: +81-29-838-8627
          Email: huenishi@affrc.go.jp
          EST project with full-length enriched cDNA libraries carried out in
          Animal Genome Research Program (Japan) by National Institute of
          Agrobiological Sciences and STAFF-Institute
          Single pass sequencing of clones derived from oligo-capped cDNA
          library
          Vector sequences were eliminated by RepeatMasker version 2002/07/13
          and crossmatch version 0.990319
          Low quality bases were trimmed based on the quality values.
TURES                Location/Qualifiers
  source             1. .763
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="LVR010002F10"
                     /tissue_type="liver"
                     /dev_stage="adult"
                     /clone_lib="full-length enriched swine cDNA library, adult
                     liver"
ORIGIN

Alignment Scores:
Pred. No.:                505             Length:         763
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              2.7%            Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-56 (1-328) x BP446084 (1-763)

Qy          64 GlnSerSerGluValLeuGlySerGly 72
               ||||||||||||||||||||||||||||
Db         646 CAATCCTCAGAGGTACTTGGGAGCGGA 620

RESULT 87
BU375548
LOCUS       BU375548                780 bp    mRNA    linear   EST 28-NOV-2002
DEFINITION  603807808F1 CSEQCHN74 Gallus gallus cDNA clone ChEST789p2 5', mRNA
            sequence.
ACCESSION   BU375548
VERSION     BU375548.1  GI:25883549
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST789p2"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN74"
                     /note="Organ: kidney + adrenal; Vector: pBluescript II
                     KS(+); Site_1: EcoRI; Site_2: Not1; This normalized
                     library was constructed from 1 million independent clones.
                     cDNA synthesis was initiated using an oligo(dT) primer,
                     using methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN
```

```
nment Scores:
. No.:              515             Length:         780
e:                  9.00            Matches:        9
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            2.7%            Indels:         0
                    3               Gaps:           0

0-821-670A-56 (1-328) x BU375548 (1-780)

      201 ProAlaAlaGluGluSerLeuProIle 209
          ||||||||||||||||||||||||||||
      682 CCTGCCGCGGAAGAGAGCTTGCCTATC 708

LT 88
6171/c
S       BZ056171                796 bp    DNA     linear   GSS 09-OCT-2002
NITION  l1b95f10.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
        sequence.
SSION   BZ056171
ION     BZ056171.1  GI:23661434
ORDS    GSS.
CE      Brassica oleracea
GANISM  Brassica oleracea
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
RENCE   1  (bases 1 to 796)
THORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
        Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TLE     Whole genome shotgun reads from Brassica oleracea
URNAL   Unpublished (2002)
ENT     Contact: Richard K. Wilson
        Genome Sequencing Center
        Washington University School of Medicine
        Email: submissions@watson.wustl.edu
        Plate: l1b95  row: f  column: 10
        Seq primer: -21UPpOT forward
        Class: shotgun
        High quality sequence start: 23
        High quality sequence stop: 551.
URES            Location/Qualifiers
 source         1. .796
                /organism="Brassica oleracea"
                /mol_type="genomic DNA"
                /db_xref="taxon:3712"
                /clone_lib="B.oleracea002"
                /note="Vector: pOTw13; Whole genome shotgun library from
                flowering buds. DNA was purified  from a crude nuclear
                prep using Brassica oleracea TO1000DH3 buds  provided by
                Thosmas Osborn at the University of Wisconsin. Genomic
                DNA was provided by Pablo Rabinowicz (CSHL) and the
                shotgun library  prepared at Washington University Genome
                Sequencing Center."
IN

nment Scores:
. No.:              524             Length:         796
e:                  9.00            Matches:        9
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            2.7%            Indels:         0
                    11              Gaps:           0

0-821-670A-56 (1-328) x BZ056171 (1-796)

       73 LysThrLeuThrIleGlnValLysGlu 81
          |||||||||||||||||||||||||||
      651 AAAACATTAACAATCCAAGTGAAAGAA 625

LT 89
0584
```

```
LOCUS       BZ020584                798 bp    DNA     linear   GSS 08-OCT-2002
DEFINITION  oeg90c01.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BZ020584
VERSION     BZ020584.1  GI:23580317
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: oeg90  row: c  column: 01
            Seq primer: -21UPpOT forward
            Class: shotgun
            High quality sequence start: 120
            High quality sequence stop: 335.
FEATURES            Location/Qualifiers
     source         1. .798
                    /organism="Brassica oleracea"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:3712"
                    /clone_lib="B.oleracea002"
                    /note="Vector: pOTw13; Whole genome shotgun library from
                    flowering buds. DNA was purified  from a crude nuclear
                    prep using Brassica oleracea TO1000DH3 buds  provided by
                    Thosmas Osborn at the University of Wisconsin. Genomic
                    DNA was provided by Pablo Rabinowicz (CSHL) and the
                    shotgun library  prepared at Washington University Genome
                    Sequencing Center."
ORIGIN

Alignment Scores:
Pred. No.:              526             Length:         798
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     11              Gaps:           0

US-10-821-670A-56 (1-328) x BZ020584 (1-798)

Qy        217 HisLysLeuLysTyrGluAsnTyrThr 225
              |||||||||||||||||||||||||||
Db        687 CATAAGTTAAAATATGAAAATTATACT 713

RESULT 90
CT202661/c
LOCUS       CT202661                798 bp    DNA     linear   GSS 02-NOV-2005
DEFINITION  Sus scrofa genomic clone CH242-149M11, genomic survey sequence.
ACCESSION   CT202661
VERSION     CT202661.1  GI:79718123
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 149M11. 149M11
```

```
        is part of the CHORI-242 BAC Library created by P. de Jong. Further
        details: http://www.sanger.ac.uk/Projects/S_scrofa/.
TURES               Location/Qualifiers
  source            1. .798
                    /organism="Sus scrofa"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9823"
                    /clone="CH242-149M11"
                    /tissue_type="White blood cells"
                    /note="vector pTARBAC1.3_BamHI
                    sex female"
GIN

gnment Scores:
i. No.:               526             Length:         798
ce:                   9.00            Matches:        9
cent Similarity:      100.0%          Conservative:   0
: Local Similarity:   100.0%          Mismatches:     0
cy Match:             2.7%            Indels:         0
                      14              Gaps:           0

10-821-670A-56 (1-328) x CT202661 (1-798)

       100 SerPheLeuLeuIleHisLysLysGlu 108
           ||||||||||||||||||||||||||||
       728 TCTTTTTTACTCATCCATAAAAAAGAA 702

JLT 91
18405/c
JS        DN518405                  802 bp    mRNA    linear   EST 10-MAR-2005
INITION   1259097 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
SSION     DN518405
SION      DN518405.1  GI:60728595
WORDS     EST.
RCE       Bos taurus (cattle)
RGANISM   Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bos.
ERENCE    1  (bases 1 to 802)
UTHORS    Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
          Wray,J.E. and Keele,J.W.
ITLE      A second set of bovine ESTs from pooled-tissue normalized libraries
OURNAL    Unpublished (2003)
MENT      Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called with phred v0.020425.c and
          trimmed with the aid of the trim_alt option. Vector identified with
          cross_match v0.990329.
          Plate: RLK8037  row: F  column: 24
          Seq primer: TAGAAGGCACAGTCGAGG.
TURES               Location/Qualifiers
  source            1. .802
                    /organism="Bos taurus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9913"
                    /tissue_type="pooled"
                    /lab_host="DH10B"
                    /clone_lib="MARC 7BOV"
                    /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                    Library made with RNA pooled from multiple tissues
                    including ovary, hindbrain, uterus, and day-30 whole
                    embryos."
GIN

gnment Scores:
i. No.:               528             Length:         802
ce:                   9.00            Matches:        9
cent Similarity:      100.0%          Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.7%          Indels:         0
DB:                     9             Gaps:           0

US-10-821-670A-56 (1-328) x DN518405 (1-802)

Qy          69 LeuGlySerGlyLysThrLeuThrIle 77
               |||||||||||||||||||||||||||
Db         312 TTGGGATCAGGGAAAACATTAACCATT 286

RESULT 92
BG332928/c
LOCUS       BG332928                819 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602430781F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4548381 5',
            mRNA sequence.
ACCESSION   BG332928
VERSION     BG332928.1  GI:13139366
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1238  row: a  column: 22
            High quality sequence stop: 151.
FEATURES            Location/Qualifiers
     source         1. .819
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:4548381"
                    /tissue_type="large cell carcinoma"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_18"
                    /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCACGAG(G). Library constructed  by Ling Hong in the
                    laboratory of Gerald M. Rubin (University of  California,
                    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                    Superscript II RT (Life Technologies). Note: this is a
                    NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              538             Length:         819
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-56 (1-328) x BG332928 (1-819)

Qy          10 TrpPheSerLeuValLeuLeuAlaPro 18
               ||||||||||||||||||||||||||
Db         653 TGGTTTTCTTTAGTTCTTCTTGCTCCT 627

RESULT 93
DN521145
```

```
S       DN521145                819 bp    mRNA    linear   EST 11-MAR-2005
NITION  1263973 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
SSION   DN521145
ION     DN521145.1  GI:60961723
ORDS    EST.
CE      Bos taurus (cattle)
GANISM  Bos taurus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
        Pecora; Bovidae; Bovinae; Bos.
RENCE   1  (bases 1 to 819)
THORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
        Wray,J.E. and Keele,J.W.
TLE     A second set of bovine ESTs from pooled-tissue normalized libraries
URNAL   Unpublished (2003)
ENT     Contact: Smith TPL
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called with phred v0.020425.c and
        trimmed with the aid of the trim_alt option. Vector identified with
        cross_match v0.990329.
        Plate: RLK8037  row: F  column: 24
        Seq primer: GTAATACGACTCACTATAGGG.
URES            Location/Qualifiers
 source         1. .819
                /organism="Bos taurus"
                /mol_type="mRNA"
                /db_xref="taxon:9913"
                /tissue_type="pooled"
                /lab_host="DH10B"
                /clone_lib="MARC 7BOV"
                /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                Library made with RNA pooled from multiple tissues
                including ovary, hindbrain, uterus, and day-30 whole
                embryos."
IN

nment Scores:
. No.:              538           Length:        819
e:                  9.00          Matches:       9
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            2.7%          Indels:        0
                    9             Gaps:          0

0-821-670A-56 (1-328) x DN521145 (1-819)

       69 LeuGlySerGlyLysThrLeuThrIle 77
          |||||||||||||||||||||||||||
      512 TTGGGATCAGGGAAAACATTAACCATT 538

LT 94
6281/c
S       BF616281                829 bp    mRNA    linear   EST 22-OCT-2001
NITION  HVSMEc0006B06f Hordeum vulgare seedling shoot EST library
        HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare subsp.
        vulgare cDNA clone HVSMEc0006B06f, mRNA sequence.
SSION   BF616281
ION     BF616281.2  GI:16312057
ORDS    EST.
CE      Hordeum vulgare subsp. vulgare
GANISM  Hordeum vulgare subsp. vulgare
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
        clade; Pooideae; Triticeae; Hordeum.
RENCE   1  (bases 1 to 829)
THORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
        Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
        Fenton,R.D., Oates,R. and Main,D.
TLE     Development of a genetically and physically anchored EST resource
        for barley genomics: Morex unstressed seedling shoot cDNA library
 JOURNAL  Unpublished (2001)
COMMENT  On Dec 18, 2000 this sequence version replaced gi:11880015.
        Contact: Wing RA
        Clemson University Genomics Institute
        Clemson University
        100 Jordan Hall, Clemson, SC 29634, USA
        Tel: 864 656 7288
        Fax: 864 656 4293
        Email: rwing@clemson.edu
        Total hq bases = 100
        Seq primer: AATTAACCCTCACTAAAGGG
        High quality sequence start: 10
        High quality sequence stop: 640.
FEATURES            Location/Qualifiers
     source         1. .829
                    /organism="Hordeum vulgare subsp. vulgare"
                    /mol_type="mRNA"
                    /cultivar="Morex"
                    /sub_species="vulgare"
                    /db_xref="taxon:112509"
                    /clone="HVSMEc0006B06f"
                    /tissue_type="Seedling shoot"
                    /lab_host="TJC121"
                    /clone_lib="Hordeum vulgare seedling shoot EST library
                    HVcDNA0003 (Etiolated and unstressed)"
                    /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                    Seeds were surface sterilized then germinated under axenic
                    conditions in the dark at room temperature on filter paper
                    with water, nystatin and cefotaxime in covered
                    crystallization dishes. Five-day old seedling shoots were
                    then harvested, total RNA was prepared, poly(A) RNA was
                    purified, one primary unamplified cDNA library was made,
                    and 1 million pfu were in vivo excised to give pBluescript
                    SK(-) cDNA phagemids. These steps were performed in the TJ
                    Close laboratory at the University of California,
                    Riverside (Choi, Close, Fenton). Phagemids were plated and
                    picked at the Clemson University Genomics Institute (CUGI)
                    (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                    preparations, DNA sequencing and sequence analysis were
                    performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
                    Oates, Rambo, Main). The sequence has been trimmed to
                    remove vector sequence and contains a minimum of 100 bases
                    of phred value 20 or above. For more details on library
                    preparation and sequence analysis see
                    http://www.genome.clemson.edu/projects/barley. To order
                    this clone see http://www.genome.clemson.edu/orders Also
                    see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                    Genetically and physically anchored EST resources for
                    barley genomics. Barley Genetics Newsletter 31:29-30.
                    (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
ORIGIN

Alignment Scores:
Pred. No.:              544           Length:        829
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-56 (1-328) x BF616281 (1-829)

Qy          11 PheSerLeuValLeuLeuAlaProPro 19
               |||||||||||||||||||||||||||
Db         466 TTTTCTCTTGTCCTCCTGGCCCCCCCC 440

RESULT 95
BG582789/c
LOCUS       BG582789                841 bp    mRNA    linear   EST 11-APR-2001
DEFINITION  EST484535 GVN Medicago truncatula cDNA clone pGVN-70P19 5' end,
            mRNA sequence.
ACCESSION   BG582789
```

```
SION      BG582789.1  GI:13597853
WORDS     EST.
RCE       Medicago truncatula (barrel medic)
RGANISM   Medicago truncatula
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
          Medicago.
ERENCE    1  (bases 1 to 841)
UTHORS    Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S.,
          Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ITLE      ESTs from one month old nitrogen-fixing root nodules of Medicago
          truncatula, 2001
OURNAL    Unpublished (2001)
MENT      Contact: Carroll P. Vance
          Department of Agronomy and Plant Genetics
          University of Minnesota
          411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
          Tel: 612 625 5715
          Fax: 651-649-5058
          Email: vance004@maroon.tc.umn.edu
          University of Minnesota name: M383861e TIGR sequence name:
          MTCDY94TK More information is available at: http://www.medicago.org
          Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
TURES               Location/Qualifiers
  source            1. .841
                    /organism="Medicago truncatula"
                    /mol_type="mRNA"
                    /cultivar="genotype A17"
                    /db_xref="taxon:3880"
                    /clone="pGVN-70P19"
                    /tissue_type="N2-fixing root nodules"
                    /dev_stage="effective root nodules harvested one month
                    post inoculation with Sinorhizobium meliloti"
                    /lab_host="E. coli strain XLOLR"
                    /clone_lib="GVN"
                    /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                    XhoI; cDNA was prepared from polyA+ enriched RNA from
                    effective root nodules harvested one month post
                    inoculation with Sinorhizobium meliloti. The cDNA was
                    directionally ligated into the Uni-ZAP XR vector from
                    Stratagene and packaged using Gigapack III Gold packaging
                    extracts. Plasmids containing cDNA inserts were excised
                    from the recombinant lambda-ZAP phage using Ex-Assist
                    helper phage and propagated in XLOLR cells."
GIN

gnment Scores:
i. No.:              551            Length:        841
ce:                  9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
: Local Similarity:  100.0%         Mismatches:    0
cy Match:            2.7%           Indels:        0
                     2              Gaps:          0

10-821-670A-56 (1-328) x BG582789 (1-841)

       281 LysAsnAsnArgGluLysLysAspArg 289
           |||||||||||||||||||||||||||
       136 AAAAACAATAGAGAAAAAAAAGATAGA 110

ULT 96
51254/c
JS        CR551254                 864 bp    mRNA    linear   EST 24-MAR-2005
INITION   CR551254 Normalized and Subtracted bovine embryonic and
          extraembryonic tissues (bcaz/BE03) Bos taurus cDNA clone
          bcaz0001.m.23 5', mRNA sequence.
SSION     CR551254
SION      CR551254.2  GI:61760533
WORDS     EST.
RCE       Bos taurus (cattle)
RGANISM   Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1  (bases 1 to 864)
  AUTHORS Renard,J.P., Lewin,H.A., Yang,J., Hernandez,A., Degrelle,S.,
          Everts,R.E. and Hue,I.
  TITLE   Embryonic ESTs (bcaz)
  JOURNAL Unpublished (2004)
COMMENT   On Jul 12, 2004 this sequence version replaced gi:50246164.
          Contact: Renard JP
          Biologie du Developpement et Reproduction
          INRA
          Domaine de Vilvert 78350 Jouy en Josas, FRANCE
          Email: jean-paul.renard@jouy.inra.fr
          Sequence cleaned of vector, adaptator and repetitions. Contact us
          at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
          sequence. AGENAE Resource centre. Francois PIUMI,
          Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
          genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
          FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
          Plate: bcaz0001a  row: m  column: 23.
FEATURES            Location/Qualifiers
     source         1. .864
                    /organism="Bos taurus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9913"
                    /clone="bcaz0001.m.23"
                    /tissue_type="embryo (day 36 and day 64), extra-embryonic
                    tissue (day 14 to 25)"
                    /lab_host="DH10B"
                    /clone_lib="Normalized and Subtracted bovine embryonic and
                    extraembryonic tissues (bcaz/BE03)"
                    /note="Vector: pGEMZf11; Funding for EST sequencing was
                    provided by funds dedicated to J.P.RENARD (BDR, Inra).
                    Funding for construction and subtraction of the cDNA
                    library was provided by USDA ARS contract No 58-1275-2-020
                    to H. A. Lewin The cDNA library was constructed,
                    normalized and subtracted by Dr. A. Hernandez (W.M. Keck
                    Center, University of Illinois Urbana-Champaign) and S.
                    Degrelle (BDR, Inra) as described in Bonaldo et al.(1996),
                    Genome Research 6, 791-806. BE03 library is a normalized
                    library of embryonic tissues subtracted with 7800 known
                    EST sequences. The double-stranded cDNA was size selected
                    (>450 bp), adaptored with EcoRI adaptors at both ends and
                    digested with NotI. The cDNA was then directionally cloned
                    into EcoRI-NotI digested pGEM11Zf(+) phagemid vector.
                    Insert size was between 450-2200 bp. Tagged oligo-dT was
                    used to identify the origin of the ESTs where possible.
                    (A18)TGCGT = extraembryonic tissue; (A18)TCGGT = 36-day
                    oldfetus; (A18)TGCGA = 64-day old fetus (organs);
                    (A18)TCGGA = 64-day old fetus (body)"
ORIGIN

Alignment Scores:
Pred. No.:              564            Length:        864
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            2.7%           Indels:        0
DB:                     8              Gaps:          0

US-10-821-670A-56 (1-328) x CR551254 (1-864)

Qy          99 HisSerPheLeuLeuIleHisLysLys 107
               |||||||||||||||||||||||||||
Db         791 CATTCATTTCTTTTAATTCACAAAAAG 765

RESULT 97
AQ895672/c
LOCUS       AQ895672                 876 bp    DNA     linear   GSS 10-NOV-1999
DEFINITION  HS_4861_B1_B07_T7A CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=4861 Col=13 Row=D, genomic survey
            sequence.
ACCESSION   AQ895672
```

```
ION     AQ895672.1  GI:6351862
ORDS    GSS.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 876)
THORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
        Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
        Hood,L.
TLE     Sequence-tagged connectors: A sequence approach to mapping and
        scanning the human genome
URNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
UBMED   10449764
ENT     Contact: Mahairas GG, Wallace JC, Hood L
        High Throughput Sequencing Center
        University of Washington
        401 Queen Anne Avenue North, Seattle, WA 98109, USA
        Tel: (206) 616-3618
        Fax: (206) 616-3887
        Email: jwallace@u.washington.edu
        Clones may be purchased from Research Genetics (info@resgen.com).
        BAC end Web Server: http://www.htsc.washington.edu
        Plate: 4861  row: D  column: 13
        Seq primer: T7
        Class: BAC ends
        High quality sequence stop: 876.
URES            Location/Qualifiers
 source         1. .876
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Plate=4861 Col=13 Row=D"
                /sex="male"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                E-Coli DH10B"
IN
```

nment Scores:			
. No.:	571	Length:	876
e:	9.00	Matches:	9
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	2.7%	Indels:	0
	11	Gaps:	0

```
0-821-670A-56 (1-328) x AQ895672 (1-876)

       14 ValLeuLeuAlaProProLeuMetAla 22
          ||||||||||||||||||||||||||||
      642 GTCCTCCTGGCTCCCCCACTCATGGCC 616

LT 98
5638/c
S       CX115638                 893 bp    mRNA    linear   EST 03-JUN-2005
NITION  EI100A06 A normalized whole-life-cycle cDNA library of rice Oryza
        sativa (indica cultivar-group) cDNA clone EI100A06 5', mRNA
        sequence.
SSION   CX115638
ION     CX115638.1  GI:66928790
ORDS    EST.
CE      Oryza sativa (indica cultivar-group)
GANISM  Oryza sativa (indica cultivar-group)
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
        clade; Ehrhartoideae; Oryzeae; Oryza.
RENCE   1  (bases 1 to 893)
THORS   Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan,D.,
        Han,B., Zhang,Q. and Wang,S.
TLE     Features of the expressed sequences revealed by a large-scale
        analysis of ESTs from a normalized cDNA library of the elite indica
        rice cultivar Minghui 63
  JOURNAL   Plant J. 42 (5), 772-780 (2005)
   PUBMED   15918889
COMMENT     Contact: Wang S
            National Key Laboratory of Crop Genetic Improvement
            Hauzhong Agricultural University
            Wuhan 430070, China
            Tel: 86-27-87282044
            Fax: 86-27-87287092
            Email: shipingwang@hotmail.com
            Seq primer: T7.
FEATURES            Location/Qualifiers
     source         1. .893
                    /organism="Oryza sativa (indica cultivar-group)"
                    /mol_type="mRNA"
                    /strain="indica"
                    /cultivar="Minghui 63"
                    /db_xref="taxon:39946"
                    /clone="EI100A06"
                    /tissue_type="whole plant"
                    /dev_stage="whole-life-cycle"
                    /lab_host="E. coli DH10B"
                    /clone_lib="A normalized whole-life-cycle cDNA library of
                    rice"
                    /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; The
                    library is constructed based on the strategy of satuation
                    hybridization with genomic DNA using rice cultivar Minghui
                    63. This library consists of cDNA from 15 directionally
                    cloned cDNA libraries constructed with different tissues
                    from 9 developmental stages."
ORIGIN

Alignment Scores:
```

Pred. No.:	581	Length:	893
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	8	Gaps:	0

```
US-10-821-670A-56 (1-328) x CX115638 (1-893)

Qy         12 SerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||
Db        680 AGCTTGGTCCTTTTAGCCCCCCCCCTC 654

RESULT 99
BI258748
LOCUS       BI258748                 894 bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  602970329F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109966 5',
            mRNA sequence.
ACCESSION   BI258748
VERSION     BI258748.1  GI:14815408
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11266  row: i  column: 07
```

```
        High quality sequence stop: 851.
TURES             Location/Qualifiers
  source          1. .894
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:5109966"
                  /tissue_type="cervical carcinoma cell line"
                  /lab_host="DH10B"
                  /clone_lib="NIH_MGC_12"
                  /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                  Average insert size 1.4 kb. Library prepared by Life
                  Technologies."
GIN

gnment Scores:
d. No.:              582           Length:        894
re:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
: Local Similarity:  100.0%        Mismatches:    0
ry Match:            2.7%          Indels:        0
                     2             Gaps:          0

10-821-670A-56 (1-328) x BI258748 (1-894)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       699 TTTTTACTGATTCACAAAAAGGAAGAC 725

JLT 100
38766
JS       BI088766                 895 bp    mRNA    linear   EST 20-JUN-2001
INITION  602851556F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4993380 5',
         mRNA sequence.
SSION    BI088766
SION     BI088766.1  GI:14507096
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 895)
UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL   Unpublished (1999)
MENT     Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: Incyte Genomics, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM11013  row: o  column: 13
         High quality sequence stop: 623.
TURES             Location/Qualifiers
  source          1. .895
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:4993380"
                  /cell_line="MGC36"
                  /lab_host="DH10B"
                  /clone_lib="NIH_MGC_10"
                  /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                  Average insert size 1.5 kb. Library prepared by Life
                  Technologies."
GIN
```

```
Alignment Scores:
Pred. No.:              582           Length:        895
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     2             Gaps:          0

US-10-821-670A-56 (1-328) x BI088766 (1-895)

Qy        279 GlnGlyLysAsnAsnArgGluLysLys 287
              |||||||||||||||||||||||||||
Db        837 CAGGGGAAAAACAATAGAGAGAAGAAA 863


Search completed: June 10, 2006, 16:34:56
Job time : 4560.78 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

on: June 10, 2006, 01:43:45 ; Search time 186.981 Seconds
(without alignments)
4923.420 Million cell updates/sec

le: US-10-821-670A-56
ect score: 328
ience: 1 MHPQQLVIAWFSLVLLAPPL.....VQARDRYYSSSWSNWASVSC 328

ring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

rched: 1403666 seqs, 935554401 residues

d size: 1

al number of hits satisfying chosen parameters: 2800955

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Listing first 200 summaries

mand line parameters:
DEL=frame+_p2n.model -DEV=xlp
/abss/ABSSWEB_spool/US10821670/runat_07062006_110458_27682/app_query.fasta_1
=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rni
NMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
ANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
IGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
XLEN=2000000000 -HOST=abss05p
ER=US10821670_@CGN_1_1_677_@runat_07062006_110458_27682 -NCPU=6 -ICPU=3
_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
RN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
APOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

abase : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt No.	Score	% Query Match	Length	DB	ID	Description
1	328	100.0	985	3	US-09-917-265A-55	Sequence 55, Appl
2	328	100.0	985	3	US-09-917-265A-57	Sequence 57, Appl
3	328	100.0	987	3	US-09-917-265A-29	Sequence 29, Appl
4	328	100.0	987	3	US-09-917-265A-31	Sequence 31, Appl
5	316	96.3	2193	3	US-09-011-143-5	Sequence 5, Appli
6	316	96.3	2193	3	US-09-302-495-5	Sequence 5, Appli
7	316	96.3	2193	3	US-10-079-616-5	Sequence 5, Appli
8	306	93.3	921	3	US-09-011-143-6	Sequence 6, Appli
9	306	93.3	921	3	US-09-011-143-7	Sequence 7, Appli
10	306	93.3	921	3	US-09-302-495-6	Sequence 6, Appli
11	306	93.3	921	3	US-09-302-495-7	Sequence 7, Appli
12	306	93.3	921	3	US-10-079-616-6	Sequence 6, Appli
13	306	93.3	921	3	US-10-079-616-7	Sequence 7, Appli
14	216	65.9	1599	3	US-09-917-265A-38	Sequence 38, Appl
c 15	216	65.9	1599	3	US-09-917-265A-40	Sequence 40, Appl
16	205	62.5	921	3	US-09-917-265A-26	Sequence 26, Appl
c 17	205	62.5	921	3	US-09-917-265A-28	Sequence 28, Appl
18	205	62.5	1533	3	US-09-917-265A-43	Sequence 43, Appl
c 19	205	62.5	1533	3	US-09-917-265A-45	Sequence 45, Appl
20	37	11.3	921	3	US-09-917-265A-52	Sequence 52, Appl
c 21	37	11.3	921	3	US-09-917-265A-54	Sequence 54, Appl
22	37	11.3	987	3	US-09-917-265A-58	Sequence 58, Appl
c 23	37	11.3	987	3	US-09-917-265A-60	Sequence 60, Appl
24	37	11.3	990	3	US-09-079-984A-1	Sequence 1, Appli
25	37	11.3	990	3	US-09-079-984A-11	Sequence 11, Appl
26	37	11.3	990	3	US-09-390-729-1	Sequence 1, Appli
27	37	11.3	990	3	US-09-390-729-11	Sequence 11, Appl
28	37	11.3	1533	3	US-09-917-265A-66	Sequence 66, Appl
c 29	37	11.3	1533	3	US-09-917-265A-68	Sequence 68, Appl
30	37	11.3	1599	3	US-09-917-265A-61	Sequence 61, Appl
c 31	37	11.3	1599	3	US-09-917-265A-63	Sequence 63, Appl
32	37	11.3	2267	3	US-09-917-265A-107	Sequence 107, App
c 33	37	11.3	2267	3	US-09-917-265A-109	Sequence 109, App
34	35	10.7	987	2	US-08-186-529-1	Sequence 1, Appli
35	35	10.7	987	2	US-08-640-386A-1	Sequence 1, Appli
36	35	10.7	1018	2	US-08-184-009-194	Sequence 194, App
37	35	10.7	1018	2	US-08-458-356-194	Sequence 194, App
38	35	10.7	1018	3	US-08-460-736-194	Sequence 194, App
39	35	10.7	1018	3	US-09-535-370-194	Sequence 194, App
40	35	10.7	1018	3	US-09-663-667-194	Sequence 194, App
41	35	10.7	1389	3	US-09-634-368-4	Sequence 4, Appli
42	35	10.7	1399	2	US-08-751-767A-3	Sequence 3, Appli
43	35	10.7	1560	2	US-08-751-767A-11	Sequence 11, Appl
44	35	10.7	1623	2	US-08-751-767A-9	Sequence 9, Appli
45	35	10.7	2307	3	US-09-949-016-5452	Sequence 5452, Ap
46	35	10.7	2362	2	US-08-265-087-1	Sequence 1, Appli
47	35	10.7	2362	2	US-08-621-493-1	Sequence 1, Appli
48	35	10.7	2362	2	US-08-965-688-1	Sequence 1, Appli
49	35	10.7	2362	3	US-09-260-173-1	Sequence 1, Appli
50	35	10.7	2362	3	US-09-924-703-3	Sequence 3, Appli
51	35	10.7	6139	2	US-08-751-767A-7	Sequence 7, Appli
52	23	7.0	987	3	US-08-848-760B-24	Sequence 24, Appl
53	23	7.0	987	3	US-09-826-025-24	Sequence 24, Appl
54	23	7.0	1870	3	US-09-310-842-4	Sequence 4, Appli
55	23	7.0	2318	3	US-09-851-062-3	Sequence 3, Appli
56	23	7.0	2318	3	US-09-949-016-315	Sequence 315, App
57	22	6.7	16002	3	US-09-949-016-12057	Sequence 12057, A
58	22	6.7	16003	3	US-09-949-016-17194	Sequence 17194, A
59	17	5.2	73	3	US-09-823-549-77	Sequence 77, Appl
c 60	17	5.2	601	3	US-09-949-016-24253	Sequence 24253, A
c 61	17	5.2	601	3	US-09-949-016-190686	Sequence 190686,
62	17	5.2	1061	2	US-08-385-335A-13	Sequence 13, Appl
63	17	5.2	1409	3	US-09-634-368-3	Sequence 3, Appli
64	17	5.2	1472	3	US-09-634-368-2	Sequence 2, Appli
65	17	5.2	1569	3	US-09-634-368-12	Sequence 12, Appl
66	17	5.2	2013	3	US-09-634-368-11	Sequence 11, Appl
67	17	5.2	2709	3	US-09-634-368-13	Sequence 13, Appl
68	17	5.2	6295	2	US-08-659-206A-4	Sequence 4, Appli
69	17	5.2	7287	2	US-08-659-206A-1	Sequence 1, Appli
70	12	3.7	38	3	US-09-011-143-12	Sequence 12, Appl
71	12	3.7	38	3	US-09-302-495-12	Sequence 12, Appl
72	12	3.7	38	3	US-10-079-616-12	Sequence 12, Appl
c 73	12	3.7	601	3	US-09-949-016-24250	Sequence 24250, A
c 74	12	3.7	601	3	US-09-949-016-24251	Sequence 24251, A
c 75	12	3.7	601	3	US-09-949-016-190683	Sequence 190683,
c 76	12	3.7	601	3	US-09-949-016-190684	Sequence 190684,
77	9	2.7	28	3	US-09-917-265A-85	Sequence 85, Appl
78	9	2.7	37	3	US-09-917-265A-87	Sequence 87, Appl
79	9	2.7	532	3	US-09-513-999C-4018	Sequence 4018, Ap
80	8	2.4	25	3	US-09-887-145-37	Sequence 37, Appl

81	8	2.4	25	3	US-09-917-265A-86	Sequence 86, Appl
82	8	2.4	32	3	US-09-011-143-13	Sequence 13, Appl
83	8	2.4	32	3	US-09-302-495-13	Sequence 13, Appl
84	8	2.4	32	3	US-10-079-616-13	Sequence 13, Appl
85	8	2.4	37	3	US-09-917-265A-99	Sequence 99, Appl
86	8	2.4	39	3	US-09-079-984A-13	Sequence 13, Appl
87	8	2.4	39	3	US-09-390-729-13	Sequence 13, Appl
88	8	2.4	44	3	US-09-011-143-14	Sequence 14, Appl
89	8	2.4	44	3	US-09-302-495-14	Sequence 14, Appl
90	8	2.4	44	3	US-10-079-616-14	Sequence 14, Appl
91	8	2.4	427	3	US-09-270-767-2298	Sequence 2298, Ap
92	8	2.4	427	3	US-09-270-767-17580	Sequence 17580, A
93	8	2.4	540	3	US-09-445-724B-13	Sequence 13, Appl
94	8	2.4	549	3	US-09-533-559-4743	Sequence 4743, Ap
95	8	2.4	601	3	US-09-949-016-70299	Sequence 70299, A
96	8	2.4	601	3	US-09-949-016-87513	Sequence 87513, A
97	8	2.4	601	3	US-09-949-016-110703	Sequence 110703,
98	8	2.4	601	3	US-09-949-016-110704	Sequence 110704,
99	8	2.4	601	3	US-09-949-016-110705	Sequence 110705,
00	8	2.4	601	3	US-09-949-016-138629	Sequence 138629,
01	8	2.4	601	3	US-09-949-016-168993	Sequence 168993,
02	8	2.4	601	3	US-09-949-016-168994	Sequence 168994,
03	8	2.4	601	3	US-09-949-016-168995	Sequence 168995,
04	8	2.4	601	3	US-09-949-016-202770	Sequence 202770,
05	8	2.4	633	5	US-09-974-300-5194	Sequence 5194, Ap
06	8	2.4	830	3	US-09-621-976-1463	Sequence 1463, Ap
07	8	2.4	885	3	US-09-328-352-1423	Sequence 1423, Ap
08	8	2.4	2961	3	US-09-949-016-2226	Sequence 2226, Ap
09	8	2.4	3342	2	US-08-254-989-1	Sequence 1, Appli
10	8	2.4	5874	3	US-08-843-417-9	Sequence 9, Appli
11	8	2.4	5874	3	US-09-527-013-9	Sequence 9, Appli
12	8	2.4	6758	3	US-09-902-540-1033	Sequence 1033, Ap
13	8	2.4	7173	3	US-09-949-016-17491	Sequence 17491, A
14	8	2.4	14185	3	US-09-949-016-14809	Sequence 14809, A
15	8	2.4	17085	3	US-09-949-016-16507	Sequence 16507, A
16	8	2.4	28976	3	US-09-949-002-689	Sequence 689, App
17	8	2.4	28976	3	US-09-949-002-698	Sequence 698, App
18	8	2.4	41815	3	US-09-949-016-17447	Sequence 17447, A
19	8	2.4	68444	3	US-09-949-016-13968	Sequence 13968, A
20	8	2.4	72843	3	US-09-949-016-12574	Sequence 12574, A
21	8	2.4	81927	3	US-09-949-016-15623	Sequence 15623, A
22	8	2.4	87350	3	US-08-781-891-79	Sequence 79, Appl
23	8	2.4	87350	3	US-09-618-166-79	Sequence 79, Appl
24	8	2.4	87543	3	US-09-791-211-3	Sequence 3, Appli
25	8	2.4	104428	3	US-09-949-016-12737	Sequence 12737, A
26	8	2.4	104429	3	US-09-949-016-13814	Sequence 13814, A
27	8	2.4	145320	3	US-09-949-016-15858	Sequence 15858, A
28	8	2.4	168575	3	US-09-426-290-1	Sequence 1, Appli
29	8	2.4	194889	3	US-09-949-016-15654	Sequence 15654, A
30	8	2.4	393753	3	US-09-949-016-14573	Sequence 14573, A
31	8	2.4	393753	3	US-09-949-016-14574	Sequence 14574, A
32	8	2.4	670689	3	US-09-949-016-12505	Sequence 12505, A
33	8	2.4	670690	3	US-09-949-016-14207	Sequence 14207, A
34	8	2.4	784019	3	US-09-949-016-14033	Sequence 14033, A
35	8	2.4	818128	3	US-09-949-016-14546	Sequence 14546, A
36	8	2.4	818128	3	US-09-949-016-14547	Sequence 14547, A
37	8	2.4	818128	3	US-09-949-016-14548	Sequence 14548, A
38	8	2.4	818128	3	US-09-949-016-14549	Sequence 14549, A
39	8	2.4	818128	3	US-09-949-016-14550	Sequence 14550, A
40	8	2.4	818128	3	US-09-949-016-14551	Sequence 14551, A
41	8	2.4	818128	3	US-09-949-016-14552	Sequence 14552, A
42	8	2.4	818128	3	US-09-949-016-14553	Sequence 14553, A
43	8	2.4	818128	3	US-09-949-016-14554	Sequence 14554, A
44	8	2.4	818128	3	US-09-949-016-14555	Sequence 14555, A
45	8	2.4	818128	3	US-09-949-016-14556	Sequence 14556, A
46	8	2.4	818128	3	US-09-949-016-14557	Sequence 14557, A
47	8	2.4	818128	3	US-09-949-016-14558	Sequence 14558, A
48	8	2.4	818128	3	US-09-949-016-14559	Sequence 14559, A
49	8	2.4	818128	3	US-09-949-016-14560	Sequence 14560, A
50	8	2.4	818128	3	US-09-949-016-14561	Sequence 14561, A
51	8	2.4	818128	3	US-09-949-016-14562	Sequence 14562, A
52	8	2.4	818128	3	US-09-949-016-14564	Sequence 14564, A
53	8	2.4	818128	3	US-09-949-016-14565	Sequence 14565, A
c 154	8	2.4	818128	3	US-09-949-016-14566	Sequence 14566, A
c 155	8	2.4	818128	3	US-09-949-016-14567	Sequence 14567, A
c 156	8	2.4	828152	3	US-09-949-016-12777	Sequence 12777, A
157	8	2.4	1830121	3	US-09-557-884-1	Sequence 1, Appli
158	8	2.4	1830121	3	US-09-643-990A-1	Sequence 1, Appli
159	8	2.4	1830121	3	US-10-158-865-1	Sequence 1, Appli
160	7	2.1	24	3	US-09-823-549-48	Sequence 48, Appl
161	7	2.1	25	3	US-09-396-196G-42419	Sequence 42419, A
162	7	2.1	25	3	US-09-396-196G-42420	Sequence 42420, A
c 163	7	2.1	37	4	US-09-701-271A-7	Sequence 7, Appli
164	7	2.1	44	2	US-08-823-516-115	Sequence 115, App
165	7	2.1	44	3	US-08-759-038-123	Sequence 123, App
166	7	2.1	44	3	US-08-758-314-123	Sequence 123, App
167	7	2.1	44	3	US-09-684-938-123	Sequence 123, App
168	7	2.1	44	3	US-09-308-825A-123	Sequence 123, App
169	7	2.1	44	3	US-09-940-244-115	Sequence 115, App
170	7	2.1	44	3	US-09-381-212-115	Sequence 115, App
171	7	2.1	44	3	US-09-713-601A-115	Sequence 115, App
172	7	2.1	45	3	US-09-777-430C-60	Sequence 60, Appl
173	7	2.1	50	2	US-08-823-516-118	Sequence 118, App
174	7	2.1	50	3	US-08-759-038-126	Sequence 126, App
175	7	2.1	50	3	US-08-758-314-126	Sequence 126, App
176	7	2.1	50	3	US-09-940-244-118	Sequence 118, App
177	7	2.1	50	3	US-09-381-212-118	Sequence 118, App
178	7	2.1	50	3	US-09-713-601A-118	Sequence 118, App
179	7	2.1	51	3	US-09-684-938-126	Sequence 126, App
180	7	2.1	51	3	US-09-308-825A-126	Sequence 126, App
181	7	2.1	178	3	US-09-513-999C-35523	Sequence 35523, A
182	7	2.1	186	3	US-09-489-039A-260	Sequence 260, App
183	7	2.1	241	3	US-09-270-767-8558	Sequence 8558, Ap
184	7	2.1	241	3	US-09-270-767-23840	Sequence 23840, A
c 185	7	2.1	259	3	US-09-513-999C-29666	Sequence 29666, A
186	7	2.1	287	3	US-09-313-294A-2940	Sequence 2940, Ap
c 187	7	2.1	295	3	US-09-082-092-2	Sequence 2, Appli
c 188	7	2.1	295	3	US-09-885-722A-2	Sequence 2, Appli
189	7	2.1	300	4	US-09-297-648-247	Sequence 247, App
c 190	7	2.1	327	3	US-09-513-999C-320	Sequence 320, App
c 191	7	2.1	331	3	US-09-513-999C-33699	Sequence 33699, A
c 192	7	2.1	338	3	US-09-513-999C-30716	Sequence 30716, A
c 193	7	2.1	378	3	US-09-513-999C-21946	Sequence 21946, A
c 194	7	2.1	383	3	US-09-621-976-15609	Sequence 15609, A
195	7	2.1	405	3	US-09-270-767-8945	Sequence 8945, Ap
196	7	2.1	405	3	US-09-270-767-24227	Sequence 24227, A
197	7	2.1	414	3	US-09-893-737-103	Sequence 103, App
198	7	2.1	421	4	US-09-880-107-3615	Sequence 3615, Ap
199	7	2.1	423	5	US-09-974-300-6739	Sequence 6739, Ap
c 200	7	2.1	430	3	US-09-621-976-1556	Sequence 1556, Ap

ALIGNMENTS

```
RESULT 1
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
```

LOCATION: (1)..(984)
09-917-265A-55

gnment Scores:

d. No.:	0	Length:	985
ce:	328.00	Matches:	328
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
cy Match:	100.0%	Indels:	0
	3	Gaps:	0

10-821-670A-56 (1-328) x US-09-917-265A-55 (1-985)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
```

```
Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984
```

RESULT 2
US-09-917-265A-57/c
; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-57

Alignment Scores:

Pred. No.:	0	Length:	985
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-917-265A-57 (1-985)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
```

```
      505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
      445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
      385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
      325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
      265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
      205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
      145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
       85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

      321 SerAsnTrpAlaSerValSerCys 328
       25 AGCAACTGGGCATCCGTGTCCTGC 2
```

```
LT 3
9-917-265A-29
quence 29, Application US/09917265A
tent No. 6818444
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 29
LENGTH: 987
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(987)
9-917-265A-29

nment Scores:
. No.:              0           Length:        987
e:                  328.00      Matches:       328
ent Similarity:     100.0%      Conservative:  0
 Local Similarity:  100.0%      Mismatches:    0
y Match:            100.0%      Indels:        0
                    3           Gaps:          0

0-821-670A-56 (1-328) x US-09-917-265A-29 (1-987)

        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
        1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
```

```
Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984
```

```
RESULT 4
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
```

```
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 31
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Felis catus
09-917-265A-31

gnment Scores:
i. No.:              0              Length:        987
ce:                  328.00         Matches:       328
cent Similarity:     100.0%         Conservative:  0
: Local Similarity:  100.0%         Mismatches:    0
cy Match:            100.0%         Indels:        0
                     3              Gaps:          0

10-821-670A-56 (1-328) x US-09-917-265A-31 (1-987)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||
Db       27 AGCAACTGGGCATCCGTGTCCTGC 4

RESULT 5
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

Alignment Scores:
Pred. No.:              0              Length:        2193
Score:                  316.00         Matches:       316
Percent Similarity:     100.0%         Conservative:  0
```

```
 Local Similarity:  100.0%          Mismatches:     0
y Match:            96.3%           Indels:         0
                    3               Gaps:           0

0-821-670A-56 (1-328) x US-09-011-143-5 (1-2193)

       13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

       33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

       53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

       73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

       93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

      113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

      133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

      153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

      173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

      193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

      213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

      233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

      253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

      273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

      293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

      313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
          |||||||||||||||||||||||||||||||||||||||||||||||||
     1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 1047

LT 6
9-302-495-5
quence 5, Application US/09302495
```

```
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

Alignment Scores:
Pred. No.:                0              Length:         2193
Score:                    316.00         Matches:        316
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              96.3%          Indels:         0
DB:                       3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-302-495-5 (1-2193)

Qy          13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

Qy          33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy          53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy          73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

 93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
    ||||||||||||||||||||||||||||||||||||||||||||||||
1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 1047

JLT 7
L0-079-616-5
equence 5, Application US/10079616
itent No. 6566097
GENERAL INFORMATION:
     APPLICANT: IMAMURA, Takayuki
                MAEDA, Hiroaki
                FUJIYASU, Takeshi
                IMAGAWA, Yoshitaka
                TOKIYOSHI, Sachio
     TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
     NUMBER OF SEQUENCES: 26
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: BROWDY AND NEIMARK
          STREET: 419 Seventh Street, N.W., Suite 300
          CITY: Washington
          STATE: D.C.
          COUNTRY: USA
          ZIP: 20004
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2193 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.:                0                Length:          2193
Score:                    316.00           Matches:         316
Percent Similarity:       100.0%           Conservative:    0
Best Local Similarity:    100.0%           Mismatches:      0
Query Match:              96.3%            Indels:          0
DB:                       3                Gaps:            0

US-10-821-670A-56 (1-328) x US-10-079-616-5 (1-2193)

Qy          13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

Qy          33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy          53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy          73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

Qy          93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

Qy         113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

Qy         133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

Qy         153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

Qy         173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
      580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

      193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

      213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

      233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

      253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

      273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

      293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

      313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
          ||||||||||||||||||||||||||||||||||||||||||||||||
     1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 1047

LT 8
9-011-143-6
quence 6, Application US/09011143
tent No. 6472509
ENERAL INFORMATION:
 APPLICANT:  IMAMURA, Takayuki
 APPLICANT:  MAEDA, Hiroaki
 APPLICANT:  FUJIYASU, Takeshi
 APPLICANT:  IMAGAWA, Yoshitaka
 APPLICANT:  TOKIYOSHI, Sachio
 TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
 NUMBER OF SEQUENCES:  26
 CORRESPONDENCE ADDRESS:
   ADDRESSEE:  BROWDY AND NEIMARK
   STREET:  419 Seventh Street, N.W., Suite 300
   CITY:  Washington
   STATE:  D.C.
   COUNTRY:  USA
   ZIP:  20004
 COMPUTER READABLE FORM:
   MEDIUM TYPE:  Floppy disk
   COMPUTER:  IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:  PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/09/011,143
   FILING DATE:  04-FEB-1998
   CLASSIFICATION:  536
 PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  PCT/JP97/01824
   FILING DATE:  29-MAY-1997
 PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  JP 165249/1996
   FILING DATE:  04-JUN-1996
 ATTORNEY/AGENT INFORMATION:
   NAME:  BROWDY, Roger L.
   REGISTRATION NUMBER:  25,618
   REFERENCE/DOCKET NUMBER:  IMAMURA=1
 TELECOMMUNICATION INFORMATION:
   TELEPHONE:  202-628-5197
   TELEFAX:  202-737-3528
NFORMATION FOR SEQ ID NO:  6:
 SEQUENCE CHARACTERISTICS:

;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6

Alignment Scores:
Pred. No.:                0              Length:          921
Score:                    306.00         Matches:         306
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              93.3%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-56 (1-328) x US-09-011-143-6 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
```

```
      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

      323 TrpAlaSerValSerCys 328
          ||||||||||||||||||
      901 TGGGCATCCGTGTCCTGC 918

JLT 9
)9-011-143-7
equence 7, Application US/09011143
atent No. 6472509
GENERAL INFORMATION:
  APPLICANT:  IMAMURA, Takayuki
  APPLICANT:  MAEDA, Hiroaki
  APPLICANT:  FUJIYASU, Takeshi
  APPLICANT:  IMAGAWA, Yoshitaka
  APPLICANT:  TOKIYOSHI, Sachio
  TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
  NUMBER OF SEQUENCES:  26
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  BROWDY AND NEIMARK
    STREET:  419 Seventh Street, N.W., Suite 300
    CITY:  Washington
    STATE:  D.C.
    COUNTRY:  USA
    ZIP:  20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/011,143
    FILING DATE:  04-FEB-1998
    CLASSIFICATION:  536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/JP97/01824
    FILING DATE:  29-MAY-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  JP 165249/1996
    FILING DATE:  04-JUN-1996
  ATTORNEY/AGENT INFORMATION:
    NAME:  BROWDY, Roger L.
    REGISTRATION NUMBER:  25,618
    REFERENCE/DOCKET NUMBER:  IMAMURA=1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  202-628-5197
    TELEFAX:  202-737-3528
NFORMATION FOR SEQ ID NO:  7:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  921 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
)9-011-143-7

gnment Scores:
l. No.:                0              Length:          921
re:                    306.00         Matches:         306
cent Similarity:       100.0%         Conservative:    0
: Local Similarity:    100.0%         Mismatches:      0
cy Match:              93.3%          Indels:          0
                       3              Gaps:            0

10-821-670A-56 (1-328) x US-09-011-143-7 (1-921)

       23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

       43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

       63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

       83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

      103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

      123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

      143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

      163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

      243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

      323 TrpAlaSerValSerCys 328
          ||||||||||||||||||
      901 TGGGCATCCGTGTCCTGC 918

RESULT 10
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
```

```
        STREET: 419 Seventh Street, N.W., Suite 300
        CITY: Washington
        STATE: D.C.
        COUNTRY: USA
        ZIP: 20004
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/302,495
        FILING DATE: 30-Apr-1999
        CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/09/011,143
        FILING DATE: 04-FEB-1998
        APPLICATION NUMBER: PCT/JP97/01824
        FILING DATE: 29-MAY-1997
        APPLICATION NUMBER: JP 165249/1996
        FILING DATE: 04-JUN-1996
    ATTORNEY/AGENT INFORMATION:
        NAME: BROWDY, Roger L.
        REGISTRATION NUMBER: 25,618
        REFERENCE/DOCKET NUMBER: IMAMURA=1
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 202-628-5197
        TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 921 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: cDNA
    SEQUENCE DESCRIPTION: SEQ ID NO: 6:
9-302-495-6

nment Scores:
. No.:              0              Length:         921
e:                  306.00         Matches:        306
ent Similarity:     100.0%         Conservative:   0
 Local Similarity:  100.0%         Mismatches:     0
y Match:            93.3%          Indels:         0
                    3              Gaps:           0

0-821-670A-56 (1-328) x US-09-302-495-6 (1-921)

       23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

       43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

       63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

       83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

      103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

      123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

      143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy    163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy    183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy    203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy    223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy    243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy    263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy    283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy    303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy    323 TrpAlaSerValSerCys 328
          |||||||||||||||||
Db    901 TGGGCATCCGTGTCCTGC 918

RESULT 11
US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
```

```
        FILING DATE: 04-JUN-1996
      ATTORNEY/AGENT INFORMATION:
        NAME: BROWDY, Roger L.
        REGISTRATION NUMBER: 25,618
        REFERENCE/DOCKET NUMBER: IMAMURA=1
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 202-628-5197
        TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 7:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 921 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
09-302-495-7

gnment Scores:
i. No.:              0            Length:        921
re:                  306.00       Matches:       306
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            93.3%        Indels:        0
                     3            Gaps:          0

10-821-670A-56 (1-328) x US-09-302-495-7 (1-921)

        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy     263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy     283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy     303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy     323 TrpAlaSerValSerCys 328
           |||||||||||||||||
Db     901 TGGGCATCCGTGTCCTGC 918

RESULT 12
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

Alignment Scores:
Pred. No.:           0            Length:        921
```

```
e:                  306.00          Matches:        306
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            93.3%           Indels:         0
                    3               Gaps:           0

0-821-670A-56 (1-328) x US-10-079-616-6 (1-921)

       23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

       43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

       63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

       83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

      103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

      123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

      143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

      163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

      243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

      323 TrpAlaSerValSerCys 328
          |||||||||||||||||
      901 TGGGCATCCGTGTCCTGC 918
```



```
US-10-079-616-7
; Sequence 7, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

Alignment Scores:
Pred. No.:              0               Length:         921
Score:                  306.00          Matches:        306
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            93.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-079-616-7 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
```

```
 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
901 TGGGCATCCGTGTCCTGC 918
```

```
ULT 14
09-917-265A-38
equence 38, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE:  2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 38
 LENGTH: 1599
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
```

```
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:
Pred. No.:              1.55e-223       Length:         1599
Score:                  216.00          Matches:        316
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            65.9%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-38 (1-1599)

Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933
```

```
      312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 984

LT 15
9-917-265A-40/c
quence 40, Application US/09917265A
tent No. 6818444
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 40
LENGTH: 1599
TYPE: DNA
ORGANISM: Felis catus
9-917-265A-40

nment Scores:
. No.:              1.55e-223      Length:         1599
e:                  216.00         Matches:        316
ent Similarity:     99.7%          Conservative:   0
 Local Similarity:  99.7%          Mismatches:     1
y Match:            65.9%          Indels:         0
                    3              Gaps:           0

.0-821-670A-56 (1-328) x US-09-917-265A-40 (1-1599)

       12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

       32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

       52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

       72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

       92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

      112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

      132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

      152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

      172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy       192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy       212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy       232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy       252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy       272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

Qy       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 616

RESULT 16
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-26

Alignment Scores:
Pred. No.:              7.09e-212      Length:         921
Score:                  205.00         Matches:        305
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            62.5%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-26 (1-921)

Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
901 TGGGCATCCGTGTCCTGC 918
```

```
ULT 17
09-917-265A-28/c
equence 28, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE:  2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 28
 LENGTH: 921
 TYPE: DNA
```

```
;   ORGANISM: Felis catus
US-09-917-265A-28

Alignment Scores:
Pred. No.:              7.09e-212       Length:         921
Score:                  205.00          Matches:        305
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            62.5%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-28 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22
```

```
       323 TrpAlaSerValSerCys 328
           ||||||||||||||||||
        21 TGGGCATCCGTGTCCTGC 4

/LT 18
)9-917-265A-43
:quence 43, Application US/09917265A
:tent No. 6818444
:NERAL INFORMATION:
\PPLICANT: Wonderling, Ramani S.
\PPLICANT:  Boroughs, Karen L.
:ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
:ITLE OF INVENTION:  THEREOF
'ILE REFERENCE: IM-5
:URRENT APPLICATION NUMBER: US/09/917,265A
:URRENT FILING DATE:  2001-07-27
'RIOR APPLICATION NUMBER: 60/223,016
'RIOR FILING DATE: 2000-08-04
JUMBER OF SEQ ID NOS: 111
)OFTWARE: PatentIn version 3.2
)Q ID NO 43
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1533)
)9-917-265A-43

jnment Scores:
i. No.:              1.17e-211      Length:         1533
:e:                  205.00         Matches:        305
:ent Similarity:     99.7%          Conservative:   0
 Local Similarity:   99.7%          Mismatches:     1
:y Match:            62.5%          Indels:         0
                     3              Gaps:           0

.0-821-670A-56 (1-328) x US-09-917-265A-43 (1-1533)

        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy     203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy     223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy     243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy     263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy     283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy     303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy     323 TrpAlaSerValSerCys 328
           ||||||||||||||||||
Db     901 TGGGCATCCGTGTCCTGC 918

RESULT 19
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.:              1.17e-211      Length:         1533
Score:                  205.00         Matches:        305
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            62.5%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-45 (1-1533)

Qy      23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy      43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy      63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354
```

```
 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
633 TGGGCATCCGTGTCCTGC 616
```

```
ULT 20
09-917-265A-52
equence 52, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE:  2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 52
 LENGTH: 921
 TYPE: DNA
 ORGANISM: Canis familiaris
```

```
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-52

Alignment Scores:
Pred. No.:                3.24e-30        Length:         921
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-52 (1-921)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 21
US-09-917-265A-54/c
; Sequence 54, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;    LENGTH: 921
;    TYPE: DNA
;    ORGANISM: Canis familiaris
US-09-917-265A-54

Alignment Scores:
Pred. No.:                3.24e-30        Length:         921
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-54 (1-921)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 22
US-09-917-265A-58
; Sequence 58, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
```

```
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 58
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(987)
9-917-265A-58

nment Scores:
. No.:                3.46e-30        Length:         987
e:                    37.00           Matches:        37
ent Similarity:       100.0%          Conservative:   0
 Local Similarity:    100.0%          Mismatches:     0
y Match:              11.3%           Indels:         0
                      3               Gaps:           0

0-821-670A-56 (1-328) x US-09-917-265A-58 (1-987)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

LT 23
9-917-265A-60/c
equence 60, Application US/09917265A
tent No. 6818444
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 60
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Canis familiaris
9-917-265A-60

nment Scores:
. No.:                3.46e-30        Length:         987
e:                    37.00           Matches:        37
ent Similarity:       100.0%          Conservative:   0
 Local Similarity:    100.0%          Mismatches:     0
y Match:              11.3%           Indels:         0
                      3               Gaps:           0

0-821-670A-56 (1-328) x US-09-917-265A-60 (1-987)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271
```

```
RESULT 24
US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

Alignment Scores:
Pred. No.:                3.47e-30        Length:         990
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-079-984A-1 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 25
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
```

```
  APPLICANT:  Yamada, Katsushige
  TITLE OF INVENTION:  Canine interleukin 12, a production method
  TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
  TITLE OF INVENTION:  method using it
  NUMBER OF SEQUENCES:  16
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Miller & Christenbury Intellectual Property
    ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
    STREET:  1600 Market Street, 39th Floor
    CITY:  Philadelphia
    STATE:  PA
    COUNTRY:  USA
    ZIP:  19103
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy Disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  WordPerfect 5.1
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/079,984A
    FILING DATE:  15-MAY-1998
  ATTORNEY/AGENT INFORMATION:
    NAME:  Austin R. Miller
    REGISTRATION NUMBER:  16,602
    REFERENCE/DOCKET NUMBER:  1051-98
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (215) 563-1810
    TELEFAX:  (215) 568-6946
INFORMATION FOR SEQ ID NO:  11:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  990 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA to mRNA
  ORIGINAL SOURCE:
    ORGANISM:  Canis familiaris
  FEATURE:
    NAME/KEY:  Canine IL12
    LOCATION:  1 to 987
    IDENTIFICATION METHOD:  Similarity
09-079-984A-11

gnment Scores:
d. No.:                3.47e-30        Length:         990
re:                    37.00           Matches:        37
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              11.3%           Indels:         0
                       3               Gaps:           0

10-821-670A-56 (1-328) x US-09-079-984A-11 (1-990)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 26
09-390-729-1
equence 1, Application US/09390729
atent No. 6562334
GENERAL INFORMATION:
  APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
  APPLICANT:  Yamada, Katsushige
  TITLE OF INVENTION:  Canine interleukin 12, a production method
  TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
  TITLE OF INVENTION:  method using it
  NUMBER OF SEQUENCES:  16
  CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-1

Alignment Scores:
Pred. No.:                3.47e-30        Length:         990
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-390-729-1 (1-990)

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy         223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 27
US-09-390-729-11
; Sequence 11, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
```

```
    CITY:  Philadelphia
    STATE:  PA
    COUNTRY:  USA
    ZIP:  19103
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy Disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  WordPerfect 5.1
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/390,729
    FILING DATE:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  09/079,984
    FILING DATE:  15-MAY-1998
  ATTORNEY/AGENT INFORMATION:
    NAME:  Austin R. Miller
    REGISTRATION NUMBER:  16,602
    REFERENCE/DOCKET NUMBER:  1051-98
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (215) 563-1810
    TELEFAX:  (215) 568-6946
NFORMATION FOR SEQ ID NO:  11:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  990 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA to mRNA
  ORIGINAL SOURCE:
    ORGANISM:  Canis familiaris
  FEATURE:
    NAME/KEY:  Canine IL12
    LOCATION:  1 to 987
    IDENTIFICATION METHOD:  Similarity
)9-390-729-11

nment Scores:
l. No.:                3.47e-30        Length:         990
e:                     37.00           Matches:        37
ent Similarity:        100.0%          Conservative:   0
 Local Similarity:     100.0%          Mismatches:     0
y Match:               11.3%           Indels:         0
                       3               Gaps:           0

.0-821-670A-56 (1-328) x US-09-390-729-11 (1-990)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

JLT 28
)9-917-265A-66
equence 66, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 66
 LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-66

Alignment Scores:
Pred. No.:                5.33e-30        Length:         1533
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-66 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 29
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

Alignment Scores:
Pred. No.:                5.33e-30        Length:         1533
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-68 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 30
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
```

TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 61
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
09-917-265A-61

gnment Scores:

d. No.:	5.56e-30	Length:	1599
re:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	3	Gaps:	0

10-821-670A-56 (1-328) x US-09-917-265A-61 (1-1599)

```
203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

ULT 31
09-917-265A-63/c
equence 63, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 63
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
09-917-265A-63

gnment Scores:

d. No.:	5.56e-30	Length:	1599
re:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	3	Gaps:	0

10-821-670A-56 (1-328) x US-09-917-265A-63 (1-1599)

```
203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db 933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 32
US-09-917-265A-107
; Sequence 107, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)..(1140)
US-09-917-265A-107

Alignment Scores:

Pred. No.:	7.82e-30	Length:	2267
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-917-265A-107 (1-2267)

```
Qy      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870
```

RESULT 33
US-09-917-265A-109/c
; Sequence 109, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265A-109

Alignment Scores:

Pred. No.:	7.82e-30	Length:	2267
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0

```
                    3              Gaps:          0

.0-821-670A-56 (1-328) x US-09-917-265A-109 (1-2267)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

JLT 34
)8-186-529-1
:quence 1, Application US/08186529
itent No. 5573764
:ENERAL INFORMATION:
  APPLICANT:  Sykes, Megan
  APPLICANT:  Wolf, Stanley F.
  TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
  TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
  NUMBER OF SEQUENCES:  4
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
    STREET:  87 CambridgePark Drive
    CITY:  Cambridge
    STATE:  MA
    COUNTRY:  USA
    ZIP:  02140
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/186,529
    FILING DATE:
    CLASSIFICATION:  424
  ATTORNEY/AGENT INFORMATION:
    NAME:  McDaniels, Patricia A.
    REGISTRATION NUMBER:  33,194
    REFERENCE/DOCKET NUMBER:  GI 5225
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  617-498-8401
    TELEFAX:  617-876-5851
:NFORMATION FOR SEQ ID NO:  1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  987 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
  ORIGINAL SOURCE:
    ORGANISM:  Homo sapiens
    CELL TYPE:  Lymphoblast
    CELL LINE:  RPMI 8866
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  1..987
8-186-529-1

:nment Scores:
l. No.:              5.04e-28       Length:        987
e:                   35.00          Matches:       35
ent Similarity:      100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
y Match:             10.7%          Indels:        0
                     2              Gaps:          0

.0-821-670A-56 (1-328) x US-08-186-529-1 (1-987)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||
Db         706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 35
US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1

Alignment Scores:
Pred. No.:              5.04e-28       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-56 (1-328) x US-08-640-386A-1 (1-987)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||
Db         706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

```
ULT 36
08-184-009-194
equence 194, Application US/08184009
atent No. 5833975
GENERAL INFORMATION:
  APPLICANT:  Paoletti, Enzo
  APPLICANT:  Tartaglia, James
  APPLICANT:  Cox, William I.
  TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
  NUMBER OF SEQUENCES:  217
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Curtis, Morris & Safford
    STREET:  530 Fifth Avenue
    CITY:  New York
    STATE:  NY
    COUNTRY:  USA
    ZIP:  10036
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/184,009
    FILING DATE:  19-JAN-1994
    CLASSIFICATION:  435
  ATTORNEY/AGENT INFORMATION:
    NAME:  Frommer, William S.
    REGISTRATION NUMBER:  25,506
    REFERENCE/DOCKET NUMBER:  454310-2530
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (212) 840-3333
    TELEFAX:  (212) 840-0712
    TELEX:  425066CURTMS
INFORMATION FOR SEQ ID NO:  194:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1018 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
08-184-009-194

gnment Scores:
d. No.:                5.19e-28        Length:         1018
re:                    35.00           Matches:        35
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              10.7%           Indels:         0
                       2               Gaps:           0

10-821-670A-56 (1-328) x US-08-184-009-194 (1-1018)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

ULT 37
08-458-356-194
equence 194, Application US/08458356
atent No. 5942235
GENERAL INFORMATION:
  APPLICANT:  Paoletti, Enzo
  APPLICANT:  Tartaglia, James
  APPLICANT:  Cox, William I.
  TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
  NUMBER OF SEQUENCES:  217
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Curtis, Morris & Safford
;     STREET:  530 Fifth Avenue
;     CITY:  New York
;     STATE:  NY
;     COUNTRY:  USA
;     ZIP:  10036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/458,356
;     FILING DATE:  02-JUN-1995
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/184,009
;     FILING DATE:  19-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Frommer, William S.
;     REGISTRATION NUMBER:  25,506
;     REFERENCE/DOCKET NUMBER:  454310-2530
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 840-3333
;     TELEFAX:  (212) 840-0712
;     TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1018 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
US-08-458-356-194

Alignment Scores:
Pred. No.:                5.19e-28        Length:         1018
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              10.7%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-56 (1-328) x US-08-458-356-194 (1-1018)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||
Db         737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 38
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/460,736
    FILING DATE:  02-JUN-1995
    CLASSIFICATION:  514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/184,009
    FILING DATE:  19-JAN-1994
  ATTORNEY/AGENT INFORMATION:
    NAME:  Frommer, William S.
    REGISTRATION NUMBER:  25,506
    REFERENCE/DOCKET NUMBER:  454310-2530
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (212) 840-3333
    TELEFAX:  (212) 840-0712
    TELEX:  425066CURTMS
NFORMATION FOR SEQ ID NO:  194:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1018 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
)8-460-736-194

nment Scores:
i. No.:                5.19e-28        Length:         1018
:e:                    35.00           Matches:        35
:ent Similarity:       100.0%          Conservative:   0
: Local Similarity:    100.0%          Mismatches:     0
:y Match:              10.7%           Indels:         0
                       3               Gaps:           0

.0-821-670A-56 (1-328) x US-08-460-736-194 (1-1018)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

:LT 39
9-535-370-194
:quence 194, Application US/09535370
itent No. 6537594
GENERAL INFORMATION:
     APPLICANT: Paoletti, Enzo
                Tartaglia, James
                Cox, William I.
     TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
     NUMBER OF SEQUENCES: 217
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Curtis, Morris & Safford
          STREET: 530 Fifth Avenue
          CITY: New York
          STATE: NY
          COUNTRY: USA
          ZIP: 10036
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.25
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/535,370
          FILING DATE: 24-Mar-2000
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 08/460,736
          FILING DATE: <Unknown>
     ATTORNEY/AGENT INFORMATION:
          NAME: Frommer, William S.
          REGISTRATION NUMBER: 25,506
          REFERENCE/DOCKET NUMBER: 454310-2530
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (212) 840-3333
          TELEFAX: (212) 840-0712
          TELEX: 425066CURTMS
  INFORMATION FOR SEQ ID NO: 194:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 1018 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: cDNA
     SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-535-370-194

Alignment Scores:
Pred. No.:             5.19e-28        Length:         1018
Score:                 35.00           Matches:        35
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           10.7%           Indels:         0
DB:                    3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-535-370-194 (1-1018)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 40
US-09-663-667-194
; Sequence 194, Application US/09663667
; Patent No. 6780407
;  GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/663,667
;            FILING DATE: 15-Sep-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/184,009
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 840-3333
;            TELEFAX: (212) 840-0712
;            TELEX: 425066CURTMS
;  INFORMATION FOR SEQ ID NO: 194:
```

```
      SEQUENCE CHARACTERISTICS:
           LENGTH: 1018 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 194:
09-663-667-194

gnment Scores:
d. No.:                5.19e-28        Length:         1018
re:                    35.00           Matches:        35
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              10.7%           Indels:         0
                       3               Gaps:           0

10-821-670A-56 (1-328) x US-09-663-667-194 (1-1018)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

ULT 41
09-634-368-4
equence 4, Application US/09634368
atent No. 6617135
ENERAL INFORMATION:
APPLICANT:  Gillies, Stephen
APPLICANT:  Lo, Kin Ming
TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
FILE REFERENCE:  LEX-010
CURRENT APPLICATION NUMBER: US/09/634,368
CURRENT FILING DATE:  2000-08-09
PRIOR APPLICATION NUMBER:  60/147,924
PRIOR FILING DATE:  1999-08-09
NUMBER OF SEQ ID NOS:  32
SOFTWARE:  PatentIn Ver. 2.0
EQ ID NO 4
 LENGTH: 1389
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: human
 OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
09-634-368-4

gnment Scores:
d. No.:                7.04e-28        Length:         1389
re:                    35.00           Matches:        35
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              10.7%           Indels:         0
                       3               Gaps:           0

10-821-670A-56 (1-328) x US-09-634-368-4 (1-1389)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ULT 42
08-751-767A-3
equence 3, Application US/08751767A
atent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..1026
US-08-751-767A-3

Alignment Scores:
Pred. No.:             7.09e-28        Length:         1399
Score:                 35.00           Matches:        35
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           10.7%           Indels:         0
DB:                    2               Gaps:           0

US-10-821-670A-56 (1-328) x US-08-751-767A-3 (1-1399)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 43
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
```

```
    STATE:  VA
    COUNTRY:  USA
    ZIP:  22201
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/751,767A
    FILING DATE:  08-NOV-1996
    CLASSIFICATION:  536
  ATTORNEY/AGENT INFORMATION:
    NAME:  SADOFF, B.J.
    REGISTRATION NUMBER:  36,663
    REFERENCE/DOCKET NUMBER:  117-221
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  7038164091
    TELEFAX:  7038164100
NFORMATION FOR SEQ ID NO:  11:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1560 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  1..1557
)8-751-767A-11

gnment Scores:
l. No.:                7.89e-28        Length:         1560
:e:                    35.00           Matches:        35
:ent Similarity:       100.0%          Conservative:   0
': Local Similarity:   100.0%          Mismatches:     0
:y Match:              10.7%           Indels:         0
                       2               Gaps:           0

.0-821-670A-56 (1-328) x US-08-751-767A-11 (1-1560)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       583 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 642

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       643 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 687

JLT 44
)8-751-767A-9
equence 9, Application US/08751767A
itent No. 5994104
ENERAL INFORMATION:
  APPLICANT:  ANDERSON, ROBERT J.
  APPLICANT:  GRANT, HUGH
  APPLICANT:  MACDONALD, IAN D.
  TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
  NUMBER OF SEQUENCES:  80
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  NIXON & VANDERHYE P.C.
    STREET:  1100 NORTH GLEBE ROAD
    CITY:  ARLINGTON
    STATE:  VA
    COUNTRY:  USA
    ZIP:  22201
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/751,767A
;     FILING DATE:  08-NOV-1996
;     CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  SADOFF, B.J.
;     REGISTRATION NUMBER:  36,663
;     REFERENCE/DOCKET NUMBER:  117-221
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  7038164091
;     TELEFAX:  7038164100
; INFORMATION FOR SEQ ID NO:  9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1623 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  1..1620
US-08-751-767A-9

Alignment Scores:
Pred. No.:                8.2e-28         Length:         1623
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              10.7%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-56 (1-328) x US-08-751-767A-9 (1-1623)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 45
US-09-949-016-5452
; Sequence 5452, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5452
;   LENGTH: 2307
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5452

Alignment Scores:
Pred. No.:                1.16e-27        Length:         2307
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              10.7%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-949-016-5452 (1-2307)
```

```
       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       648 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 707

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       708 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 752

ULT 46
08-265-087-1
equence 1, Application US/08265087
atent No. 5571515
GENERAL INFORMATION:
  APPLICANT:  Scott, Phillip
  APPLICANT:  Trinchieri, Giorgio
  TITLE OF INVENTION:  Compositions and Methods for Use of
  TITLE OF INVENTION:  IL-12 as an Adjuvant
  NUMBER OF SEQUENCES:  4
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Howson and Howson
    STREET:  Spring House Corporate Center, PO Box 457
    CITY:  Spring House
    STATE:  Pennsylvania
    COUNTRY:  USA
    ZIP:  19477
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/265,087
    FILING DATE:
    CLASSIFICATION:  424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/229,282
    FILING DATE:  18-APR-1994
  ATTORNEY/AGENT INFORMATION:
    NAME:  Bak, Mary E.
    REGISTRATION NUMBER:  31,215
    REFERENCE/DOCKET NUMBER:  WST51AUSA
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  215-540-9206
    TELEFAX:  215-540-5818
INFORMATION FOR SEQ ID NO:  1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  2362 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  unknown
  MOLECULE TYPE:  cDNA
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  33..1016
08-265-087-1

gnment Scores:
d. No.:                1.18e-27        Length:         2362
re:                    35.00           Matches:        35
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              10.7%           Indels:         0
                       2               Gaps:           0

10-821-670A-56 (1-328) x US-08-265-087-1 (1-2362)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 47
US-08-621-493-1
; Sequence 1, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-621-493-1

Alignment Scores:
Pred. No.:                1.18e-27        Length:         2362
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              10.7%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-56 (1-328) x US-08-621-493-1 (1-2362)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||
Db         738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 48
US-08-965-688-1
; Sequence 1, Application US/08965688
```

```
itent No. 5976539
ENERAL INFORMATION:
  APPLICANT:  Scott, Phillip
  APPLICANT:  Trinchieri, Giorgio
  TITLE OF INVENTION:  Compositions and Methods for Use of
  TITLE OF INVENTION:  IL-12 as an Adjuvant
  NUMBER OF SEQUENCES:  4
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Howson and Howson
    STREET:  Spring House Corporate Center, PO Box 457
    CITY:  Spring House
    STATE:  Pennsylvania
    COUNTRY:  USA
    ZIP:  19477
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/965,688
    FILING DATE:
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  08/621,493
    FILING DATE:  25-MAR-1996
    APPLICATION NUMBER:  08/265,087
    FILING DATE:  17-JUN-1994
    APPLICATION NUMBER:  US 08/229,282
    FILING DATE:  18-APR-1994
  ATTORNEY/AGENT INFORMATION:
    NAME:  Bak, Mary E.
    REGISTRATION NUMBER:  31,215
    REFERENCE/DOCKET NUMBER:  WST51AUSA
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  215-540-9206
    TELEFAX:  215-540-5818
NFORMATION FOR SEQ ID NO:  1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  2362 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  unknown
  MOLECULE TYPE:  cDNA
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  33..1016
)8-965-688-1

gnment Scores:
l. No.:                1.18e-27        Length:         2362
ce:                    35.00           Matches:        35
cent Similarity:       100.0%          Conservative:   0
: Local Similarity:    100.0%          Mismatches:     0
cy Match:              10.7%           Indels:         0
                       2               Gaps:           0

.0-821-670A-56 (1-328) x US-08-965-688-1 (1-2362)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

JLT 49
)9-260-173-1
equence 1, Application US/09260173
itent No. 6168923
 GENERAL INFORMATION:
      APPLICANT: Scott, Phillip
;                Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2362 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  33..1016
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

Alignment Scores:
Pred. No.:              1.18e-27        Length:         2362
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-260-173-1 (1-2362)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 50
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
```

```
APPLICANT:  PERUSSIA, BICE
APPLICANT:  CLARK, STEVEN C.
APPLICANT:  WONG, GORDON G.
APPLICANT:  HEWICK, RODNEY
APPLICANT:  KOBAYASHI, MICHIKO
TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
FILE REFERENCE: 01142.0142.0100
CURRENT APPLICATION NUMBER: US/09/924,703
CURRENT FILING DATE:  2001-08-09
PRIOR APPLICATION NUMBER: 09/325,958
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 08/858,000
PRIOR FILING DATE: 1997-05-16
PRIOR APPLICATION NUMBER: 08/403,013
PRIOR FILING DATE: 1995-03-13
PRIOR APPLICATION NUMBER: 07/584,941
PRIOR FILING DATE: 1990-09-18
PRIOR APPLICATION NUMBER: 07/307,817
PRIOR FILING DATE: 1989-02-07
PRIOR APPLICATION NUMBER: 07/269,945
PRIOR FILING DATE: 1988-11-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 3
 LENGTH: 2362
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
 OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
 NAME/KEY: CDS
 LOCATION: (33)..(1016)
09-924-703-3

gnment Scores:
d. No.:                1.18e-27        Length:         2362
re:                    35.00           Matches:        35
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              10.7%           Indels:         0
                       3               Gaps:           0

10-821-670A-56 (1-328) x US-09-924-703-3 (1-2362)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

ULT 51
08-751-767A-7
equence 7, Application US/08751767A
atent No. 5994104
GENERAL INFORMATION:
  APPLICANT:  ANDERSON, ROBERT J.
  APPLICANT:  GRANT, HUGH
  APPLICANT:  MACDONALD, IAN D.
  TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
  NUMBER OF SEQUENCES:  80
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  NIXON & VANDERHYE P.C.
    STREET:  1100 NORTH GLEBE ROAD
    CITY:  ARLINGTON
    STATE:  VA
    COUNTRY:  USA
    ZIP:  22201
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/751,767A
;     FILING DATE:  08-NOV-1996
;     CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  SADOFF, B.J.
;     REGISTRATION NUMBER:  36,663
;     REFERENCE/DOCKET NUMBER:  117-221
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  7038164091
;     TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  6139 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  both
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  3222..4841
US-08-751-767A-7

Alignment Scores:
Pred. No.:              3.02e-27        Length:         6139
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-56 (1-328) x US-08-751-767A-7 (1-6139)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3867 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3926

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db       3927 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3971

RESULT 52
US-08-848-760B-24
; Sequence 24, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
```

```
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (352) 375-8100
           TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 24:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
           DESCRIPTION: /desc = "DNA"
      SEQUENCE DESCRIPTION: SEQ ID NO: 24:
'8-848-760B-24

:nment Scores:
l. No.:              4.76e-15       Length:         987
 e:                  23.00          Matches:        23
'ent Similarity:     100.0%         Conservative:   0
  Local Similarity:  100.0%         Mismatches:     0
:y Match:            7.0%           Indels:         0
                     3              Gaps:           0

.0-821-670A-56 (1-328) x US-08-848-760B-24 (1-987)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       466 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 525

       176 SerAlaGlu 178
           |||||||||
       526 TCTGCAGAG 534

ILT 53
)9-826-025-24
:quence 24, Application US/09826025
:tent No. 6730512
 GENERAL INFORMATION:
      APPLICANT: Chang, Lung-Ji
      TITLE OF INVENTION: Combination Immunogene Therapy
      NUMBER OF SEQUENCES: 25
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Medlen & Carroll, LLP
           STREET: 220 Montgomery Street, Suite 2200
           CITY: San Francisco
           STATE: California
           COUNTRY: United States of America
           ZIP: 94104
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/826,025
           FILING DATE: 04-Apr-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/838,702
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Ingolia, Diane E.
           REGISTRATION NUMBER: 40,027
           REFERENCE/DOCKET NUMBER: CHANG-02687
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (415) 705-8410
           TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 24:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

Alignment Scores:
Pred. No.:              4.76e-15       Length:         987
Score:                  23.00          Matches:        23
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            7.0%           Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-826-025-24 (1-987)

Qy         156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         466 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 525

Qy         176 SerAlaGlu 178
               |||||||||
Db         526 TCTGCAGAG 534

RESULT 54
US-09-310-842-4
; Sequence 4, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

Alignment Scores:
Pred. No.:              8.91e-15       Length:         1870
Score:                  23.00          Matches:        23
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            7.0%           Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-310-842-4 (1-1870)

Qy         156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
      1098 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1157

       176 SerAlaGlu 178
           |||||||||
      1158 TCTGCAGAG 1166

ULT 55
09-851-062-3
equence 3, Application US/09851062
atent No. 6448081
ENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT:  Susan M. Freier
ITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
ILE REFERENCE: RTS-0247
URRENT APPLICATION NUMBER: US/09/851,062
URRENT FILING DATE:  2001-05-07
UMBER OF SEQ ID NOS: 87
EQ ID NO 3
 LENGTH: 2318
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (14)...(1000)
09-851-062-3

gnment Scores:
d. No.:                1.1e-14        Length:         2318
re:                    23.00          Matches:        23
cent Similarity:       100.0%         Conservative:   0
t Local Similarity:    100.0%         Mismatches:     0
ry Match:              7.0%           Indels:         0
                       3              Gaps:           0

10-821-670A-56 (1-328) x US-09-851-062-3 (1-2318)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       479 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 538

       176 SerAlaGlu 178
           |||||||||
       539 TCTGCAGAG 547

ULT 56
09-949-016-315
equence 315, Application US/09949016
atent No. 6812339
ENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ILE REFERENCE: CL001307
URRENT APPLICATION NUMBER: US/09/949,016
URRENT FILING DATE:  2000-04-14
RIOR APPLICATION NUMBER: 60/241,755
RIOR FILING DATE: 2000-10-20
RIOR APPLICATION NUMBER: 60/237,768
RIOR FILING DATE: 2000-10-03
RIOR APPLICATION NUMBER: 60/231,498
RIOR FILING DATE: 2000-09-08
UMBER OF SEQ ID NOS: 207012
OFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 315
 LENGTH: 2318
 TYPE: DNA
 ORGANISM: Human
09-949-016-315

gnment Scores:
d. No.:                1.1e-14        Length:         2318
re:                    23.00          Matches:        23
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           7.0%           Indels:         0
DB:                    3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-949-016-315 (1-2318)

Qy         156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         479 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 538

Qy         176 SerAlaGlu 178
               |||||||||
Db         539 TCTGCAGAG 547

RESULT 57
US-09-949-016-12057
; Sequence 12057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12057
;   LENGTH: 16002
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12057

Alignment Scores:
Pred. No.:             8.81e-13       Length:         16002
Score:                 22.00          Matches:        22
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           6.7%           Indels:         0
DB:                    3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-949-016-12057 (1-16002)

Qy         253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        9948 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 10007

Qy         273 ThrPhe 274
               ||||||
Db       10008 ACATTC 10013

RESULT 58
US-09-949-016-17194
; Sequence 17194, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
```

```
:RIOR APPLICATION NUMBER: 60/231,498
:RIOR FILING DATE: 2000-09-08
:UMBER OF SEQ ID NOS: 207012
;OFTWARE: FastSEQ for Windows Version 4.0
:Q ID NO 17194
 LENGTH: 16003
 TYPE: DNA
 ORGANISM: Human
)9-949-016-17194

;nment Scores:
i. No.:                 8.81e-13        Length:         16003
:e:                     22.00           Matches:        22
:ent Similarity:        100.0%          Conservative:   0
: Local Similarity:     100.0%          Mismatches:     0
:y Match:               6.7%            Indels:         0
                        3               Gaps:           0

.0-821-670A-56 (1-328) x US-09-949-016-17194 (1-16003)

       253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      9948 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 10007

       273 ThrPhe 274
           ||||||
     10008 ACATTC 10013

:LT 59
)9-823-549-77
:quence 77, Application US/09823549
:tent No. 6664442
:NERAL INFORMATION:
:PPLICANT: McConlogue, Lisa  C
:PPLICANT:  Games, Kate D.
:PPLICANT:  Yednock, Theodore A.
:PPLICANT:  Hua, Tan
:PPLICANT:  Messersmith, Elizabeth
:PPLICANT:  Bard, Frederique
:ITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
:ILE REFERENCE: 015270-009110US
:URRENT APPLICATION NUMBER: US/09/823,549
:URRENT FILING DATE:  2001-03-30
:RIOR APPLICATION NUMBER: US 60/193,847
:RIOR FILING DATE: 2000-03-30
:UMBER OF SEQ ID NOS: 85
;OFTWARE: PatentIn version 3.1
:Q ID NO 77
 LENGTH: 73
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: IL-12 p40, #1 marker
)9-823-549-77

;nment Scores:
i. No.:                 1.14e-09        Length:         73
:e:                     17.00           Matches:        17
:ent Similarity:        100.0%          Conservative:   0
: Local Similarity:     100.0%          Mismatches:     0
:y Match:               5.2%            Indels:         0
                        3               Gaps:           0

.0-821-670A-56 (1-328) x US-09-823-549-77 (1-73)

       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           |||||||||||||||||||||||||||||||||||||||||||||||||||
         9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59

:LT 60
)9-949-016-24253/c
:quence 24253, Application US/09949016
:tent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24253
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24253

Alignment Scores:
Pred. No.:                9e-09         Length:         601
Score:                    17.00         Matches:        17
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              5.2%          Indels:         0
DB:                       3             Gaps:           0

US-10-821-670A-56 (1-328) x US-09-949-016-24253 (1-601)

Qy        162 SerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGlu 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAG 214

RESULT 61
US-09-949-016-190686/c
; Sequence 190686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190686
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190686

Alignment Scores:
Pred. No.:                9e-09         Length:         601
Score:                    17.00         Matches:        17
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              5.2%          Indels:         0
DB:                       3             Gaps:           0

US-10-821-670A-56 (1-328) x US-09-949-016-190686 (1-601)

Qy        162 SerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGlu 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAG 214
```

```
ULT 62
08-385-335A-13
equence 13, Application US/08385335A
atent No. 5891680
GENERAL INFORMATION:
  APPLICANT:  Lieschke, Graham J.
  APPLICANT:  Mulligan, Richard C.
  TITLE OF INVENTION:  Bioactive Fusion Proteins
  NUMBER OF SEQUENCES:  34
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
    STREET:  Two Militia Drive
    CITY:  Lexington
    STATE:  Massachusetts
    COUNTRY:  USA
    ZIP:  02173
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/385,335A
    FILING DATE:  08-FEB-1995
    CLASSIFICATION:  530
  ATTORNEY/AGENT INFORMATION:
    NAME:  Granahan, Patricia
    REGISTRATION NUMBER:  32,227
    REFERENCE/DOCKET NUMBER:  WHI95-01
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  617-861-6240
    TELEFAX:  617-861-9540
INFORMATION FOR SEQ ID NO:  13:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1061 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  unknown
    TOPOLOGY:  unknown
  MOLECULE TYPE:  DNA (genomic)
08-385-335A-13

gnment Scores:
d. No.:                1.57e-08        Length:         1061
re:                    17.00           Matches:        17
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              5.2%            Indels:         0
                       2               Gaps:           0

10-821-670A-56 (1-328) x US-08-385-335A-13 (1-1061)

       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
       716 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 766

ULT 63
09-634-368-3
equence 3, Application US/09634368
atent No. 6617135
ENERAL INFORMATION:
APPLICANT:  Gillies, Stephen
APPLICANT:  Lo, Kin Ming
TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
FILE REFERENCE:  LEX-010
CURRENT APPLICATION NUMBER: US/09/634,368
CURRENT FILING DATE:  2000-08-09
PRIOR APPLICATION NUMBER:  60/147,924
PRIOR FILING DATE:  1999-08-09
NUMBER OF SEQ ID NOS:  32
SOFTWARE:  PatentIn Ver. 2.0
EQ ID NO 3
 LENGTH: 1409
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-09-634-368-3

Alignment Scores:
Pred. No.:             2.08e-08        Length:         1409
Score:                 17.00           Matches:        17
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           5.2%            Indels:         0
DB:                    3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-634-368-3 (1-1409)

Qy         227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740

RESULT 64
US-09-634-368-2
; Sequence 2, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-2

Alignment Scores:
Pred. No.:             2.17e-08        Length:         1472
Score:                 17.00           Matches:        17
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           5.2%            Indels:         0
DB:                    3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-634-368-2 (1-1472)

Qy         227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740

RESULT 65
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
```

```
;OFTWARE:  PatentIn Ver. 2.0
;Q ID NO 12
 LENGTH: 1569
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: murine
 OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
)9-634-368-12

;nment Scores:
i. No.:              2.31e-08       Length:        1569
 e:                  17.00          Matches:       17
:ent Similarity:     100.0%         Conservative:  0
  Local Similarity:  100.0%         Mismatches:    0
 y Match:            5.2%           Indels:        0
                     3              Gaps:          0

.0-821-670A-56 (1-328) x US-09-634-368-12 (1-1569)

       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

;LT 66
)9-634-368-11
;quence 11, Application US/09634368
;tent No. 6617135
;NERAL INFORMATION:
;PPLICANT:  Gillies, Stephen
;PPLICANT:  Lo, Kin Ming
:ITLE OF INVENTION:  Multiple Cytokine Protein Complexes
:ILE REFERENCE:  LEX-010
:URRENT APPLICATION NUMBER: US/09/634,368
:URRENT FILING DATE:  2000-08-09
:RIOR APPLICATION NUMBER:  60/147,924
:RIOR FILING DATE:  1999-08-09
;UMBER OF SEQ ID NOS:  32
;OFTWARE:  PatentIn Ver. 2.0
;Q ID NO 11
 LENGTH: 2013
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: murine
 OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
)9-634-368-11

;nment Scores:
i. No.:              2.94e-08       Length:        2013
:e:                  17.00          Matches:       17
:ent Similarity:     100.0%         Conservative:  0
  Local Similarity:  100.0%         Mismatches:    0
 y Match:            5.2%           Indels:        0
                     3              Gaps:          0

 0-821-670A-56 (1-328) x US-09-634-368-11 (1-2013)

       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

;LT 67
)9-634-368-13
;quence 13, Application US/09634368
;tent No. 6617135
;NERAL INFORMATION:
;PPLICANT:  Gillies, Stephen
;PPLICANT:  Lo, Kin Ming
:ITLE OF INVENTION:  Multiple Cytokine Protein Complexes
:ILE REFERENCE:  LEX-010
:URRENT APPLICATION NUMBER: US/09/634,368
:URRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

Alignment Scores:
Pred. No.:              3.94e-08       Length:        2709
Score:                  17.00          Matches:       17
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            5.2%           Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-56 (1-328) x US-09-634-368-13 (1-2709)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1977

RESULT 68
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
; GENERAL INFORMATION:
;   APPLICANT:  Rakhmilevich, Alexander
;   TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;   NUMBER OF SEQUENCES:  6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Quarles & Brady
;     STREET:  1 South Pinckney Street
;     CITY:  Madison
;     STATE:  WI
;     COUNTRY:  US
;     ZIP:  53703
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/659,206A
;     FILING DATE:
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Seay, Nicholas J
;     REGISTRATION NUMBER:  27386
;     REFERENCE/DOCKET NUMBER:  110229.91144
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  608-251-5000
;     TELEFAX:  608-251-9166
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  6295 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  circular
;   MOLECULE TYPE:  other nucleic acid
;     DESCRIPTION:  /desc = "plasmid pWRG3196"
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  join(955..1260, 1334..1675)
;     OTHER INFORMATION:  /product= "p35 gene product"
;   FEATURE:
;     NAME/KEY:  CDS
```

```
    LOCATION:  2377..3384
    OTHER INFORMATION:  /product= "p40 gene product"
08-659-206A-4

gnment Scores:
d. No.:                9e-08          Length:         6295
re:                    17.00          Matches:        17
cent Similarity:       100.0%         Conservative:   0
t Local Similarity:    100.0%         Mismatches:     0
ry Match:              5.2%           Indels:         0
                       2              Gaps:           0

10-821-670A-56 (1-328) x US-08-659-206A-4 (1-6295)

       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      3046 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 3096

ULT 69
08-659-206A-1
equence 1, Application US/08659206A
atent No. 5922685
GENERAL INFORMATION:
  APPLICANT:  Rakhmilevich, Alexander
  TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
  NUMBER OF SEQUENCES:  6
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Quarles & Brady
    STREET:  1 South Pinckney Street
    CITY:  Madison
    STATE:  WI
    COUNTRY:  US
    ZIP:  53703
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/659,206A
    FILING DATE:
    CLASSIFICATION:  435
  ATTORNEY/AGENT INFORMATION:
    NAME:  Seay, Nicholas J
    REGISTRATION NUMBER:  27386
    REFERENCE/DOCKET NUMBER:  110229.91144
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  608-251-5000
    TELEFAX:  608-251-9166
INFORMATION FOR SEQ ID NO:  1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  7287 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  circular
  MOLECULE TYPE:  other nucleic acid
    DESCRIPTION:  /desc = "Plasmid DNA"
  IMMEDIATE SOURCE:
    CLONE:  pWRG3169
  FEATURE:
    NAME/KEY:  promoter
    LOCATION:  1..628
  FEATURE:
    NAME/KEY:  iDNA
    LOCATION:  629..810
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  join(953..1258, 1332..1673)
    OTHER INFORMATION:  /product= "p35 gene product"
  FEATURE:
    NAME/KEY:  polyA_site
    LOCATION:  1797..2024
  FEATURE:
;     NAME/KEY:  promoter
;     LOCATION:  2110..2737
;   FEATURE:
;     NAME/KEY:  iDNA
;     LOCATION:  2738..2919
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  2983..3990
;     OTHER INFORMATION:  /product= "p40 gene product"
;   FEATURE:
;     NAME/KEY:  polyA_site
;     LOCATION:  4075..4306
US-08-659-206A-1

Alignment Scores:
Pred. No.:             1.04e-07       Length:         7287
Score:                 17.00          Matches:        17
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           5.2%           Indels:         0
DB:                    2              Gaps:           0

US-10-821-670A-56 (1-328) x US-08-659-206A-1 (1-7287)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3652 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 3702

RESULT 70
US-09-011-143-12
; Sequence 12, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 base pairs
;      TYPE:  nucleic acid
```

```
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
)9-011-143-12

;nment Scores:
i. No.:              0.000153       Length:        38
:e:                  12.00          Matches:       12
:ent Similarity:     100.0%         Conservative:  0
: Local Similarity:  100.0%         Mismatches:    0
:y Match:            3.7%           Indels:        0
                     3              Gaps:          0

.0-821-670A-56 (1-328) x US-09-011-143-12 (1-38)

        23 IleTrpGluLeuGluLysAsnValTyrValValGlu 34
           ||||||||||||||||||||||||||||||||||||
         1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36

JLT 71
)9-302-495-12
:quence 12, Application US/09302495
itent No. 6518045
GENERAL INFORMATION:
     APPLICANT: IMAMURA, Takayuki
                MAEDA, Hiroaki
                FUJIYASU, Takeshi
                IMAGAWA, Yoshitaka
                TOKIYOSHI, Sachio
     TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
     NUMBER OF SEQUENCES: 26
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: BROWDY AND NEIMARK
          STREET: 419 Seventh Street, N.W., Suite 300
          CITY: Washington
          STATE: D.C.
          COUNTRY: USA
          ZIP: 20004
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/302,495
          FILING DATE: 30-Apr-1999
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: US/09/011,143
          FILING DATE: 04-FEB-1998
          APPLICATION NUMBER: PCT/JP97/01824
          FILING DATE: 29-MAY-1997
          APPLICATION NUMBER: JP 165249/1996
          FILING DATE: 04-JUN-1996
     ATTORNEY/AGENT INFORMATION:
          NAME: BROWDY, Roger L.
          REGISTRATION NUMBER: 25,618
          REFERENCE/DOCKET NUMBER: IMAMURA=1
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 12:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 38 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: cDNA
     SEQUENCE DESCRIPTION: SEQ ID NO: 12:
)9-302-495-12

;nment Scores:
i. No.:              0.000153       Length:        38
Score:               12.00          Matches:       12
Percent Similarity:  100.0%         Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:         3.7%           Indels:        0
DB:                  3              Gaps:          0

US-10-821-670A-56 (1-328) x US-09-302-495-12 (1-38)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGlu 34
              ||||||||||||||||||||||||||||||||||||
Db          1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36

RESULT 72
US-10-079-616-12
; Sequence 12, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 38 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-079-616-12

Alignment Scores:
Pred. No.:           0.000153       Length:        38
Score:               12.00          Matches:       12
Percent Similarity:  100.0%         Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:         3.7%           Indels:        0
DB:                  3              Gaps:          0

US-10-821-670A-56 (1-328) x US-10-079-616-12 (1-38)
```

```
        23 IleTrpGluLeuGluLysAsnValTyrValValGlu 34
           ||||||||||||||||||||||||||||||||||||
         1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36

ULT 73
09-949-016-24250/c
equence 24250, Application US/09949016
atent No. 6812339
ENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE:  2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 24250
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
09-949-016-24250

gnment Scores:
d. No.:                0.0023          Length:         601
re:                    12.00           Matches:        12
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              3.7%            Indels:         0
                       3               Gaps:           0

10-821-670A-56 (1-328) x US-09-949-016-24250 (1-601)

        39 ProAspAlaProGlyGluMetValValLeuThrCys 50
           ||||||||||||||||||||||||||||||||||||
        81 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 46

ULT 74
09-949-016-24251/c
equence 24251, Application US/09949016
atent No. 6812339
ENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE:  2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 24251
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
09-949-016-24251

gnment Scores:
d. No.:                0.0023          Length:         601
re:                    12.00           Matches:        12
cent Similarity:       100.0%          Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            3.7%           Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-949-016-24251 (1-601)

Qy         39 ProAspAlaProGlyGluMetValValLeuThrCys 50
              ||||||||||||||||||||||||||||||||||||
Db        100 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 65

RESULT 75
US-09-949-016-190683/c
; Sequence 190683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190683
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190683

Alignment Scores:
Pred. No.:             0.0023          Length:         601
Score:                 12.00           Matches:        12
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            3.7%           Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-949-016-190683 (1-601)

Qy         39 ProAspAlaProGlyGluMetValValLeuThrCys 50
              ||||||||||||||||||||||||||||||||||||
Db         81 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 46

RESULT 76
US-09-949-016-190684/c
; Sequence 190684, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190684
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190684
```

```
;nment Scores:
i. No.:              0.0023          Length:         601
:e:                  12.00           Matches:        12
:ent Similarity:     100.0%          Conservative:   0
: Local Similarity:  100.0%          Mismatches:     0
:y Match:            3.7%            Indels:         0
                     3               Gaps:           0

.0-821-670A-56 (1-328) x US-09-949-016-190684 (1-601)

        39 ProAspAlaProGlyGluMetValValLeuThrCys 50
           ||||||||||||||||||||||||||||||||||||
       100 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 65

:LT 77
)9-917-265A-85
:quence 85, Application US/09917265A
:tent No. 6818444
:NERAL INFORMATION:
\PPLICANT: Wonderling, Ramani S.
\PPLICANT:  Boroughs, Karen L.
:ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
:ITLE OF INVENTION:  THEREOF
'ILE REFERENCE: IM-5
:URRENT APPLICATION NUMBER: US/09/917,265A
:URRENT FILING DATE:  2001-07-27
'RIOR APPLICATION NUMBER: 60/223,016
'RIOR FILING DATE: 2000-08-04
JUMBER OF SEQ ID NOS: 111
;OFTWARE: PatentIn version 3.2
;Q ID NO 85
 LENGTH: 28
 TYPE: DNA
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Primer
)9-917-265A-85

;nment Scores:
i. No.:              0.199           Length:         28
:e:                  9.00            Matches:        9
:ent Similarity:     100.0%          Conservative:   0
: Local Similarity:  100.0%          Mismatches:     0
:y Match:            2.7%            Indels:         0
                     3               Gaps:           0

.0-821-670A-56 (1-328) x US-09-917-265A-85 (1-28)

        1 MetHisProGlnGlnLeuValIleAla 9
          ||||||||||||||||||||||||||
        1 ATGCATCCTCAGCAGTTGGTCATCGCC 27

:LT 78
)9-917-265A-87
:quence 87, Application US/09917265A
:tent No. 6818444
:NERAL INFORMATION:
\PPLICANT: Wonderling, Ramani S.
\PPLICANT:  Boroughs, Karen L.
:ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
:ITLE OF INVENTION:  THEREOF
'ILE REFERENCE: IM-5
:URRENT APPLICATION NUMBER: US/09/917,265A
:URRENT FILING DATE:  2001-07-27
'RIOR APPLICATION NUMBER: 60/223,016
'RIOR FILING DATE: 2000-08-04
JUMBER OF SEQ ID NOS: 111
;OFTWARE: PatentIn version 3.2
;Q ID NO 87
 LENGTH: 37
 TYPE: DNA
 ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-87

Alignment Scores:
Pred. No.:           0.262           Length:         37
Score:               9.00            Matches:        9
Percent Similarity:  100.0%          Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:         2.7%            Indels:         0
DB:                  3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-87 (1-37)

Qy          1 MetHisProGlnGlnLeuValIleAla 9
              ||||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATCGCC 36

RESULT 79
US-09-513-999C-4018
; Sequence 4018, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 4018
;   LENGTH: 532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 144..503
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 29
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 30
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 289
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 460
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 461
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 503
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 513
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 518
```

OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: UNSURE
LOCATION: 49
OTHER INFORMATION: Xaa=Leu or Arg
FEATURE:
NAME/KEY: UNSURE
LOCATION: 106
OTHER INFORMATION: Xaa=Ile or Lys or Met or Asn or Arg or Ser or Thr
09-513-999C-4018

gnment Scores:

d. No.:	3.57	Length:	532
re:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.7%	Indels:	0
	3	Gaps:	0

10-821-670A-56 (1-328) x US-09-513-999C-4018 (1-532)

```
       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       462 TTTTTACTGATTCACAAAAAGGAAGAC 488
```

ULT 80
09-887-145-37
equence 37, Application US/09887145
atent No. 6780641
GENERAL INFORMATION:
APPLICANT: Kim, Seung U
TITLE OF INVENTION: Immortalized human microglia
cell and continuous cell line
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Microsoft Word version 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,145
FILING DATE: 22-Jun-2001
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: UBC-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
09-887-145-37

gnment Scores:

d. No.:	2.15	Length:	25
re:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.4%	Indels:	0
	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-887-145-37 (1-25)

```
Qy         91 HisLysGlyGlyGluValLeuSer 98
              |||||||||||||||||||||||
Db          2 CACAAAGGAGGCGAGGTTCTAAGC 25
```

RESULT 81
US-09-917-265A-86/c
; Sequence 86, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-917-265A-86

Alignment Scores:

Pred. No.:	2.15	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-917-265A-86 (1-25)

```
Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 82
US-09-011-143-13/c
; Sequence 13, Application US/09011143
; Patent No. 6472509
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: FUJIYASU, Takeshi
; APPLICANT: IMAGAWA, Yoshitaka
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,143
; FILING DATE: 04-FEB-1998
; CLASSIFICATION: 536

```
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/JP97/01824
    FILING DATE:  29-MAY-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  JP 165249/1996
    FILING DATE:  04-JUN-1996
  ATTORNEY/AGENT INFORMATION:
    NAME:  BROWDY, Roger L.
    REGISTRATION NUMBER:  25,618
    REFERENCE/DOCKET NUMBER:  IMAMURA=1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  202-628-5197
    TELEFAX:  202-737-3528
:NFORMATION FOR SEQ ID NO:  13:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  32 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
)9-011-143-13

;nment Scores:
i. No.:                2.74          Length:        32
:e:                    8.00          Matches:       8
:ent Similarity:       100.0%        Conservative:  0
: Local Similarity:    100.0%        Mismatches:    0
:y Match:              2.4%          Indels:        0
                       3             Gaps:          0

.0-821-670A-56 (1-328) x US-09-011-143-13 (1-32)

       176 SerAlaGluLysValArgValAsp 183
           |||||||||||||||||||||||||
        32 TCAGCAGAGAAGGTCAGAGTCGAC 9

'LT 83
'9-302-495-13/c
'quence 13, Application US/09302495
'tent No. 6518045
GENERAL INFORMATION:
     APPLICANT: IMAMURA, Takayuki
                MAEDA, Hiroaki
                FUJIYASU, Takeshi
                IMAGAWA, Yoshitaka
                TOKIYOSHI, Sachio
     TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
     NUMBER OF SEQUENCES: 26
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: BROWDY AND NEIMARK
          STREET: 419 Seventh Street, N.W., Suite 300
          CITY: Washington
          STATE: D.C.
          COUNTRY: USA
          ZIP: 20004
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/302,495
          FILING DATE: 30-Apr-1999
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: US/09/011,143
          FILING DATE: 04-FEB-1998
          APPLICATION NUMBER: PCT/JP97/01824
          FILING DATE: 29-MAY-1997
          APPLICATION NUMBER: JP 165249/1996
          FILING DATE: 04-JUN-1996
     ATTORNEY/AGENT INFORMATION:
          NAME: BROWDY, Roger L.
          REGISTRATION NUMBER: 25,618
          REFERENCE/DOCKET NUMBER: IMAMURA=1
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
     INFORMATION FOR SEQ ID NO: 13:
          SEQUENCE CHARACTERISTICS:
               LENGTH: 32 base pairs
               TYPE: nucleic acid
               STRANDEDNESS: single
               TOPOLOGY: linear
          MOLECULE TYPE: cDNA
          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-302-495-13

Alignment Scores:
Pred. No.:                2.74          Length:        32
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.4%          Indels:        0
DB:                       3             Gaps:          0

US-10-821-670A-56 (1-328) x US-09-302-495-13 (1-32)

Qy        176 SerAlaGluLysValArgValAsp 183
              |||||||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGTCGAC 9

RESULT 84
US-10-079-616-13/c
; Sequence 13, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
```

LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
10-079-616-13

gnment Scores:

d. No.:	2.74	Length:	32
re:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.4%	Indels:	0
	3	Gaps:	0

10-821-670A-56 (1-328) x US-10-079-616-13 (1-32)

```
       176 SerAlaGluLysValArgValAsp 183
           |||||||||||||||||||||||
        32 TCAGCAGAGAAGGTCAGAGTCGAC 9
```

ULT 85
09-917-265A-99
equence 99, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 99
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Primer
09-917-265A-99

gnment Scores:

d. No.:	3.16	Length:	37
re:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.4%	Indels:	0
	3	Gaps:	0

10-821-670A-56 (1-328) x US-09-917-265A-99 (1-37)

```
         1 MetHisProGlnGlnLeuValIle 8
           ||||||||||||||||||||||||
        11 ATGCACCCTCAGCAGTTGGTCATC 34
```

ULT 86
09-079-984A-13
equence 13, Application US/09079984A
atent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other DNA; synthetic DNA
US-09-079-984A-13

Alignment Scores:

Pred. No.:	3.33	Length:	39
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-079-984A-13 (1-39)

```
Qy          1 MetHisProGlnGlnLeuValIle 8
              ||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATC 33
```

RESULT 87
US-09-390-729-13
Sequence 13, Application US/09390729
Patent No. 6562334
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/390,729
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/079,984

```
    FILING DATE:  15-MAY-1998
  ATTORNEY/AGENT INFORMATION:
    NAME:  Austin R. Miller
    REGISTRATION NUMBER:  16,602
    REFERENCE/DOCKET NUMBER:  1051-98
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (215) 563-1810
    TELEFAX:  (215) 568-6946
:NFORMATION FOR SEQ ID NO:  13:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  39 bases
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  other DNA; synthetic DNA
)9-390-729-13

:nment Scores:
i. No.:              3.33          Length:        39
e:                   8.00          Matches:       8
'ent Similarity:     100.0%        Conservative:  0
  Local Similarity:  100.0%        Mismatches:    0
y Match:             2.4%          Indels:        0
                     3             Gaps:          0

.0-821-670A-56 (1-328) x US-09-390-729-13 (1-39)

         1 MetHisProGlnGlnLeuValIle 8
           ||||||||||||||||||||||||
        10 ATGCATCCTCAGCAGTTGGTCATC 33

JLT 88
)9-011-143-14
:quence 14, Application US/09011143
itent No. 6472509
:ENERAL INFORMATION:
  APPLICANT:  IMAMURA, Takayuki
  APPLICANT:  MAEDA, Hiroaki
  APPLICANT:  FUJIYASU, Takeshi
  APPLICANT:  IMAGAWA, Yoshitaka
  APPLICANT:  TOKIYOSHI, Sachio
  TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
  NUMBER OF SEQUENCES:  26
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  BROWDY AND NEIMARK
    STREET:  419 Seventh Street, N.W., Suite 300
    CITY:  Washington
    STATE:  D.C.
    COUNTRY:  USA
    ZIP:  20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/011,143
    FILING DATE:  04-FEB-1998
    CLASSIFICATION:  536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/JP97/01824
    FILING DATE:  29-MAY-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  JP 165249/1996
    FILING DATE:  04-JUN-1996
  ATTORNEY/AGENT INFORMATION:
    NAME:  BROWDY, Roger L.
    REGISTRATION NUMBER:  25,618
    REFERENCE/DOCKET NUMBER:  IMAMURA=1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  202-628-5197
    TELEFAX:  202-737-3528
:NFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-14

Alignment Scores:
Pred. No.:              3.74          Length:        44
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.4%          Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-56 (1-328) x US-09-011-143-14 (1-44)

Qy        182 ValAspAsnArgAspTyrLysLys 189
              ||||||||||||||||||||||
Db         21 GTCGACAACAGGGATTATAAGAAG 44

RESULT 89
US-09-302-495-14
; Sequence 14, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 44 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-302-495-14
```

gnment Scores:
d. No.: 3.74 Length: 44
re: 8.00 Matches: 8
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 2.4% Indels: 0
3 Gaps: 0

10-821-670A-56 (1-328) x US-09-302-495-14 (1-44)

182 ValAspAsnArgAspTyrLysLys 189
||||||||||||||||||||||
21 GTCGACAACAGGGATTATAAGAAG 44

JLT 90
10-079-616-14
equence 14, Application US/10079616
atent No. 6566097
GENERAL INFORMATION:
APPLICANT: IMAMURA, Takayuki
MAEDA, Hiroaki
FUJIYASU, Takeshi
IMAGAWA, Yoshitaka
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/079,616
FILING DATE: 22-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/011,143
FILING DATE: 04-FEB-1998
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
10-079-616-14

gnment Scores:
d. No.: 3.74 Length: 44
re: 8.00 Matches: 8
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-56 (1-328) x US-10-079-616-14 (1-44)

Qy 182 ValAspAsnArgAspTyrLysLys 189
||||||||||||||||||||||
Db 21 GTCGACAACAGGGATTATAAGAAG 44

RESULT 91
US-09-270-767-2298/c
; Sequence 2298, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2298
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-2298

Alignment Scores:
Pred. No.: 34.7 Length: 427
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-56 (1-328) x US-09-270-767-2298 (1-427)

Qy 13 LeuValLeuLeuAlaProProLeu 20
||||||||||||||||||||||
Db 223 TTAGTTCTGCTAGCCCCGCCTCTG 200

RESULT 92
US-09-270-767-17580/c
; Sequence 17580, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17580
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-17580

Alignment Scores:
Pred. No.: 34.7 Length: 427
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-56 (1-328) x US-09-270-767-17580 (1-427)

Qy 13 LeuValLeuLeuAlaProProLeu 20
||||||||||||||||||||||
Db 223 TTAGTTCTGCTAGCCCCGCCTCTG 200

RESULT 93

```
,9-445-724B-13
quence 13, Application US/09445724B
tent No. 6600020
NERAL INFORMATION:
PPLICANT: OKANO, FUMIYOSHI
ITLE OF INVENTION: CANINE INTERLEUKIN 18, CANINE INTERLEUKIN 1 CONVERTING
ITLE OF INVENTION:  ENZYME, DNA SEQUENCES ENCODING THESE, INTERLEUKIN 18
ITLE OF INVENTION:  PRODUCTION METHOD AND CANINE IMMUNE DISEASE REMEDY
ILE REFERENCE: 2109-15
URRENT APPLICATION NUMBER: US/09/445,724B
URRENT FILING DATE:  1999-12-13
UMBER OF SEQ ID NOS: 14
OFTWARE: PatentIn Ver. 2.1
Q ID NO 13
 LENGTH: 540
 TYPE: DNA
 ORGANISM: Caninus sp.
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(537)
)9-445-724B-13

nment Scores:
i. No.:              43.7          Length:        540
e:                   8.00          Matches:       8
ent Similarity:      100.0%        Conservative:  0
 Local Similarity:   100.0%        Mismatches:    0
y Match:             2.4%          Indels:        0
                     3             Gaps:          0

.0-821-670A-56 (1-328) x US-09-445-724B-13 (1-540)

        1 MetHisProGlnGlnLeuValIle 8
          ||||||||||||||||||||||||
        1 ATGCATCCTCAGCAGTTGGTCATC 24

LT 94
9-533-559-4743
quence 4743, Application US/09533559
tent No. 6902887
NERAL INFORMATION:
PPLICANT: Randy M. Berka
PPLICANT: Michael W. Rey
PPLICANT: Jeffrey R.Shuster
PPLICANT: Sakari Kauppinen
PPLICANT: Ib Groth Clausen
PPLICANT: Peter Bjarke Olsen
ITLE OF INVENTION: Methods For Monitoring Multiple Gene
ITLE OF INVENTION: Expression
ILE REFERENCE: 5849.200-US
URRENT APPLICATION NUMBER: US/09/533,559
URRENT FILING DATE: 2000-03-22
ARLIER APPLICATION NUMBER: 09/273,623
ARLIER FILING DATE: 1999-03-22
UMBER OF SEQ ID NOS: 7860
OFTWARE: FastSEQ for Windows Version 4.0
Q ID NO 4743
 LENGTH: 549
 TYPE: DNA
 ORGANISM: Aspergillus oryzae
)9-533-559-4743

nment Scores:
i. No.:              44.4          Length:        549
e:                   8.00          Matches:       8
ent Similarity:      100.0%        Conservative:  0
 Local Similarity:   100.0%        Mismatches:    0
y Match:             2.4%          Indels:        0
                     3             Gaps:          0

.0-821-670A-56 (1-328) x US-09-533-559-4743 (1-549)

        13 LeuValLeuLeuAlaProProLeu 20
```

```
                   ||||||||||||||||||||||||
Db        321 CTGGTCTTGTTGGCGCCCCCGCTT 344

RESULT 95
US-09-949-016-70299
; Sequence 70299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70299
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-70299

Alignment Scores:
Pred. No.:              48.5          Length:        601
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.4%          Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-56 (1-328) x US-09-949-016-70299 (1-601)

Qy          97 LeuSerHisSerPheLeuLeuIle 104
               ||||||||||||||||||||||||
Db        506 CTCAGTCATTCTTTTTTACTAATT 529

RESULT 96
US-09-949-016-87513
; Sequence 87513, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87513
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87513

Alignment Scores:
Pred. No.:              48.5          Length:        601
Score:                  8.00          Matches:       8
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.4%          Indels:        0
```

```
                    3              Gaps:          0

10-821-670A-56 (1-328) x US-09-949-016-87513 (1-601)

        97 LeuSerHisSerPheLeuLeuIle 104
           ||||||||||||||||||||||||
       440 CTATCACATTCCTTTCTCTTAATC 463

ULT 97
09-949-016-110703
equence 110703, Application US/09949016
atent No. 6812339
ENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE:  2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 110703
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
09-949-016-110703

gnment Scores:
d. No.:              48.5          Length:        601
re:                  8.00          Matches:       8
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            2.4%          Indels:        0
                     3             Gaps:          0

10-821-670A-56 (1-328) x US-09-949-016-110703 (1-601)

        11 PheSerLeuValLeuLeuAlaPro 18
           ||||||||||||||||||||||||
       345 TTTTCATTAGTTCTCCTGGCTCCT 368

ULT 98
09-949-016-110704
equence 110704, Application US/09949016
atent No. 6812339
ENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE:  2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 110704
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
09-949-016-110704

gnment Scores:
Pred. No.:           48.5          Length:        601
Score:               8.00          Matches:       8
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         2.4%          Indels:        0
DB:                  3             Gaps:          0

US-10-821-670A-56 (1-328) x US-09-949-016-110704 (1-601)

Qy          11 PheSerLeuValLeuLeuAlaPro 18
               ||||||||||||||||||||||||
Db         271 TTTTCATTAGTTCTCCTGGCTCCT 294

RESULT 99
US-09-949-016-110705
; Sequence 110705, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110705
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-110705

Alignment Scores:
Pred. No.:           48.5          Length:        601
Score:               8.00          Matches:       8
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         2.4%          Indels:        0
DB:                  3             Gaps:          0

US-10-821-670A-56 (1-328) x US-09-949-016-110705 (1-601)

Qy          11 PheSerLeuValLeuLeuAlaPro 18
               ||||||||||||||||||||||||
Db          71 TTTTCATTAGTTCTCCTGGCTCCT 94

RESULT 100
US-09-949-016-138629
; Sequence 138629, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138629
;   LENGTH: 601
```

TYPE: DNA
ORGANISM: Human
)9-949-016-138629

;nment Scores:

i. No.:	48.5	Length:	601
:e:	8.00	Matches:	8
:ent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
:y Match:	2.4%	Indels:	0
	3	Gaps:	0

.0-821-670A-56 (1-328) x US-09-949-016-138629 (1-601)

```
        12 SerLeuValLeuLeuAlaProPro 19
           ||||||||||||||||||||||
       367 TCCCTAGTACTTCTAGCGCCCCCC 390
```

ch completed: June 10, 2006, 04:52:33
time : 236.981 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

on: June 11, 2006, 22:10:55 ; Search time 1584.01 Seconds
(without alignments)
3816.589 Million cell updates/sec

le: US-10-821-670A-56
fect score: 328
uence: 1 MHPQQLVIAWFSLVLLAPPL.....VQARDRYYSSSWSNWASVSC 328

ring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

rched: 18892170 seqs, 6143817638 residues

d size: 1

al number of hits satisfying chosen parameters: 37767826

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Listing first 200 summaries

mand line parameters:
DEL=frame+_p2n.model -DEV=xlh
/abss/ABSSWEB_spool/US10821670/runat_07062006_110503_27781/app_query.fasta_1
=Published_Applications_NA_Main -QFMT=fastap
FFIX=oligo.p2n.200scores.rnpbm -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
ITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
CALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
RM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
ER=US10821670_@CGN_1_1_4932_@runat_07062006_110503_27781 -NCPU=6 -ICPU=3
_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
RN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
APOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

abase : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	% Query Match	Length	DB	ID	Description
1	328	100.0	985	3	US-09-917-265-55	Sequence 55, Appl
c 2	328	100.0	985	3	US-09-917-265-57	Sequence 57, Appl
3	328	100.0	985	9	US-10-821-670-55	Sequence 55, Appl
c 4	328	100.0	985	9	US-10-821-670-57	Sequence 57, Appl
5	328	100.0	987	3	US-09-917-265-29	Sequence 29, Appl
c 6	328	100.0	987	3	US-09-917-265-31	Sequence 31, Appl
7	328	100.0	987	9	US-10-821-670-29	Sequence 29, Appl
c 8	328	100.0	987	9	US-10-821-670-31	Sequence 31, Appl
9	328	100.0	990	7	US-10-041-672C-1	Sequence 1, Appli
10	328	100.0	4522	7	US-10-041-672C-10	Sequence 10, Appl
11	316	96.3	2193	6	US-10-079-616-5	Sequence 5, Appli
12	306	93.3	921	6	US-10-079-616-6	Sequence 6, Appli
13	306	93.3	921	6	US-10-079-616-7	Sequence 7, Appli
14	216	65.9	1599	3	US-09-917-265-38	Sequence 38, Appl
c 15	216	65.9	1599	3	US-09-917-265-40	Sequence 40, Appl
16	216	65.9	1599	9	US-10-821-670-38	Sequence 38, Appl
c 17	216	65.9	1599	9	US-10-821-670-40	Sequence 40, Appl
18	205	62.5	921	3	US-09-917-265-26	Sequence 26, Appl
c 19	205	62.5	921	3	US-09-917-265-28	Sequence 28, Appl
20	205	62.5	921	9	US-10-821-670-26	Sequence 26, Appl
c 21	205	62.5	921	9	US-10-821-670-28	Sequence 28, Appl
22	205	62.5	1533	3	US-09-917-265-43	Sequence 43, Appl
c 23	205	62.5	1533	3	US-09-917-265-45	Sequence 45, Appl
24	205	62.5	1533	9	US-10-821-670-43	Sequence 43, Appl
c 25	205	62.5	1533	9	US-10-821-670-45	Sequence 45, Appl
26	37	11.3	921	3	US-09-917-265-52	Sequence 52, Appl
c 27	37	11.3	921	3	US-09-917-265-54	Sequence 54, Appl
28	37	11.3	921	9	US-10-821-670-52	Sequence 52, Appl
c 29	37	11.3	921	9	US-10-821-670-54	Sequence 54, Appl
30	37	11.3	987	3	US-09-917-265-58	Sequence 58, Appl
c 31	37	11.3	987	3	US-09-917-265-60	Sequence 60, Appl
32	37	11.3	987	9	US-10-821-670-58	Sequence 58, Appl
c 33	37	11.3	987	9	US-10-821-670-60	Sequence 60, Appl
34	37	11.3	1533	3	US-09-917-265-66	Sequence 66, Appl
c 35	37	11.3	1533	3	US-09-917-265-68	Sequence 68, Appl
36	37	11.3	1533	9	US-10-821-670-66	Sequence 66, Appl
c 37	37	11.3	1533	9	US-10-821-670-68	Sequence 68, Appl
38	37	11.3	1599	3	US-09-917-265-61	Sequence 61, Appl
c 39	37	11.3	1599	3	US-09-917-265-63	Sequence 63, Appl
40	37	11.3	1599	9	US-10-821-670-61	Sequence 61, Appl
c 41	37	11.3	1599	9	US-10-821-670-63	Sequence 63, Appl
42	37	11.3	2267	3	US-09-917-265-107	Sequence 107, App
c 43	37	11.3	2267	3	US-09-917-265-109	Sequence 109, App
44	37	11.3	2267	9	US-10-821-670-107	Sequence 107, App
c 45	37	11.3	2267	9	US-10-821-670-109	Sequence 109, App
46	35	10.7	987	3	US-09-754-014-2	Sequence 2, Appli
47	35	10.7	987	3	US-09-754-014-3	Sequence 3, Appli
48	35	10.7	987	3	US-09-754-014-4	Sequence 4, Appli
49	35	10.7	987	3	US-09-836-866-2	Sequence 2, Appli
50	35	10.7	1007	8	US-10-221-975A-1	Sequence 1, Appli
51	35	10.7	1018	7	US-10-267-384-194	Sequence 194, App
52	35	10.7	1389	8	US-10-603-064-4	Sequence 4, Appli
53	35	10.7	1397	7	US-10-349-507-2	Sequence 2, Appli
54	35	10.7	1397	7	US-10-267-565-2	Sequence 2, Appli
55	35	10.7	1399	10	US-10-929-182-22	Sequence 22, Appl
56	35	10.7	2347	7	US-10-429-802-44	Sequence 44, Appl
57	35	10.7	2347	7	US-10-430-503-35	Sequence 35, Appl
58	35	10.7	2362	3	US-09-924-703-3	Sequence 3, Appli
59	35	10.7	2362	8	US-10-358-395-3	Sequence 3, Appli
60	35	10.7	5686	7	US-10-136-837-1	Sequence 1, Appli
61	35	10.7	11569	10	US-10-511-237-1	Sequence 1, Appli
62	28	8.5	2390	10	US-10-528-644A-53	Sequence 53, Appl
63	23	7.0	987	3	US-09-826-025-24	Sequence 24, Appl
64	23	7.0	987	9	US-10-785-577-24	Sequence 24, Appl
65	23	7.0	1005	7	US-10-373-456-18	Sequence 18, Appl
66	23	7.0	1017	7	US-10-373-456-20	Sequence 20, Appl
67	23	7.0	1580	9	US-10-742-405-7	Sequence 7, Appli
68	23	7.0	1828	7	US-10-373-456-2	Sequence 2, Appli
69	23	7.0	1870	6	US-10-228-811-4	Sequence 4, Appli
70	23	7.0	2318	6	US-10-172-399-7	Sequence 7, Appli
71	23	7.0	2318	9	US-10-476-961-3	Sequence 3, Appli
72	23	7.0	2466	7	US-10-373-456-1	Sequence 1, Appli
73	23	7.0	8578	3	US-09-828-825-1	Sequence 1, Appli
74	23	7.0	8578	3	US-09-828-825-3	Sequence 3, Appli

75	23	7.0	8608	3	US-09-828-825-7	Sequence 7, Appli
76	23	7.0	8623	3	US-09-828-825-5	Sequence 5, Appli
77	23	7.0	8629	3	US-09-828-825-15	Sequence 15, Appl
78	23	7.0	8638	3	US-09-828-825-9	Sequence 9, Appli
79	23	7.0	8644	3	US-09-828-825-13	Sequence 13, Appl
80	23	7.0	8659	3	US-09-828-825-11	Sequence 11, Appl
81	23	7.0	11453	10	US-10-511-237-3	Sequence 3, Appli
82	22	6.7	18340	8	US-10-240-376A-130	Sequence 130, App
83	20	6.1	270	7	US-10-029-386-16833	Sequence 16833, A
84	20	6.1	399	16	US-11-128-061-661	Sequence 661, App
85	20	6.1	399	16	US-11-128-061-4303	Sequence 4303, Ap
86	20	6.1	399	16	US-11-128-049-661	Sequence 661, App
87	20	6.1	399	16	US-11-128-049-4303	Sequence 4303, Ap
88	20	6.1	556	7	US-10-029-386-3133	Sequence 3133, Ap
89	17	5.2	73	3	US-09-823-549-77	Sequence 77, Appl
90	17	5.2	73	9	US-10-685-992-77	Sequence 77, Appl
91	17	5.2	600	16	US-11-136-527-4408	Sequence 4408, Ap
92	17	5.2	1024	16	US-11-136-527-312	Sequence 312, App
93	17	5.2	1409	8	US-10-603-064-3	Sequence 3, Appli
94	17	5.2	1472	8	US-10-603-064-2	Sequence 2, Appli
95	17	5.2	1569	8	US-10-603-064-12	Sequence 12, Appl
96	17	5.2	1610	9	US-10-742-405-5	Sequence 5, Appli
97	17	5.2	1840	6	US-10-172-399-3	Sequence 3, Appli
98	17	5.2	2013	8	US-10-603-064-11	Sequence 11, Appl
99	17	5.2	2709	8	US-10-603-064-13	Sequence 13, Appl
.00	17	5.2	5966	7	US-10-136-837-3	Sequence 3, Appli
.01	17	5.2	11458	10	US-10-511-237-2	Sequence 2, Appli
.02	12	3.7	38	6	US-10-079-616-12	Sequence 12, Appl
.03	10	3.0	21925	7	US-10-017-161-2415	Sequence 2415, Ap
.04	10	3.0	21925	7	US-10-292-798-2055	Sequence 2055, Ap
.05	10	3.0	26184	7	US-10-017-161-2043	Sequence 2043, Ap
.06	10	3.0	26184	7	US-10-292-798-1689	Sequence 1689, Ap
.07	9	2.7	28	3	US-09-917-265-85	Sequence 85, Appl
.08	9	2.7	28	9	US-10-821-670-85	Sequence 85, Appl
.09	9	2.7	30	8	US-10-240-376A-9	Sequence 9, Appli
.10	9	2.7	37	3	US-09-917-265-87	Sequence 87, Appl
11	9	2.7	37	9	US-10-821-670-87	Sequence 87, Appl
.12	9	2.7	353	9	US-10-357-930-7460	Sequence 7460, Ap
.13	9	2.7	381	3	US-09-796-692-7886	Sequence 7886, Ap
.14	9	2.7	381	6	US-10-040-862-7886	Sequence 7886, Ap
.15	9	2.7	381	7	US-10-057-475B-7886	Sequence 7886, Ap
.16	9	2.7	381	7	US-10-154-884B-7886	Sequence 7886, Ap
.17	9	2.7	381	9	US-10-764-324-7886	Sequence 7886, Ap
.18	9	2.7	400	8	US-10-242-535A-51196	Sequence 51196, A
.19	9	2.7	400	8	US-10-085-783A-51196	Sequence 51196, A
.20	9	2.7	419	8	US-10-240-376A-1	Sequence 1, Appli
.21	9	2.7	419	8	US-10-240-376A-2	Sequence 2, Appli
.22	9	2.7	426	9	US-10-357-930-37422	Sequence 37422, A
.23	9	2.7	540	4	US-09-925-065A-564824	Sequence 564824,
.24	9	2.7	540	5	US-09-925-065A-564824	Sequence 564824,
.25	9	2.7	600	10	US-10-972-079-50704	Sequence 50704, A
.26	9	2.7	858	6	US-10-198-846-9631	Sequence 9631, Ap
.27	9	2.7	2256	9	US-10-357-930-22505	Sequence 22505, A
.28	9	2.7	2256	9	US-10-357-930-24790	Sequence 24790, A
.29	9	2.7	2256	9	US-10-357-930-28340	Sequence 28340, A
.30	9	2.7	2433	7	US-10-369-493-24162	Sequence 24162, A
.31	9	2.7	2659	6	US-10-198-846-13710	Sequence 13710, A
.32	9	2.7	2709	10	US-10-750-185-41680	Sequence 41680, A
.33	9	2.7	2709	10	US-10-750-623-41680	Sequence 41680, A
.34	9	2.7	3284	7	US-10-108-260A-630	Sequence 630, App
.35	9	2.7	179687	10	US-10-981-277-29	Sequence 29, Appl
.36	9	2.7	1503841	3	US-09-795-668-1	Sequence 1, Appli
.37	9	2.7	1503841	3	US-09-795-686-1	Sequence 1, Appli
.38	9	2.7	1503841	3	US-09-946-807-1	Sequence 1, Appli
.39	9	2.7	1503841	10	US-10-995-011-1	Sequence 1, Appli
.40	8	2.4	25	3	US-09-917-265-86	Sequence 86, Appl
.41	8	2.4	25	3	US-09-887-145-37	Sequence 37, Appl
.42	8	2.4	25	8	US-10-719-956-231796	Sequence 231796,
.43	8	2.4	25	9	US-10-821-670-86	Sequence 86, Appl
.44	8	2.4	25	13	US-11-036-317-431048	Sequence 431048,
.45	8	2.4	25	16	US-11-136-527-18285	Sequence 18285, A
46	8	2.4	25	16	US-11-136-527-18288	Sequence 18288, A
47	8	2.4	30	7	US-10-349-507-39	Sequence 39, Appl
148	8	2.4	30	7	US-10-267-565-34	Sequence 34, Appl
c 149	8	2.4	32	6	US-10-079-616-13	Sequence 13, Appl
150	8	2.4	37	3	US-09-917-265-99	Sequence 99, Appl
151	8	2.4	37	9	US-10-821-670-99	Sequence 99, Appl
152	8	2.4	44	6	US-10-079-616-14	Sequence 14, Appl
c 153	8	2.4	50	16	US-11-175-859-25436	Sequence 25436, A
154	8	2.4	182	9	US-10-425-115-66404	Sequence 66404, A
c 155	8	2.4	201	9	US-10-741-600-54203	Sequence 54203, A
c 156	8	2.4	201	10	US-10-995-561-40384	Sequence 40384, A
157	8	2.4	201	10	US-10-995-561-56659	Sequence 56659, A
158	8	2.4	201	10	US-10-995-561-56702	Sequence 56702, A
c 159	8	2.4	201	10	US-10-995-561-56721	Sequence 56721, A
c 160	8	2.4	201	10	US-10-995-561-56753	Sequence 56753, A
c 161	8	2.4	201	16	US-11-124-367A-32612	Sequence 32612, A
c 162	8	2.4	229	8	US-10-437-963-26379	Sequence 26379, A
c 163	8	2.4	252	3	US-09-864-761-32006	Sequence 32006, A
164	8	2.4	280	3	US-09-560-863-932	Sequence 932, App
c 165	8	2.4	296	8	US-10-424-599-57914	Sequence 57914, A
c 166	8	2.4	366	8	US-10-424-599-104364	Sequence 104364,
c 167	8	2.4	369	8	US-10-424-599-118136	Sequence 118136,
c 168	8	2.4	374	3	US-09-770-791-289	Sequence 289, App
169	8	2.4	381	8	US-10-437-963-45090	Sequence 45090, A
c 170	8	2.4	397	3	US-09-864-761-15492	Sequence 15492, A
c 171	8	2.4	416	3	US-09-783-590-7899	Sequence 7899, Ap
c 172	8	2.4	436	7	US-10-062-674-978	Sequence 978, App
c 173	8	2.4	441	4	US-09-925-065A-458395	Sequence 458395,
c 174	8	2.4	441	5	US-09-925-065A-458395	Sequence 458395,
175	8	2.4	443	12	US-10-301-480-516016	Sequence 516016,
176	8	2.4	443	12	US-10-301-480-1129425	Sequence 1129425,
c 177	8	2.4	462	7	US-10-341-961A-368	Sequence 368, App
178	8	2.4	467	12	US-10-301-480-28499	Sequence 28499, A
179	8	2.4	467	12	US-10-301-480-641908	Sequence 641908,
c 180	8	2.4	474	6	US-10-027-632-48724	Sequence 48724, A
c 181	8	2.4	474	7	US-10-027-632-48724	Sequence 48724, A
c 182	8	2.4	474	12	US-10-301-480-3946	Sequence 3946, Ap
c 183	8	2.4	474	12	US-10-301-480-3947	Sequence 3947, Ap
c 184	8	2.4	474	12	US-10-301-480-617355	Sequence 617355,
c 185	8	2.4	474	12	US-10-301-480-617356	Sequence 617356,
186	8	2.4	476	3	US-09-918-995-25870	Sequence 25870, A
187	8	2.4	491	4	US-09-925-065A-538665	Sequence 538665,
188	8	2.4	491	5	US-09-925-065A-538665	Sequence 538665,
c 189	8	2.4	494	6	US-10-027-632-198942	Sequence 198942,
c 190	8	2.4	494	7	US-10-027-632-198942	Sequence 198942,
c 191	8	2.4	500	4	US-09-925-065A-376272	Sequence 376272,
c 192	8	2.4	500	4	US-09-925-065A-376273	Sequence 376273,
c 193	8	2.4	500	4	US-09-925-065A-376274	Sequence 376274,
c 194	8	2.4	500	5	US-09-925-065A-376272	Sequence 376272,
c 195	8	2.4	500	5	US-09-925-065A-376273	Sequence 376273,
c 196	8	2.4	500	5	US-09-925-065A-376274	Sequence 376274,
197	8	2.4	507	4	US-09-925-065A-511562	Sequence 511562,
198	8	2.4	507	4	US-09-925-065A-511564	Sequence 511564,
199	8	2.4	507	5	US-09-925-065A-511562	Sequence 511562,
200	8	2.4	507	5	US-09-925-065A-511564	Sequence 511564,

ALIGNMENTS

```
RESULT 1
US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
```

```
 LENGTH: 985
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(984)
 OTHER INFORMATION:
09-917-265-55

gnment Scores:
d. No.:                0              Length:        985
re:                    328.00         Matches:       328
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              100.0%         Indels:        0
                       3              Gaps:          0

10-821-670A-56 (1-328) x US-09-917-265-55 (1-985)

        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

       21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

       41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

       61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

       81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

      101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

      121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

      141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

      161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              ||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 2
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-57

Alignment Scores:
Pred. No.:             0              Length:        985
Score:                 328.00         Matches:       328
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           100.0%         Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-56 (1-328) x US-09-917-265-57 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566
```

```
      141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

      161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

      321 SerAsnTrpAlaSerValSerCys 328
          |||||||||||||||||||||||
       25 AGCAACTGGGCATCCGTGTCCTGC 2

:LT 3
.0-821-670-55
'quence 55, Application US/10821670
.blication No. US20040248261A1
:NERAL INFORMATION:
 PPLICANT: Wonderling, Ramani S.
 PPLICANT:  Boroughs, Karen L.
 ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 ITLE OF INVENTION:  THEREOF
 ILE REFERENCE: IM-5
 URRENT APPLICATION NUMBER: US/10/821,670
 URRENT FILING DATE:  2004-04-09
 RIOR APPLICATION NUMBER: 60/223,016
 RIOR FILING DATE: 2000-08-04
 UMBER OF SEQ ID NOS: 111
 OFTWARE: PatentIn version 3.2
 Q ID NO 55
 LENGTH: 985
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(984)
.0-821-670-55

 nment Scores:
 . No.:              0              Length:        985
 e:                  328.00         Matches:       328
 ent Similarity:     100.0%         Conservative:  0
  Local Similarity:  100.0%         Mismatches:    0
 y Match:            100.0%         Indels:        0
                     9              Gaps:          0
```

```
US-10-821-670A-56 (1-328) x US-10-821-670-55 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 4
US-10-821-670-57/c
; Sequence 57, Application US/10821670
```

ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION: THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE: 2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 57
LENGTH: 985
TYPE: DNA
ORGANISM: Felis catus
10-821-670-57

gnment Scores:

d. No.:	0	Length:	985
re:	328.00	Matches:	328
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	100.0%	Indels:	0
	9	Gaps:	0

10-821-670A-56 (1-328) x US-10-821-670-57 (1-985)

```
          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326
```

```
Qy      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||
Db       25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 5
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
; OTHER INFORMATION:
US-09-917-265-29

Alignment Scores:

Pred. No.:	0	Length:	987
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-917-265-29 (1-987)

```
Qy        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy       21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy       41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy       61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

 81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

321 SerAsnTrpAlaSerValSerCys 328
    |||||||||||||||||||||||
961 AGCAACTGGGCATCCGTGTCCTGC 984
```

```
:LT 6
)9-917-265-31/c
:quence 31, Application US/09917265
:tent No. US20020052030A1
:NERAL INFORMATION:
\PPLICANT: Wonderling, Ramani S.
\PPLICANT:  Boroughs, Karen L.
:ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
:ILE REFERENCE: IM-5
:URRENT APPLICATION NUMBER: US/09/917,265
:URRENT FILING DATE:  2001-07-27
>RIOR APPLICATION NUMBER: 60/223,016
>RIOR FILING DATE: 2000-08-04
:UMBER OF SEQ ID NOS: 109
;OFTWARE: PatentIn version 3.1
:Q ID NO 31
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Felis catus
```

US-09-917-265-31

Alignment Scores:

Pred. No.:	0	Length:	987
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-917-265-31 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

321 SerAsnTrpAlaSerValSerCys 328
    |||||||||||||||||||||||||
 27 AGCAACTGGGCATCCGTGTCCTGC 4

ULT 7
10-821-670-29
equence 29, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 29
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(987)
10-821-670-29

gnment Scores:
d. No.:                0              Length:         987
re:                    328.00         Matches:        328
cent Similarity:       100.0%         Conservative:   0
t Local Similarity:    100.0%         Mismatches:     0
ry Match:              100.0%         Indels:         0
                       9              Gaps:           0

10-821-670A-56 (1-328) x US-10-821-670-29 (1-987)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy      161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||||
Db      961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 8
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-31

Alignment Scores:
Pred. No.:             0              Length:         987
Score:                 328.00         Matches:        328
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           100.0%         Indels:         0
DB:                    9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-31 (1-987)

Qy        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928
```

```
 21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

 41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

 61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

 81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

321 SerAsnTrpAlaSerValSerCys 328
    |||||||||||||||||||||||
 27 AGCAACTGGGCATCCGTGTCCTGC 4
```

```
;LT 9
.0-041-672C-1
equence 1, Application US/10041672C
iblication No. US20030157059A1
ENERAL INFORMATION:
\PPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
\PPLICANT:  Universitat Zurich
ITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
ILE REFERENCE: NHL-NP-36
```

```
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

Alignment Scores:
Pred. No.:              0               Length:         990
Score:                  328.00          Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-041-672C-1 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
```

```
       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

       321 SerAsnTrpAlaSerValSerCys 328
           |||||||||||||||||||||||||
       961 AGCAACTGGGCATCCGTGTCCTGC 984

ULT 10
10-041-672C-10
equence 10, Application US/10041672C
ublication No. US20030157059A1
ENERAL INFORMATION:
APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
APPLICANT:  Universitat Zurich
ITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
ILE REFERENCE: NHL-NP-36
URRENT APPLICATION NUMBER: US/10/041,672C
URRENT FILING DATE:  2002-01-08
UMBER OF SEQ ID NOS: 11
OFTWARE: PatentIn version 3.1
EQ ID NO 10
 LENGTH: 4522
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: pMol-fil12p40
10-041-672C-10

gnment Scores:
d. No.:              0              Length:        4522
re:                  328.00         Matches:       328
cent Similarity:     100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
ty Match:            100.0%         Indels:        0
                     7              Gaps:          0

10-821-670A-56 (1-328) x US-10-041-672C-10 (1-4522)

         1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

        21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy     141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy     161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy     181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy     201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy     221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy     241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy     261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy     281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy     301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy     321 SerAsnTrpAlaSerValSerCys 328
           |||||||||||||||||||||||||
Db    4007 AGCAACTGGGCATCCGTGTCCTGC 4030

RESULT 11
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
```

```
          FILING DATE: 04-FEB-1998
          APPLICATION NUMBER: PCT/JP97/01824
          FILING DATE: 29-MAY-1997
          APPLICATION NUMBER: JP 165249/1996
          FILING DATE: 04-JUN-1996
     ATTORNEY/AGENT INFORMATION:
          NAME: BROWDY, Roger L.
          REGISTRATION NUMBER: 25,618
          REFERENCE/DOCKET NUMBER: IMAMURA=1
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 5:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 2193 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: cDNA
     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
0-079-616-5

nment Scores:
. No.:              0              Length:        2193
e:                  316.00         Matches:       316
ent Similarity:     100.0%         Conservative:  0
 Local Similarity:  100.0%         Mismatches:    0
y Match:            96.3%          Indels:        0
                    6              Gaps:          0

0-821-670A-56 (1-328) x US-10-079-616-5 (1-2193)

       13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

       33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

       53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

       73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

       93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

      113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

      133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

      153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

      173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

      193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

      213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

Qy        273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

Qy        293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

Qy        313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 12
US-10-079-616-6
; Sequence 6, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
```

10-079-616-6

gnment Scores:

d. No.:	3.84e-310	Length:	921
re:	306.00	Matches:	306
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	93.3%	Indels:	0
	6	Gaps:	0

10-821-670A-56 (1-328) x US-10-079-616-6 (1-921)

```
        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

       323 TrpAlaSerValSerCys 328
```

```
           ||||||||||||||||||
Db     901 TGGGCATCCGTGTCCTGC 918
```

RESULT 13
US-10-079-616-7
; Sequence 7, Application US/10079616
; Publication No. US20020107366A1
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,616
; FILING DATE: 22-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/011,143
; FILING DATE: 04-FEB-1998
; APPLICATION NUMBER: PCT/JP97/01824
; FILING DATE: 29-MAY-1997
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: IMAMURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

Alignment Scores:

Pred. No.:	3.84e-310	Length:	921
Score:	306.00	Matches:	306
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	93.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-079-616-7 (1-921)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
```

```
 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
901 TGGGCATCCGTGTCCTGC 918

;LT 14
)9-917-265-38
:quence 38, Application US/09917265
:tent No. US20020052030A1
:NERAL INFORMATION:
\PPLICANT: Wonderling, Ramani S.
\PPLICANT:  Boroughs, Karen L.
:ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
:ILE REFERENCE: IM-5
:URRENT APPLICATION NUMBER: US/09/917,265
:URRENT FILING DATE:  2001-07-27
?RIOR APPLICATION NUMBER: 60/223,016
?RIOR FILING DATE: 2000-08-04
vUMBER OF SEQ ID NOS: 109
;OFTWARE: PatentIn version 3.1
:Q ID NO 38
 LENGTH: 1599
```

```
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.:              1.56e-215       Length:         1599
Score:                  216.00          Matches:        316
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            65.9%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265-38 (1-1599)

Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873
```

```
       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
       934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 984

ULT 15
09-917-265-40/c
equence 40, Application US/09917265
atent No. US20020052030A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 109
OFTWARE: PatentIn version 3.1
EQ ID NO 40
 LENGTH: 1599
 TYPE: DNA
 ORGANISM: Felis catus
09-917-265-40

gnment Scores:
d. No.:                1.56e-215      Length:          1599
ce:                    216.00         Matches:         316
cent Similarity:       99.7%          Conservative:    0
t Local Similarity:    99.7%          Mismatches:      1
ry Match:              65.9%          Indels:          0
                       3              Gaps:            0

10-821-670A-56 (1-328) x US-09-917-265-40 (1-1599)

        12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

        32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

        72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

        92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

       112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

       132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

       152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

       172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy     192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy     212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy     232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy     252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy     272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy     292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

Qy     312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 616

RESULT 16
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:
Pred. No.:             1.56e-215      Length:          1599
Score:                 216.00         Matches:         316
Percent Similarity:    99.7%          Conservative:    0
Best Local Similarity: 99.7%          Mismatches:      1
Query Match:           65.9%          Indels:          0
DB:                    9              Gaps:            0

US-10-821-670A-56 (1-328) x US-10-821-670-38 (1-1599)

Qy      12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy      32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153
```

```
 52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

 72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

 92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
    ||||||||||||||||||||||||||||||||||||||||||||||||||
934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 984
```

```
:LT 17
.0-821-670-40/c
'quence 40, Application US/10821670
;blication No. US20040248261A1
 NERAL INFORMATION:
 PPLICANT: Wonderling, Ramani S.
 PPLICANT:  Boroughs, Karen L.
 ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 ITLE OF INVENTION:  THEREOF
 ILE REFERENCE: IM-5
 URRENT APPLICATION NUMBER: US/10/821,670
 URRENT FILING DATE:  2004-04-09
 RIOR APPLICATION NUMBER: 60/223,016
 RIOR FILING DATE: 2000-08-04
 UMBER OF SEQ ID NOS: 111
 OFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:
Pred. No.:              1.56e-215     Length:          1599
Score:                  216.00        Matches:         316
Percent Similarity:     99.7%         Conservative:    0
Best Local Similarity:  99.7%         Mismatches:      1
Query Match:            65.9%         Indels:          0
DB:                     9             Gaps:            0

US-10-821-670A-56 (1-328) x US-10-821-670-40 (1-1599)

Qy        12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

Qy        32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

Qy        52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

Qy        72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

Qy        92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

Qy       112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

Qy       132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

Qy       152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

Qy       172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy       192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy       212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy       232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy       252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy       272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
```

```
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

  312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
  666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGC 616

ULT 18
09-917-265-26
equence 26, Application US/09917265
atent No. US20020052030A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 109
OFTWARE: PatentIn version 3.1
Q ID NO 26
 LENGTH: 921
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(921)
 OTHER INFORMATION:
09-917-265-26

gnment Scores:
d. No.:                3.22e-204      Length:          921
re:                    205.00         Matches:         305
cent Similarity:       99.7%          Conservative:    0
t Local Similarity:    99.7%          Mismatches:      1
ry Match:              62.5%          Indels:          0
                       3              Gaps:            0

10-821-670A-56 (1-328) x US-09-917-265-26 (1-921)

   23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

   43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

   63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

   83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

  103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

  123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

  143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

  163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
      |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
  421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCys 328
              |||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGC 918

RESULT 19
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-28

Alignment Scores:
Pred. No.:             3.22e-204      Length:          921
Score:                 205.00         Matches:         305
Percent Similarity:    99.7%          Conservative:    0
Best Local Similarity: 99.7%          Mismatches:      1
Query Match:           62.5%          Indels:          0
DB:                    3              Gaps:            0

US-10-821-670A-56 (1-328) x US-09-917-265-28 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
```

```
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

   83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

  103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

  123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

  143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

  163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
      ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

  183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

  203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

  223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

  243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

  263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

  283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

  303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

  323 TrpAlaSerValSerCys 328
      ||||||||||||||||||
   21 TGGGCATCCGTGTCCTGC 4
```

```
:LT 20
.0-821-670-26
:quence 26, Application US/10821670
:blication No. US20040248261A1
:NERAL INFORMATION:
:PPLICANT: Wonderling, Ramani S.
:PPLICANT:  Boroughs, Karen L.
:ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
:ITLE OF INVENTION:  THEREOF
:ILE REFERENCE: IM-5
:URRENT APPLICATION NUMBER: US/10/821,670
:URRENT FILING DATE:  2004-04-09
:RIOR APPLICATION NUMBER: 60/223,016
:RIOR FILING DATE: 2000-08-04
:UMBER OF SEQ ID NOS: 111
:OFTWARE: PatentIn version 3.2
:Q ID NO 26
 LENGTH: 921
```

```
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-26

Alignment Scores:
Pred. No.:              3.22e-204       Length:         921
Score:                  205.00          Matches:        305
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            62.5%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-26 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
```

```
Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCys 328
              |||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGC 918

ULT 21
10-821-670-28/c
equence 28, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 28
 LENGTH: 921
 TYPE: DNA
 ORGANISM: Felis catus
10-821-670-28

gnment Scores:
d. No.:              3.22e-204      Length:          921
ce:                  205.00         Matches:         305
cent Similarity:     99.7%          Conservative:    0
t Local Similarity:  99.7%          Mismatches:      1
ry Match:            62.5%          Indels:          0
                     9              Gaps:            0

10-821-670A-56 (1-328) x US-10-821-670-28 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        323 TrpAlaSerValSerCys 328
              |||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGC 4

RESULT 22
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:
Pred. No.:           5.15e-204      Length:          1533
Score:               205.00         Matches:         305
Percent Similarity:  99.7%          Conservative:    0
Best Local Similarity: 99.7%        Mismatches:      1
Query Match:         62.5%          Indels:          0
DB:                  3              Gaps:            0

US-10-821-670A-56 (1-328) x US-09-917-265-43 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
```

```
 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
901 TGGGCATCCGTGTCCTGC 918

LT 23
9-917-265-45/c
quence 45, Application US/09917265
tent No. US20020052030A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 109
OFTWARE: PatentIn version 3.1
Q ID NO 45
```

```
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

Alignment Scores:
Pred. No.:                5.15e-204      Length:          1533
Score:                    205.00         Matches:         305
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              62.5%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-56 (1-328) x US-09-917-265-45 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

323 TrpAlaSerValSerCys 328
    |||||||||||||||||
633 TGGGCATCCGTGTCCTGC 616
```

ULT 24
10-821-670-43
equence 43, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION: THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE: 2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 43
LENGTH: 1533
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
10-821-670-43

gnment Scores:

d. No.:	5.15e-204	Length:	1533
re:	205.00	Matches:	305
cent Similarity:	99.7%	Conservative:	0
t Local Similarity:	99.7%	Mismatches:	1
ry Match:	62.5%	Indels:	0
	9	Gaps:	0

10-821-670A-56 (1-328) x US-10-821-670-43 (1-1533)

```
 23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

 43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
```

```
Qy      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy      243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy      323 TrpAlaSerValSerCys 328
            |||||||||||||||||
Db      901 TGGGCATCCGTGTCCTGC 918
```

RESULT 25
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:

Pred. No.:	5.15e-204	Length:	1533
Score:	205.00	Matches:	305
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	62.5%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-821-670-45 (1-1533)

```
Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
```

```
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

  83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

 103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

 123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

 143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

 163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
     ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

 183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

 243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

 263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

 283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

 303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

 323 TrpAlaSerValSerCys 328
     |||||||||||||||||
 633 TGGGCATCCGTGTCCTGC 616
```

```
LT 26
9-917-265-52
quence 52, Application US/09917265
tent No. US20020052030A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 109
OFTWARE: PatentIn version 3.1
Q ID NO 52
LENGTH: 921
TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-52

Alignment Scores:
Pred. No.:              4.99e-28        Length:         921
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265-52 (1-921)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 27
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-54

Alignment Scores:
Pred. No.:              4.99e-28        Length:         921
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265-54 (1-921)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 28
US-10-821-670-52
; Sequence 52, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
```

FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 52
LENGTH: 921
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(921)
10-821-670-52

gnment Scores:

d. No.:	4.99e-28	Length:	921
re:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	9	Gaps:	0

10-821-670A-56 (1-328) x US-10-821-670-52 (1-921)

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651
```

JLT 29
10-821-670-54/c
equence 54, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 54
LENGTH: 921
TYPE: DNA
ORGANISM: Canis familiaris
10-821-670-54

gnment Scores:

d. No.:	4.99e-28	Length:	921
re:	37.00	Matches:	37
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	11.3%	Indels:	0
	9	Gaps:	0

10-821-670A-56 (1-328) x US-10-821-670-54 (1-921)

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271
```

RESULT 30
US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
; OTHER INFORMATION:
US-09-917-265-58

Alignment Scores:

Pred. No.:	5.31e-28	Length:	987
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-917-265-58 (1-987)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

RESULT 31
US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-60

Alignment Scores:

Pred. No.:	5.31e-28	Length:	987
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.3%	Indels:	0
DB:	3	Gaps:	0

```
0-821-670A-56 (1-328) x US-09-917-265-60 (1-987)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

LT 32
0-821-670-58
quence 58, Application US/10821670
blication No. US20040248261A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 58
LENGTH: 987
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(987)
0-821-670-58

nment Scores:
. No.:              5.31e-28       Length:          987
e:                  37.00          Matches:         37
ent Similarity:     100.0%         Conservative:    0
 Local Similarity:  100.0%         Mismatches:      0
y Match:            11.3%          Indels:          0
                    9              Gaps:            0

0-821-670A-56 (1-328) x US-10-821-670-58 (1-987)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

LT 33
0-821-670-60/c
quence 60, Application US/10821670
blication No. US20040248261A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 60
LENGTH: 987
TYPE: DNA
ORGANISM: Canis familiaris

US-10-821-670-60

Alignment Scores:
Pred. No.:              5.31e-28       Length:          987
Score:                  37.00          Matches:         37
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            11.3%          Indels:          0
DB:                     9              Gaps:            0

US-10-821-670A-56 (1-328) x US-10-821-670-60 (1-987)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 34
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:
Pred. No.:              7.96e-28       Length:          1533
Score:                  37.00          Matches:         37
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            11.3%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-56 (1-328) x US-09-917-265-66 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 35
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
```

```
CURRENT FILING DATE:  2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SQ ID NO 68
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Canis familiaris
09-917-265-68

gnment Scores:
i. No.:                7.96e-28        Length:         1533
ce:                    37.00           Matches:        37
ent Similarity:        100.0%          Conservative:   0
 Local Similarity:     100.0%          Mismatches:     0
y Match:               11.3%           Indels:         0
                       3               Gaps:           0

10-821-670A-56 (1-328) x US-09-917-265-68 (1-1533)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

ULT 36
10-821-670-66
equence 66, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 66
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1533)
10-821-670-66

gnment Scores:
i. No.:                7.96e-28        Length:         1533
ce:                    37.00           Matches:        37
ent Similarity:        100.0%          Conservative:   0
 Local Similarity:     100.0%          Mismatches:     0
y Match:               11.3%           Indels:         0
                       9               Gaps:           0

10-821-670A-56 (1-328) x US-10-821-670-66 (1-1533)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

ULT 37
```

```
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;    LENGTH: 1533
;    TYPE: DNA
;    ORGANISM: Canis familiaris
US-10-821-670-68

Alignment Scores:
Pred. No.:              7.96e-28        Length:         1533
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.3%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-68 (1-1533)

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy         223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 38
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;    LENGTH: 1599
;    TYPE: DNA
;    ORGANISM: Canis familiaris
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)..(1599)
;    OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:
Pred. No.:              8.28e-28        Length:         1599
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265-61 (1-1599)
```

```
      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

LT 39
9-917-265-63/c
quence 63, Application US/09917265
tent No. US20020052030A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 109
OFTWARE: PatentIn version 3.1
Q ID NO 63
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
9-917-265-63

nment Scores:
. No.:              8.28e-28       Length:         1599
e:                  37.00          Matches:        37
ent Similarity:     100.0%         Conservative:   0
 Local Similarity:  100.0%         Mismatches:     0
y Match:            11.3%          Indels:         0
                    3              Gaps:           0

0-821-670A-56 (1-328) x US-09-917-265-63 (1-1599)

      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

LT 40
0-821-670-61
quence 61, Application US/10821670
blication No. US20040248261A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 61
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
0-821-670-61

Alignment Scores:
Pred. No.:              8.28e-28       Length:         1599
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            11.3%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-61 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 41
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-63

Alignment Scores:
Pred. No.:              8.28e-28       Length:         1599
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            11.3%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-63 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 42
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
```

```
3Q ID NO 107
 LENGTH: 2267
 TYPE: DNA
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (154)..(1140)
 OTHER INFORMATION:
)9-917-265-107

gnment Scores:
i. No.:              1.14e-27       Length:         2267
re:                  37.00          Matches:        37
ent Similarity:      100.0%         Conservative:   0
: Local Similarity:  100.0%         Mismatches:     0
cy Match:            11.3%          Indels:         0
                     3              Gaps:           0

10-821-670A-56 (1-328) x US-09-917-265-107 (1-2267)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

ULT 43
)9-917-265-109/c
equence 109, Application US/09917265
atent No. US20020052030A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 109
OFTWARE: PatentIn version 3.1
3Q ID NO 109
 LENGTH: 2267
 TYPE: DNA
 ORGANISM: Canis familiaris
)9-917-265-109

gnment Scores:
i. No.:              1.14e-27       Length:         2267
re:                  37.00          Matches:        37
ent Similarity:      100.0%         Conservative:   0
: Local Similarity:  100.0%         Mismatches:     0
cy Match:            11.3%          Indels:         0
                     3              Gaps:           0

10-821-670A-56 (1-328) x US-09-917-265-109 (1-2267)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
      1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

ULT 44
10-821-670-107
equence 107, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
US-10-821-670-107

Alignment Scores:
Pred. No.:              1.14e-27       Length:         2267
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            11.3%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-107 (1-2267)

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy         223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 45
US-10-821-670-109/c
; Sequence 109, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-109

Alignment Scores:
Pred. No.:              1.14e-27       Length:         2267
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            11.3%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-109 (1-2267)

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449
```

```
      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
     1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

LT 46
9-754-014-2
quence 2, Application US/09754014
tent No. US20020119940A1
GENERAL INFORMATION:
     APPLICANT: Jeff No. US20020119940A1dstrom
                Bruce Freimark
                Deepa Deshpande
     TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                         AND USES
     NUMBER OF SEQUENCES: 12
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Lyon & Lyon
          STREET: 633 West Fifth Street
                  Suite 4700
          CITY: Los Angeles
          STATE: California
          COUNTRY: U.S.A.
          ZIP: 90071-2066
     COMPUTER READABLE FORM:
          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                       storage
          COMPUTER: IBM Compatible
          OPERATING SYSTEM: IBM P.C. DOS 5.0
          SOFTWARE: FastSEQ for Windows 2.0
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/754,014
          FILING DATE: 03-Jan-2001
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 08/948,958
          FILING DATE: <Unknown>
     ATTORNEY/AGENT INFORMATION:
          NAME: Berkman, Charles S.
          REGISTRATION NUMBER: 38,077
          REFERENCE/DOCKET NUMBER: 226/284
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (213) 489-1600
          TELEFAX: (213) 955-0440
          TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 987 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
9-754-014-2

nment Scores:
. No.:              6.65e-26       Length:         987
e:                  35.00          Matches:        35
ent Similarity:     100.0%         Conservative:   0
 Local Similarity:  100.0%         Mismatches:     0
y Match:            10.7%          Indels:         0
                    3              Gaps:           0

0-821-670A-56 (1-328) x US-09-754-014-2 (1-987)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

LT 47
9-754-014-3
```

```
; Sequence 3, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-754-014-3

Alignment Scores:
Pred. No.:              6.65e-26       Length:         987
Score:                  35.00          Matches:        35
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            10.7%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-754-014-3 (1-987)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 48
US-09-754-014-4
; Sequence 4, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
```

```
      TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                          AND USES
      NUMBER OF SEQUENCES: 12
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Lyon & Lyon
           STREET: 633 West Fifth Street
                   Suite 4700
           CITY: Los Angeles
           STATE: California
           COUNTRY: U.S.A.
           ZIP: 90071-2066
      COMPUTER READABLE FORM:
           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                        storage
           COMPUTER: IBM Compatible
           OPERATING SYSTEM: IBM P.C. DOS 5.0
           SOFTWARE: FastSEQ for Windows 2.0
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/754,014
           FILING DATE: 03-Jan-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/948,958
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Berkman, Charles S.
           REGISTRATION NUMBER: 38,077
           REFERENCE/DOCKET NUMBER: 226/284
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 4:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
)9-754-014-4

ignment Scores:
id. No.:                6.65e-26        Length:         987
re:                     35.00           Matches:        35
cent Similarity:        100.0%          Conservative:   0
: Local Similarity:     100.0%          Mismatches:     0
ry Match:               10.7%           Indels:         0
                        3               Gaps:           0

10-821-670A-56 (1-328) x US-09-754-014-4 (1-987)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

JLT 49
)9-836-866-2
equence 2, Application US/09836866
atent No. US20020123473A1
 GENERAL INFORMATION:
      APPLICANT: No. US20020123473A1dstrom, Jeff
                 Freimark, Bruce
                 Deshpande, Deepa
      TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
                          DELIVERY SYTEMS AND USES
      NUMBER OF SEQUENCES: 8
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Lyon & Lyon
           STREET: 633 West Fifth Street
                   Suite 4700
           CITY: Los Angeles
           STATE: California
           COUNTRY: U.S.A.
           ZIP: 90071-2066
      COMPUTER READABLE FORM:
           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                        storage
           COMPUTER: IBM Compatible
           OPERATING SYSTEM: IBM P.C. DOS 5.0
           SOFTWARE: FastSEQ for Windows 2.0
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/836,866
           FILING DATE: 16-Apr-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/949,160
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Warburg, Richard J.
           REGISTRATION NUMBER: 32,327
           REFERENCE/DOCKET NUMBER: 226/285
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-836-866-2

Alignment Scores:
Pred. No.:              6.65e-26        Length:         987
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-836-866-2 (1-987)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 50
US-10-221-975A-1
; Sequence 1, Application US/10221975A
; Publication No. US20040023332A1
; GENERAL INFORMATION:
;  APPLICANT: Pohang University of Science and Technology
;  APPLICANT:  Progen Co., Ltd.
;  APPLICANT:  Sung, Young Chul
;  APPLICANT:  Lee, Sung Hee
;  APPLICANT:  Ha, Sang Jun
;  APPLICANT:  Song, Man Ki
;  APPLICANT:  Chang, Jun
;  TITLE OF INVENTION: Genes of IL-12p40 Subunit Mutated for Improving the Activity of
;  TITLE OF INVENTION:  IL-12 and Use Thereof for DNA Vaccine Adjuvant
;  FILE REFERENCE: 59520-00005
;  CURRENT APPLICATION NUMBER: US/10/221,975A
;  CURRENT FILING DATE:  2003-04-02
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
```

```
LENGTH: 1007
TYPE: DNA
ORGANISM: Homo sapiens
0-221-975A-1

nment Scores:
. No.:              6.77e-26        Length:         1007
e:                  35.00           Matches:        35
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            10.7%           Indels:         0
                    8               Gaps:           0

0-821-670A-56 (1-328) x US-10-221-975A-1 (1-1007)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756

LT 51
0-267-384-194
quence 194, Application US/10267384
blication No. US20030198623A1
GENERAL INFORMATION:
     APPLICANT: Paoletti, Enzo
                Tartaglia, James
                Cox, William I.
     TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
     NUMBER OF SEQUENCES: 217
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Curtis, Morris & Safford
          STREET: 530 Fifth Avenue
          CITY: New York
          STATE: NY
          COUNTRY: USA
          ZIP: 10036
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.25
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/10/267,384
          FILING DATE: 09-Oct-2002
          CLASSIFICATION: 435
     ATTORNEY/AGENT INFORMATION:
          NAME: Frommer, William S.
          REGISTRATION NUMBER: 25,506
          REFERENCE/DOCKET NUMBER: 454310-2530
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (212) 840-3333
          TELEFAX: (212) 840-0712
          TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 194:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 1018 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: cDNA
     SEQUENCE DESCRIPTION: SEQ ID NO: 194:
0-267-384-194

nment Scores:
. No.:              6.84e-26        Length:         1018
e:                  35.00           Matches:        35
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            10.7%           Indels:         0
DB:                 7               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-267-384-194 (1-1018)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 52
US-10-603-064-4
; Sequence 4, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1389
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-4

Alignment Scores:
Pred. No.:              9.1e-26         Length:         1389
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     8               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-603-064-4 (1-1389)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 53
US-10-349-507-2
; Sequence 2, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
;  APPLICANT: Hekimi , Siegfried
;  APPLICANT:  Jiang , Ning
;  APPLICANT:  Benard, Claire
;  APPLICANT:  Kebir , Hania
;  APPLICANT:  McCright, Brenton
;  APPLICANT:  Lakowski , Bernard
;  TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
;  FILE REFERENCE: 11202-006-999
;  CURRENT APPLICATION NUMBER: US/10/349,507
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 10/312,187
;  PRIOR FILING DATE: 2002-12-20
```

```
RIOR APPLICATION NUMBER: PCT/CA01/00913
RIOR FILING DATE: 2001-06-20
RIOR APPLICATION NUMBER: 60/213,174
RIOR FILING DATE: 2000-06-22
RIOR APPLICATION NUMBER: 60/254,932
RIOR FILING DATE: 2000-12-13
UMBER OF SEQ ID NOS: 41
OFTWARE: PatentIn version 3.2
Q ID NO 2
 LENGTH: 1397
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (41)...(1024)
10-349-507-2

nment Scores:
i. No.:                 9.15e-26        Length:         1397
e:                      35.00           Matches:        35
ent Similarity:         100.0%          Conservative:   0
 Local Similarity:      100.0%          Mismatches:     0
y Match:                10.7%           Indels:         0
                        7               Gaps:           0

10-821-670A-56 (1-328) x US-10-349-507-2 (1-1397)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
      746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

LT 54
10-267-565-2
equence 2, Application US/10267565
ublication No. US20030204059A1
ENERAL INFORMATION:
APPLICANT: Gately, Maurice
APPLICANT:  Gubler, Ulrich
APPLICANT:  Hulmes, Jeffery
APPLICANT:  Podlaski, Frank
APPLICANT:  Stern, Alvin
ITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
ITLE OF INVENTION:  LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
ITLE OF INVENTION:  ANTIBODIES THERETO
ILE REFERENCE: 11126-005
URRENT APPLICATION NUMBER: US/10/267,565
URRENT FILING DATE:  2003-01-23
RIOR APPLICATION NUMBER: 09/401,839
RIOR FILING DATE: 1999-09-22
RIOR APPLICATION NUMBER: 08/459,151
RIOR FILING DATE: 1995-06-02
RIOR APPLICATION NUMBER: 08/205,011
RIOR FILING DATE: 1994-03-02
RIOR APPLICATION NUMBER: 07/857,023
RIOR FILING DATE: 1992-03-24
RIOR APPLICATION NUMBER: 07/572,284
RIOR FILING DATE: 1990-08-27
RIOR APPLICATION NUMBER: 07/520,935
RIOR FILING DATE: 1990-05-09
RIOR APPLICATION NUMBER: 07/455,708
RIOR FILING DATE: 1989-12-22
UMBER OF SEQ ID NOS: 43
OFTWARE: FastSEQ for Windows Version 3.0
Q ID NO 2
 LENGTH: 1397
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
;   LOCATION: (41)...(1024)
US-10-267-565-2

Alignment Scores:
Pred. No.:              9.15e-26        Length:         1397
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-267-565-2 (1-1397)

Qy          217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy          237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
                |||||||||||||||||||||||||||||||||||||||||||||
Db          746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 55
US-10-929-182-22
; Sequence 22, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
;  APPLICANT: Zang, Jingwu
;  APPLICANT:  Hong, Jian
;  TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
;  TITLE OF INVENTION:  Multiple Sclerosis
;  FILE REFERENCE: HO-P02859US1
;  CURRENT APPLICATION NUMBER: US/10/929,182
;  CURRENT FILING DATE:  2004-08-30
;  PRIOR APPLICATION NUMBER: US 60/498,731
;  PRIOR FILING DATE: 2003-08-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 1399
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-929-182-22

Alignment Scores:
Pred. No.:              9.16e-26        Length:         1399
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-929-182-22 (1-1399)

Qy          217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy          237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
                |||||||||||||||||||||||||||||||||||||||||||||
Db          748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 56
US-10-429-802-44
; Sequence 44, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  WONG, KA YIN
;  APPLICANT:  ZOU, YIYU
;  TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
;  FILE REFERENCE: UTSC:752US
;  CURRENT APPLICATION NUMBER: US/10/429,802
;  CURRENT FILING DATE:  2003-05-05
```

```
RIOR APPLICATION NUMBER: 60/377,672
RIOR FILING DATE: 2002-05-03
UMBER OF SEQ ID NOS: 54
OFTWARE: PatentIn Ver. 2.1
Q ID NO 44
LENGTH: 2347
TYPE: DNA
ORGANISM: Homo sapiens
0-429-802-44

nment Scores:
. No.:              1.47e-25        Length:         2347
e:                  35.00           Matches:        35
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            10.7%           Indels:         0
                    7               Gaps:           0

0-821-670A-56 (1-328) x US-10-429-802-44 (1-2347)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||||
      748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

LT 57
0-430-503-35
quence 35, Application US/10430503
blication No. US20040005684A1
NERAL INFORMATION:
PPLICANT: HUNG, MIEN-CHIE
PPLICANT:  LAN, KENG-LI
PPLICANT:  OU-YANG, FU
PPLICANT:  LIU, JAW-CHING
PPLICANT:  LAN, KENG-HSIN
ITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
ITLE OF INVENTION:  REAGENTS
ILE REFERENCE: UTSC:797US
URRENT APPLICATION NUMBER: US/10/430,503
URRENT FILING DATE:  2003-05-06
RIOR APPLICATION NUMBER: 60/383,063
RIOR FILING DATE: 2002-05-06
UMBER OF SEQ ID NOS: 42
OFTWARE: PatentIn Ver. 2.1
Q ID NO 35
LENGTH: 2347
TYPE: DNA
ORGANISM: Homo sapiens
0-430-503-35

nment Scores:
. No.:              1.47e-25        Length:         2347
e:                  35.00           Matches:        35
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            10.7%           Indels:         0
                    7               Gaps:           0

0-821-670A-56 (1-328) x US-10-430-503-35 (1-2347)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||||
      748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

LT 58
9-924-703-3
; Sequence 3, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-09-924-703-3

Alignment Scores:
Pred. No.:              1.48e-25        Length:         2362
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-924-703-3 (1-2362)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 59
US-10-358-395-3
; Sequence 3, Application US/10358395
; Publication No. US20040044186A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/10/358,395
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US/09/924,703
;  PRIOR FILING DATE: 2001-08-09
```

```
PRIOR APPLICATION NUMBER: 09/325,958
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 08/858,000
PRIOR FILING DATE: 1997-05-16
PRIOR APPLICATION NUMBER: 08/403,013
PRIOR FILING DATE: 1995-03-13
PRIOR APPLICATION NUMBER: 07/584,941
PRIOR FILING DATE: 1990-09-18
PRIOR APPLICATION NUMBER: 07/307,817
PRIOR FILING DATE: 1989-02-07
PRIOR APPLICATION NUMBER: 07/269,945
PRIOR FILING DATE: 1988-11-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SQ ID NO 3
 LENGTH: 2362
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
 OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (33)..(1016)
10-358-395-3

gnment Scores:
i. No.:              1.48e-25       Length:        2362
ce:                  35.00          Matches:       35
cent Similarity:     100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
cy Match:            10.7%          Indels:        0
                     8              Gaps:          0

10-821-670A-56 (1-328) x US-10-358-395-3 (1-2362)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

JLT 60
10-136-837-1
equence 1, Application US/10136837
iblication No. US20030181405A1
ENERAL INFORMATION:
APPLICANT: NORDSTROM, Jeffrey L
APPLICANT:  PERICLE, Federica
APPLICANT:  ROLLAND, Alain
APPLICANT:  RALSTON, Robert
ITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
ITLE OF INVENTION:  Using the Same
ILE REFERENCE: 273/082 (GM15-1USC1)
URRENT APPLICATION NUMBER: US/10/136,837
URRENT FILING DATE:  2002-04-29
RIOR APPLICATION NUMBER: US 09/268,135
RIOR FILING DATE: 1999-03-12
UMBER OF SEQ ID NOS: 5
OFTWARE: PatentIn version 3.1
EQ ID NO 1
 LENGTH: 5686
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Human IL-12 Plasmid pIN1143
10-136-837-1

gnment Scores:
i. No.:              3.32e-25       Length:        5686
ce:                  35.00          Matches:       35
Percent Similarity:  100.0%         Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:         10.7%          Indels:        0
DB:                  7              Gaps:          0

US-10-821-670A-56 (1-328) x US-10-136-837-1 (1-5686)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3864 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3923

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db       3924 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3968

RESULT 61
US-10-511-237-1
; Sequence 1, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 11569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.hscIL-12 for regulated expre
;   OTHER INFORMATION: human IL-12
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2709)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2710)..(4308)
;   OTHER INFORMATION: Human single-chain IL-12
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (4020)..(4023)
;   OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-1
```

```
nment Scores:
. No.:              6.38e-25        Length:         11569
e:                  35.00           Matches:        35
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            10.7%           Indels:         0
                    10              Gaps:           0

0-821-670A-56 (1-328) x US-10-511-237-1 (1-11569)

      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     3355 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3414

      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||||||||||||||||||||||||
     3415 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3459

LT 62
0-528-644A-53
quence 53, Application US/10528644A
blication No. US20050287117A1
NERAL INFORMATION:
PPLICANT: SUNG, Young Chul
PPLICANT:  YOUN, Jin-Won
PPLICANT:  YANG, Se-Hwan
PPLICANT:  PARK, Su-Hwan
PPLICANT:  LEE, Chang Geun
ITLE OF INVENTION: A VACCINE ENHANCING THE PROTECTIVE IMMUNITY TO
ITLE OF INVENTION:  HEPATITIS C VIRUS USING PLASMID DNA AND RECOMBINANT ADENOVIRUS
ILE REFERENCE: 428.1049
URRENT APPLICATION NUMBER: US/10/528,644A
URRENT FILING DATE:  2005-03-18
RIOR APPLICATION NUMBER: PCT/KR03/01951
RIOR FILING DATE: 2003-11-19
RIOR APPLICATION NUMBER: KR 2002-0058712
RIOR FILING DATE: 2002-09-27
RIOR APPLICATION NUMBER: KR 2002-68496
RIOR FILING DATE: 2002-11-06
UMBER OF SEQ ID NOS: 54
OFTWARE: KopatentIn 1.71
Q ID NO 53
LENGTH: 2390
TYPE: DNA
ORGANISM: Homo sapiens (hIL-12m)
0-528-644A-53

nment Scores:
. No.:              3.29e-18        Length:         2390
e:                  28.00           Matches:        28
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            8.5%            Indels:         0
                    10              Gaps:           0

0-821-670A-56 (1-328) x US-10-528-644A-53 (1-2390)

      224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     2070 TACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAG 2129

      244 LeuLysProLeuLysAsnSerArg 251
          |||||||||||||||||||||||
     2130 CTGAAGCCATTAAAGAATTCTCGG 2153

LT 63
9-826-025-24
quence 24, Application US/09826025
tent No. US20020162123A1
GENERAL INFORMATION:
     APPLICANT: Chang, Lung-Ji
     TITLE OF INVENTION: Combination Immunogene Therapy
     NUMBER OF SEQUENCES: 25
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Medlen & Carroll, LLP
;              STREET: 220 Montgomery Street, Suite 2200
;              CITY: San Francisco
;              STATE: California
;              COUNTRY: United States of America
;              ZIP: 94104
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/826,025
;              FILING DATE: 04-Apr-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/838,702
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Ingolia, Diane E.
;              REGISTRATION NUMBER: 40,027
;              REFERENCE/DOCKET NUMBER: CHANG-02687
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 705-8410
;              TELEFAX: (415) 397-8338
;    INFORMATION FOR SEQ ID NO: 24:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 987 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         MOLECULE TYPE: other nucleic acid
;              DESCRIPTION: /desc = "DNA"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

Alignment Scores:
Pred. No.:              2.56e-13        Length:         987
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-826-025-24 (1-987)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 525

Qy        176 SerAlaGlu 178
              |||||||||
Db        526 TCTGCAGAG 534

RESULT 64
US-10-785-577-24
; Sequence 24, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;         APPLICANT: Chang, Lung-Ji
;         TITLE OF INVENTION: Combination Immunogene Therapy
;         NUMBER OF SEQUENCES: 25
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Medlen & Carroll, LLP
;              STREET: 220 Montgomery Street, Suite 2200
;              CITY: San Francisco
;              STATE: California
;              COUNTRY: United States of America
;              ZIP: 94104
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/785,577
FILING DATE: 23-Feb-2004
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/838,702
FILING DATE: 9-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CHANG-02687
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
10-785-577-24

jnment Scores:

i. No.:	2.56e-13	Length:	987
ce:	23.00	Matches:	23
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	7.0%	Indels:	0
	9	Gaps:	0

10-821-670A-56 (1-328) x US-10-785-577-24 (1-987)

```
Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 525

Qy        176 SerAlaGlu 178
              |||||||||
Db        526 TCTGCAGAG 534
```

JLT 65
10-373-456-18
equence 18, Application US/10373456
ublication No. US20040009146A1
ENERAL INFORMATION:
APPLICANT: Podhajcer, Osvaldo
TITLE OF INVENTION: Anti-Tumor Vaccine and Method
FILE REFERENCE: 1423P-US/101141-14
CURRENT APPLICATION NUMBER: US/10/373,456
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/359,836
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 1005
TYPE: DNA
ORGANISM: Homo sapiens
10-373-456-18

jnment Scores:

i. No.:	2.6e-13	Length:	1005
ce:	23.00	Matches:	23
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	7.0%	Indels:	0
	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-373-456-18 (1-1005)

```
Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 533

Qy        176 SerAlaGlu 178
              |||||||||
Db        534 TCTGCAGAG 542
```

RESULT 66
US-10-373-456-20
; Sequence 20, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
; APPLICANT: Podhajcer, Osvaldo
; TITLE OF INVENTION: Anti-Tumor Vaccine and Method
; FILE REFERENCE: 1423P-US/101141-14
; CURRENT APPLICATION NUMBER: US/10/373,456
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,836
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-373-456-20

Alignment Scores:

Pred. No.:	2.63e-13	Length:	1017
Score:	23.00	Matches:	23
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-373-456-20 (1-1017)

```
Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 537

Qy        176 SerAlaGlu 178
              |||||||||
Db        538 TCTGCAGAG 546
```

RESULT 67
US-10-742-405-7
; Sequence 7, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Edward P.
; APPLICANT: Chan, Jason R.
; APPLICANT: Moore, Kevin
; APPLICANT: Nguyen, Nhung
; APPLICANT: Churakova, Tatyana
; APPLICANT: Chen, Shi-Juan
; APPLICANT: Cua, Daniel J.
; TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
; FILE REFERENCE: DX01578K
; CURRENT APPLICATION NUMBER: US/10/742,405
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1569)

0-742-405-7

nment Scores:

. No.:	3.94e-13	Length:	1580
e:	23.00	Matches:	23
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	7.0%	Indels:	0
	9	Gaps:	0

0-821-670A-56 (1-328) x US-10-742-405-7 (1-1580)

```
      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      478 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 537

      176 SerAlaGlu 178
          |||||||||
      538 TCTGCAGAG 546
```

LT 68
0-373-456-2
quence 2, Application US/10373456
blication No. US20040009146A1
NERAL INFORMATION:
PPLICANT: Podhajcer, Osvaldo
ITLE OF INVENTION: Anti-Tumor Vaccine and Method
ILE REFERENCE: 1423P-US/101141-14
URRENT APPLICATION NUMBER: US/10/373,456
URRENT FILING DATE: 2003-02-25
RIOR APPLICATION NUMBER: US 60/359,836
RIOR FILING DATE: 2002-02-26
UMBER OF SEQ ID NOS: 20
OFTWARE: PatentIn version 3.1
Q ID NO 2
LENGTH: 1828
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: p40-linker-p35 fragment cloned into MVL-hIL12lig vector (Fig. 11)
0-373-456-2

nment Scores:

. No.:	4.51e-13	Length:	1828
e:	23.00	Matches:	23
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	7.0%	Indels:	0
	7	Gaps:	0

0-821-670A-56 (1-328) x US-10-373-456-2 (1-1828)

```
      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      478 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 537

      176 SerAlaGlu 178
          |||||||||
      538 TCTGCAGAG 546
```

LT 69
0-228-811-4
quence 4, Application US/10228811
blication No. US20030054392A1
NERAL INFORMATION:
PPLICANT: Wittig, Prof. Burghardt
PPLICANT: Junghans, Claas
ITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
ITLE OF INVENTION: Therapy
ILE REFERENCE: XI 597/99
URRENT APPLICATION NUMBER: US/10/228,811
URRENT FILING DATE: 2002-08-27
RIOR APPLICATION NUMBER: DE 196 48 625.4
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1870)
; OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1869)..(1870)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
; OTHER INFORMATION: to 1870 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No
US-10-228-811-4

Alignment Scores:

Pred. No.:	4.6e-13	Length:	1870
Score:	23.00	Matches:	23
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-228-811-4 (1-1870)

```
Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1157

Qy        176 SerAlaGlu 178
              |||||||||
Db       1158 TCTGCAGAG 1166
```

RESULT 70
US-10-172-399-7
; Sequence 7, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
; APPLICANT: Li, Chuan-Yuan
; APPLICANT: Dewhirst, Mark
; APPLICANT: Huang, Qian
; TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
; FILE REFERENCE: 180-129
; CURRENT APPLICATION NUMBER: US/10/172,399
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 2318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(1000)
US-10-172-399-7

Alignment Scores:

Pred. No.:	5.6e-13	Length:	2318
Score:	23.00	Matches:	23
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.0%	Indels:	0

```
                    6              Gaps:          0

10-821-670A-56 (1-328) x US-10-172-399-7 (1-2318)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       479 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 538

       176 SerAlaGlu 178
           |||||||||
       539 TCTGCAGAG 547

JLT 71
10-476-961-3
equence 3, Application US/10476961
iblication No. US20040241843A1
ENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT:  Susan M. Freier
APPLICANT:  Isis Pharmaceuticals, Inc.
ITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
ILE REFERENCE: RTSP-0393
URRENT APPLICATION NUMBER: US/10/476,961
URRENT FILING DATE:  2003-11-05
RIOR APPLICATION NUMBER: 2001-05-07
RIOR FILING DATE: 09/851,062
UMBER OF SEQ ID NOS: 87
Q ID NO 3
 LENGTH: 2318
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (14)...(1000)
10-476-961-3

nment Scores:
. No.:              5.6e-13        Length:        2318
e:                  23.00          Matches:       23
ent Similarity:     100.0%         Conservative:  0
 Local Similarity:  100.0%         Mismatches:    0
y Match:            7.0%           Indels:        0
                    9              Gaps:          0

10-821-670A-56 (1-328) x US-10-476-961-3 (1-2318)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       479 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 538

       176 SerAlaGlu 178
           |||||||||
       539 TCTGCAGAG 547

JLT 72
10-373-456-1
equence 1, Application US/10373456
iblication No. US20040009146A1
ENERAL INFORMATION:
APPLICANT: Podhajcer, Osvaldo
ITLE OF INVENTION: Anti-Tumor Vaccine and Method
ILE REFERENCE: 1423P-US/101141-14
URRENT APPLICATION NUMBER: US/10/373,456
URRENT FILING DATE:  2003-02-25
RIOR APPLICATION NUMBER: US 60/359,836
RIOR FILING DATE: 2002-02-26
UMBER OF SEQ ID NOS: 20
OFTWARE: PatentIn version 3.1
Q ID NO 1
 LENGTH: 2466
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
;   OTHER INFORMATION: p35-IRES-p40 fragment cloned into MVL-hIL-12 and MVL-hIL-12-hIL-1
;   OTHER INFORMATION: 0 vectors (Fig 11)
US-10-373-456-1

Alignment Scores:
Pred. No.:              5.93e-13       Length:        2466
Score:                  23.00          Matches:       23
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            7.0%           Indels:        0
DB:                     7              Gaps:          0

US-10-821-670A-56 (1-328) x US-10-373-456-1 (1-2466)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1935 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1994

Qy        176 SerAlaGlu 178
              |||||||||
Db       1995 TCTGCAGAG 2003

RESULT 73
US-09-828-825-1
; Sequence 1, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV  IE
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA Promoter
;   NAME/KEY: mRNA
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: mRNA
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
;   OTHER INFORMATION: linker at 3624-3629)
;   NAME/KEY: promoter
;   LOCATION: (4352)..(4431)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4362)..(4583)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4678)..(5133)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5197)..(6564)
;   OTHER INFORMATION: Neo r expression cassette
```

```
NAME/KEY: misc_feature
LOCATION: (6975)..(7835)
OTHER INFORMATION: Ampicillin resistance
OTHER INFORMATION: Description of Artificial Sequence: Plasmid
NAME/KEY: CDS
LOCATION: (2640)..(4223)
OTHER INFORMATION: IL 12.0 coding sequence - 2 amino acid linker at
OTHER INFORMATION: 3624
9-828-825-1

nment Scores:
. No.:              1.86e-12        Length:         8578
e:                  23.00           Matches:        23
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            7.0%            Indels:         0
                    3               Gaps:           0

0-821-670A-56 (1-328) x US-09-828-825-1 (1-8578)

      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

      176 SerAlaGlu 178
          |||||||||
     3165 TCTGCAGAG 3173

LT 74
9-828-825-3
quence 3, Application US/09828825
tent No. US20020018767A1
NERAL INFORMATION:
PPLICANT: Lee, Seewoo
PPLICANT:  Kim, Han-soo
ITLE OF INVENTION: Anti-cancer Cellular Vaccine
ILE REFERENCE: 84906-102
URRENT APPLICATION NUMBER: US/09/828,825
URRENT FILING DATE:  2001-04-10
RIOR APPLICATION NUMBER: KR00-43498
RIOR FILING DATE: 2000-07-27
UMBER OF SEQ ID NOS: 16
OFTWARE: PatentIn Ver. 2.1
Q ID NO 3
LENGTH: 8578
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid
NAME/KEY: enhancer
LOCATION: (1)..(659)
OTHER INFORMATION: CMV IE Enhancer
NAME/KEY: promoter
LOCATION: (669)..(750)
OTHER INFORMATION: CMV IE Promoter
NAME/KEY: misc_feature
LOCATION: (890)..(1002)
OTHER INFORMATION: InTervening Sequence
NAME/KEY: promoter
LOCATION: (1067)..(1085)
OTHER INFORMATION: T7 RNA polymerase promoter
NAME/KEY: misc_feature
LOCATION: (1090)..(1984)
OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
NAME/KEY: RBS
LOCATION: (2013)..(2593)
OTHER INFORMATION: IRES sequence
NAME/KEY: misc_feature
LOCATION: (2627)..(4263)
OTHER INFORMATION: Human IL12.0 sequence (2640-4217 is coding
OTHER INFORMATION: sequence)
NAME/KEY: promoter
LOCATION: (4346)..(4425)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4356)..(4577)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4672)..(5127)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5191)..(6558)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6969)..(7829)
;   OTHER INFORMATION: Ampicillin resistance
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4217)
;   OTHER INFORMATION: IL12.0 coding sequence - no linker
US-09-828-825-3

Alignment Scores:
Pred. No.:              1.86e-12        Length:         8578
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-828-825-3 (1-8578)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

Qy        176 SerAlaGlu 178
              |||||||||
Db       3165 TCTGCAGAG 3173

RESULT 75
US-09-828-825-7
; Sequence 7, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
```

```
LOCATION: (2627)..(4263)
OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
OTHER INFORMATION: sequence, 13 amino acid flexible linker at
OTHER INFORMATION: 3606-3676)
NAME/KEY: CDS
LOCATION: (2640)..(4253)
OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
NAME/KEY: promoter
LOCATION: (4362)..(4383)
OTHER INFORMATION: T3 RNA Polymerase promoter
NAME/KEY: polyA_signal
LOCATION: (4393)..(4614)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal
NAME/KEY: rep_origin
LOCATION: (4709)..(5164)
OTHER INFORMATION: f1 origin of replication
NAME/KEY: misc_feature
LOCATION: (5228)..(6595)
OTHER INFORMATION: Neo r expression cassette
NAME/KEY: misc_feature
LOCATION: (7006)..(7866)
OTHER INFORMATION: Ampicillin resistance
)9-828-825-7

ınment Scores:
i. No.:                1.87e-12        Length:         8608
:e:                    23.00           Matches:        23
:ent Similarity:       100.0%          Conservative:   0
: Local Similarity:    100.0%          Mismatches:     0
:y Match:              7.0%            Indels:         0
                       3               Gaps:           0

:0-821-670A-56 (1-328) x US-09-828-825-7 (1-8608)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

       176 SerAlaGlu 178
           |||||||||
      3165 TCTGCAGAG 3173

JLT 76
)9-828-825-5
equence 5, Application US/09828825
atent No. US20020018767A1
ENERAL INFORMATION:
APPLICANT: Lee, Seewoo
APPLICANT:  Kim, Han-soo
ITLE OF INVENTION: Anti-cancer Cellular Vaccine
ILE REFERENCE: 84906-102
URRENT APPLICATION NUMBER: US/09/828,825
URRENT FILING DATE:  2001-04-10
RIOR APPLICATION NUMBER: KR00-43498
RIOR FILING DATE: 2000-07-27
UMBER OF SEQ ID NOS: 16
OFTWARE: PatentIn Ver. 2.1
Q ID NO 5
 LENGTH: 8623
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(750)
 OTHER INFORMATION: CMV enhancer and promoter
 NAME/KEY: misc_feature
 LOCATION: (890)..(1002)
 OTHER INFORMATION: Intervening sequence
 NAME/KEY: promoter
 LOCATION: (1067)..(1085)
 OTHER INFORMATION: T7 RNA polymerase promoter
 NAME/KEY: misc_feature
 LOCATION: (1090)..(1984)
;  OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;  NAME/KEY: RBS
;  LOCATION: (2013)..(2593)
;  OTHER INFORMATION: IRES sequence
;  NAME/KEY: misc_feature
;  LOCATION: (2627)..(4278)
;  OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
;  OTHER INFORMATION: flexible linker from 3606-3690
;  NAME/KEY: CDS
;  LOCATION: (2640)..(4268)
;  OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
;  OTHER INFORMATION: sequence
;  NAME/KEY: promoter
;  LOCATION: (4398)..(4407)
;  OTHER INFORMATION: T3 RNA polymerase promoter
;  NAME/KEY: polyA_signal
;  LOCATION: (4408)..(4629)
;  OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;  NAME/KEY: rep_origin
;  LOCATION: (4724)..(5179)
;  OTHER INFORMATION: f1 origin of replication
;  NAME/KEY: misc_feature
;  LOCATION: (5243)..(6610)
;  OTHER INFORMATION: Neo r expression cassette
;  NAME/KEY: misc_feature
;  LOCATION: (7021)..(7881)
;  OTHER INFORMATION: Ampicillin resistance
;  OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

Alignment Scores:
Pred. No.:              1.87e-12        Length:         8623
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-828-825-5 (1-8623)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

Qy        176 SerAlaGlu 178
              |||||||||
Db       3165 TCTGCAGAG 3173

RESULT 77
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 8629
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
```

```
LOCATION: (1067)..(1085)
OTHER INFORMATION: T7 RNA polymerase promoter
NAME/KEY: misc_feature
LOCATION: (1090)..(2726)
OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
OTHER INFORMATION: amino acid linker at 2087-2116)
NAME/KEY: CDS
LOCATION: (1103)..(2716)
OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
NAME/KEY: RBS
LOCATION: (2752)..(3332)
OTHER INFORMATION: IRES sequence
NAME/KEY: misc_feature
LOCATION: (3369)..(4263)
OTHER INFORMATION: Human B7.1 sequence
NAME/KEY: promoter
LOCATION: (4383)..(4404)
OTHER INFORMATION: T3 RNA Polymerase promoter
NAME/KEY: polyA_signal
LOCATION: (4414)..(4635)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal
NAME/KEY: rep_origin
LOCATION: (4730)..(5185)
OTHER INFORMATION: f1 origin of replication
NAME/KEY: misc_feature
LOCATION: (5249)..(6616)
OTHER INFORMATION: Neo r expression cassette
NAME/KEY: misc_feature
LOCATION: (7027)..(7887)
OTHER INFORMATION: Ampicillin resistance gene
9-828-825-15

nment Scores:
. No.:              1.87e-12        Length:         8629
e:                  23.00           Matches:        23
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            7.0%            Indels:         0
                    3               Gaps:           0

0-821-670A-56 (1-328) x US-09-828-825-15 (1-8629)

      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1568 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1627

      176 SerAlaGlu 178
          |||||||||
     1628 TCTGCAGAG 1636

LT 78
9-828-825-9
quence 9, Application US/09828825
tent No. US20020018767A1
NERAL INFORMATION:
PPLICANT: Lee, Seewoo
PPLICANT:  Kim, Han-soo
ITLE OF INVENTION: Anti-cancer Cellular Vaccine
ILE REFERENCE: 84906-102
URRENT APPLICATION NUMBER: US/09/828,825
URRENT FILING DATE:  2001-04-10
RIOR APPLICATION NUMBER: KR00-43498
RIOR FILING DATE: 2000-07-27
UMBER OF SEQ ID NOS: 16
OFTWARE: PatentIn Ver. 2.1
Q ID NO 9
LENGTH: 8638
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid
NAME/KEY: misc_feature
LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4293)
;   OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
;   OTHER INFORMATION: amino acid linker at 3606-3706)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4283)
;   OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4392)..(4413)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4423)..(4644)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4739)..(5194)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5258)..(6625)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7036)..(7896)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9

Alignment Scores:
Pred. No.:              1.88e-12        Length:         8638
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-828-825-9 (1-8638)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

Qy        176 SerAlaGlu 178
              |||||||||
Db       3165 TCTGCAGAG 3173

RESULT 79
US-09-828-825-13
; Sequence 13, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 8644
;   TYPE: DNA
```

```
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid
NAME/KEY: misc_feature
LOCATION: (1)..(750)
OTHER INFORMATION: CMV enhancer and promoter
NAME/KEY: promoter
LOCATION: (1067)..(1085)
OTHER INFORMATION: T7 RNA polymerase promoter
NAME/KEY: misc_feature
LOCATION: (1090)..(2731)
OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
OTHER INFORMATION: amino acid linker at 2087-2131)
NAME/KEY: CDS
LOCATION: (1103)..(2731)
OTHER INFORMATION: IL12.3 (15 amino acid linker)
NAME/KEY: RBS
LOCATION: (2767)..(3347)
OTHER INFORMATION: IRES sequence
NAME/KEY: misc_feature
LOCATION: (3384)..(4278)
OTHER INFORMATION: Human B7.1 sequence
NAME/KEY: promoter
LOCATION: (4398)..(4419)
OTHER INFORMATION: T3 RNA polymerase promoter
NAME/KEY: polyA_signal
LOCATION: (4429)..(4650)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal
NAME/KEY: rep_origin
LOCATION: (4745)..(5200)
OTHER INFORMATION: f1 origin of replication
NAME/KEY: misc_feature
LOCATION: (5264)..(5681)
OTHER INFORMATION: Neo r expression cassette
NAME/KEY: misc_feature
LOCATION: (7042)..(7902)
OTHER INFORMATION: Ampicillin resistance gene
)9-828-825-13

ignment Scores:
i. No.:                1.88e-12      Length:          8644
ce:                    23.00         Matches:         23
cent Similarity:       100.0%        Conservative:    0
: Local Similarity:    100.0%        Mismatches:      0
cy Match:              7.0%          Indels:          0
                       3             Gaps:            0

10-821-670A-56 (1-328) x US-09-828-825-13 (1-8644)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1568 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1627

       176 SerAlaGlu 178
           |||||||||
      1628 TCTGCAGAG 1636

JLT 80
)9-828-825-11
equence 11, Application US/09828825
itent No. US20020018767A1
ENERAL INFORMATION:
APPLICANT: Lee, Seewoo
APPLICANT:  Kim, Han-soo
ITLE OF INVENTION: Anti-cancer Cellular Vaccine
ILE REFERENCE: 84906-102
URRENT APPLICATION NUMBER: US/09/828,825
URRENT FILING DATE:  2001-04-10
RIOR APPLICATION NUMBER: KR00-43498
RIOR FILING DATE: 2000-07-27
UMBER OF SEQ ID NOS: 16
OFTWARE: PatentIn Ver. 2.1
Q ID NO 11
```

```
;   LENGTH: 8659
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2756)
;   OTHER INFORMATION: Human IL12.4 (coding sequence 1103-2746, 19 amino
;   OTHER INFORMATION: acid linker at 2087-2146)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2746)
;   OTHER INFORMATION: Human IL12.4 (19 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2782)..(3362)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3399)..(4293)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4413)..(4434)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4444)..(4665)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4760)..(5215)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5279)..(6646)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7057)..(7917)
;   OTHER INFORMATION: Ampicillin resistance gene
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-11

Alignment Scores:
Pred. No.:             1.88e-12      Length:          8659
Score:                 23.00         Matches:         23
Percent Similarity:    100.0%        Conservative:    0
Best Local Similarity: 100.0%        Mismatches:      0
Query Match:           7.0%          Indels:          0
DB:                    3             Gaps:            0

US-10-821-670A-56 (1-328) x US-09-828-825-11 (1-8659)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1627

Qy        176 SerAlaGlu 178
              |||||||||
Db       1628 TCTGCAGAG 1636

RESULT 81
US-10-511-237-3
; Sequence 3, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Express
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
```

```
LENGTH: 11453
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Adenoviral expression plasmid pShuttle.3r.hscIL-12 for regulated
OTHER INFORMATION: expression of human IL-12 following virus generation using AdEasy
FEATURE:
NAME/KEY: gene
LOCATION: (327)..(713)
OTHER INFORMATION: VP16
FEATURE:
NAME/KEY: gene
LOCATION: (714)..(1352)
OTHER INFORMATION: TetR
FEATURE:
NAME/KEY: Intron
LOCATION: (1353)..(1912)
OTHER INFORMATION:
FEATURE:
NAME/KEY: promoter
LOCATION: (1864)..(1902)
OTHER INFORMATION: TK-min
FEATURE:
NAME/KEY: protein_bind
LOCATION: (1913)..(2212)
OTHER INFORMATION: TetO7
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2213)..(2709)
OTHER INFORMATION: CMV-min + Intron
FEATURE:
NAME/KEY: promoter
LOCATION: (2226)..(2264)
OTHER INFORMATION: CMV-min
FEATURE:
NAME/KEY: gene
LOCATION: (2710)..(4308)
OTHER INFORMATION: Human singe-chain IL-12
FEATURE:
NAME/KEY: mutation
LOCATION: (4020)..(4023)
OTHER INFORMATION: T/C, A/T, G/C, T/G
0-511-237-3

nment Scores:
. No.:              2.43e-12        Length:         11453
e:                  23.00           Matches:        23
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            7.0%            Indels:         0
                    10              Gaps:           0

0-821-670A-56 (1-328) x US-10-511-237-3 (1-11453)

      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     3175 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3234

      176 SerAlaGlu 178
          |||||||||
     3235 TCTGCAGAG 3243

LT 82
0-240-376A-130
quence 130, Application US/10240376A
blication No. US20040161747A1
NERAL INFORMATION:
PPLICANT: Morahan, Grant
ITLE OF INVENTION: A METHOD FOR SCREENING FOR AUTOIMMUNE
ITLE OF INVENTION:  DISEASE BY IDENTIFYING POLYMORPHISMS IN IL-12 p40
ILE REFERENCE: DAVI186.001APC
URRENT APPLICATION NUMBER: US/10/240,376A
URRENT FILING DATE:  2002-09-27
;  PRIOR APPLICATION NUMBER: PCT/AU01/00340
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: PQ 6466
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 60/204,366
;  PRIOR FILING DATE: 2000-05-15
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 18340
;   TYPE: DNA
;   ORGANISM: mammalian
US-10-240-376A-130

Alignment Scores:
Pred. No.:              4.19e-11        Length:         18340
Score:                  22.00           Matches:        22
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.7%            Indels:         0
DB:                     8               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-240-376A-130 (1-18340)

Qy        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14078 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 14137

Qy        273 ThrPhe 274
              ||||||
Db      14138 ACATTC 14143

RESULT 83
US-10-029-386-16833/c
; Sequence 16833, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16833
;   LENGTH: 270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR5.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;   OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BF204907.1, EVALUE 9.20e-02
;   OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 4.00e-41
US-10-029-386-16833

Alignment Scores:
Pred. No.:              1.09e-10        Length:         270
Score:                  20.00           Matches:        20
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.1%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-029-386-16833 (1-270)

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
```

```
                                                                                                                    ||||||
```

```
URRENT FILING DATE:  2005-05-11
RIOR APPLICATION NUMBER: US 60/570,425
RIOR FILING DATE: 2004-05-11
UMBER OF SEQ ID NOS: 7285
OFTWARE: PatentIn version 3.3
Q ID NO 4303
LENGTH: 399
TYPE: DNA
ORGANISM: Mesocricetus auratus
1-128-049-4303

nment Scores:
. No.:              1.56e-10       Length:         399
e:                  20.00          Matches:        20
ent Similarity:     100.0%         Conservative:   0
 Local Similarity:  100.0%         Mismatches:     0
y Match:            6.1%           Indels:         0
                    16             Gaps:           0

0-821-670A-56 (1-328) x US-11-128-049-4303 (1-399)

      135 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182

LT 88
0-029-386-3133/c
quence 3133, Application US/10029386
blication No. US20030194704A1
NERAL INFORMATION:
PPLICANT: Penn, Sharron G.
PPLICANT:  Rank, David R.
PPLICANT:  Hanzel, David K.
ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
ITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
ILE REFERENCE: AEOMICA-X-2
URRENT APPLICATION NUMBER: US/10/029,386
URRENT FILING DATE:  2001-12-20
UMBER OF SEQ ID NOS: 34288
OFTWARE: Annomax Sequence Listing Engine vers. 1.1
Q ID NO 3133
LENGTH: 556
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR5.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 5.00e-43
OTHER INFORMATION: EST_HUMAN HIT: BG389008.1, EVALUE 2.00e-01
0-029-386-3133

nment Scores:
. No.:              2.11e-10       Length:         556
e:                  20.00          Matches:        20
ent Similarity:     100.0%         Conservative:   0
 Local Similarity:  100.0%         Mismatches:     0
y Match:            6.1%           Indels:         0
                    7              Gaps:           0

0-821-670A-56 (1-328) x US-10-029-386-3133 (1-556)

       63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      362 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 303

LT 89
9-823-549-77
quence 77, Application US/09823549
blication No. US20020147998A1
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/09/823,549
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-09-823-549-77

Alignment Scores:
Pred. No.:              4.59e-08       Length:         73
Score:                  17.00          Matches:        17
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            5.2%           Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-823-549-77 (1-73)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59

RESULT 90
US-10-685-992-77
; Sequence 77, Application US/10685992
; Publication No. US20040213739A1
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/10/685,992
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US/09/823,549
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-10-685-992-77

Alignment Scores:
Pred. No.:              4.59e-08       Length:         73
Score:                  17.00          Matches:        17
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            5.2%           Indels:         0
DB:                     9              Gaps:           0
```

:0-821-670A-56 (1-328) x US-10-685-992-77 (1-73)

```
      227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
        9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59
```

JLT 91
:1-136-527-4408
equence 4408, Application US/11136527
ublication No. US20050287570A1
ENERAL INFORMATION:
\PPLICANT: Wyeth
\PPLICANT: Mounts, William M
ITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
ILE REFERENCE: 031896-041000 (AM101086)
URRENT APPLICATION NUMBER: US/11/136,527
URRENT FILING DATE: 2005-05-25
RIOR APPLICATION NUMBER: US 60/574,294
RIOR FILING DATE: 2005-05-26
UMBER OF SEQ ID NOS: 362830
OFTWARE: PatentIn version 3.2
Q ID NO 4408
LENGTH: 600
TYPE: DNA
ORGANISM: Rattus norvegicus
l1-136-527-4408

gnment Scores:

i. No.:	3.17e-07	Length:	600
e:	17.00	Matches:	17
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	5.2%	Indels:	0
	16	Gaps:	0

:0-821-670A-56 (1-328) x US-11-136-527-4408 (1-600)

```
      227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      262 AGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAG 312
```

JLT 92
:1-136-527-312
equence 312, Application US/11136527
ublication No. US20050287570A1
ENERAL INFORMATION:
\PPLICANT: Wyeth
\PPLICANT: Mounts, William M
ITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
ILE REFERENCE: 031896-041000 (AM101086)
URRENT APPLICATION NUMBER: US/11/136,527
URRENT FILING DATE: 2005-05-25
RIOR APPLICATION NUMBER: US 60/574,294
RIOR FILING DATE: 2005-05-26
UMBER OF SEQ ID NOS: 362830
OFTWARE: PatentIn version 3.2
Q ID NO 312
LENGTH: 1024
TYPE: DNA
ORGANISM: Rattus norvegicus
l1-136-527-312

gnment Scores:

i. No.:	5.19e-07	Length:	1024
e:	17.00	Matches:	17
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	5.2%	Indels:	0
	16	Gaps:	0

:0-821-670A-56 (1-328) x US-11-136-527-312 (1-1024)

```
Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 AGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAG 736
```

RESULT 93
US-10-603-064-3
; Sequence 3, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1409
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-10-603-064-3

Alignment Scores:

Pred. No.:	6.96e-07	Length:	1409
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.2%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-603-064-3 (1-1409)

```
Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740
```

RESULT 94
US-10-603-064-2
; Sequence 2, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-2

Alignment Scores:

Pred. No.:	7.24e-07	Length:	1472
Score:	17.00	Matches:	17

```
ent Similarity:     100.0%          Conservative:  0
 Local Similarity:  100.0%          Mismatches:    0
y Match:            5.2%            Indels:        0
                    8               Gaps:          0

0-821-670A-56 (1-328) x US-10-603-064-2 (1-1472)

      227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740

LT 95
0-603-064-12
quence 12, Application US/10603064
blication No. US20040072299A1
NERAL INFORMATION:
PPLICANT: Gillies, Stephen
PPLICANT:  Lo, Kin Ming
ITLE OF INVENTION: Multiple Cytokine Protein Complexes
ILE REFERENCE: LEX-010
URRENT APPLICATION NUMBER: US/10/603,064
URRENT FILING DATE:  2003-06-24
RIOR APPLICATION NUMBER: US/09/634,368
RIOR FILING DATE: 2000-08-09
RIOR APPLICATION NUMBER: 60/147,924
RIOR FILING DATE: 1999-08-09
UMBER OF SEQ ID NOS: 32
OFTWARE: PatentIn Ver. 2.0
Q ID NO 12
LENGTH: 1569
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
0-603-064-12

nment Scores:
. No.:              7.68e-07        Length:        1569
e:                  17.00           Matches:       17
ent Similarity:     100.0%          Conservative:  0
 Local Similarity:  100.0%          Mismatches:    0
y Match:            5.2%            Indels:        0
                    8               Gaps:          0

0-821-670A-56 (1-328) x US-10-603-064-12 (1-1569)

      227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
     1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

LT 96
0-742-405-5
quence 5, Application US/10742405
blication No. US20040213761A1
NERAL INFORMATION:
PPLICANT: Bowman, Edward P.
PPLICANT:  Chan, Jason R.
PPLICANT:  Moore, Kevin
PPLICANT:  Nguyen, Nhung
PPLICANT:  Churakova, Tatyana
PPLICANT:  Chen, Shi-Juan
PPLICANT:  Cua, Daniel J.
ITLE OF INVENTION: Uses of mammalian cytokine; related reagents
ILE REFERENCE: DX01578K
URRENT APPLICATION NUMBER: US/10/742,405
URRENT FILING DATE:  2003-12-18
UMBER OF SEQ ID NOS: 12
OFTWARE: PatentIn version 3.2
Q ID NO 5
LENGTH: 1610
TYPE: DNA
ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1599)
US-10-742-405-5

Alignment Scores:
Pred. No.:              7.86e-07        Length:        1610
Score:                  17.00           Matches:       17
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            5.2%            Indels:        0
DB:                     9               Gaps:          0

US-10-821-670A-56 (1-328) x US-10-742-405-5 (1-1610)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 732

RESULT 97
US-10-172-399-3
; Sequence 3, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1840
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (35)..(1042)
US-10-172-399-3

Alignment Scores:
Pred. No.:              8.89e-07        Length:        1840
Score:                  17.00           Matches:       17
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            5.2%            Indels:        0
DB:                     6               Gaps:          0

US-10-821-670A-56 (1-328) x US-10-172-399-3 (1-1840)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 754

RESULT 98
US-10-603-064-11
; Sequence 11, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
```

EQ ID NO 11
LENGTH: 2013
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
10-603-064-11

gnment Scores:

i. No.:	9.65e-07	Length:	2013
ce:	17.00	Matches:	17
cent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
cy Match:	5.2%	Indels:	0
	8	Gaps:	0

10-821-670A-56 (1-328) x US-10-603-064-11 (1-2013)

```
       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281
```

LT 99
0-603-064-13
equence 13, Application US/10603064
ublication No. US20040072299A1
ENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
ITLE OF INVENTION: Multiple Cytokine Protein Complexes
ILE REFERENCE: LEX-010
URRENT APPLICATION NUMBER: US/10/603,064
URRENT FILING DATE: 2003-06-24
RIOR APPLICATION NUMBER: US/09/634,368
RIOR FILING DATE: 2000-08-09
RIOR APPLICATION NUMBER: 60/147,924
RIOR FILING DATE: 1999-08-09
UMBER OF SEQ ID NOS: 32
OFTWARE: PatentIn Ver. 2.0
EQ ID NO 13
LENGTH: 2709
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
OTHER INFORMATION: sequence
10-603-064-13

gnment Scores:

i. No.:	1.27e-06	Length:	2709
ce:	17.00	Matches:	17
cent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
cy Match:	5.2%	Indels:	0
	8	Gaps:	0

10-821-670A-56 (1-328) x US-10-603-064-13 (1-2709)

```
       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1927 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1977
```

LT 100
0-136-837-3
equence 3, Application US/10136837
ublication No. US20030181405A1
ENERAL INFORMATION:
APPLICANT: NORDSTROM, Jeffrey L
APPLICANT: PERICLE, Federica
APPLICANT: ROLLAND, Alain
APPLICANT: RALSTON, Robert

; TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 273/082 (GM15-1USC1)
; CURRENT APPLICATION NUMBER: US/10/136,837
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/268,135
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5966
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse IL-12 pIN0961
US-10-136-837-3

Alignment Scores:

Pred. No.:	2.62e-06	Length:	5966
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-136-837-3 (1-5966)

```
Qy       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5343 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 5393
```

Search completed: June 12, 2006, 17:16:57
Job time : 1609.01 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

rotein - nucleic search, using frame_plus_p2n model

on: June 10, 2006, 02:09:37 ; Search time 22.3541 Seconds
(without alignments)
2793.504 Million cell updates/sec

e: US-10-821-670A-56
ect score: 328
ience: 1 MHPQQLVIAWFSLVLLAPPL.....VQARDRYYSSSWSNWASVSC 328

ring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

rched: 253354 seqs, 63461778 residues

i size: 1

al number of hits satisfying chosen parameters: 506227

imum DB seq length: 0
imum DB seq length: 2000000000

:-processing: Listing first 200 summaries

mand line parameters:
DEL=frame+_p2n.model -DEV=xlh
/abss/ABSSWEB_spool/US10821670/runat_07062006_110508_27905/app_query.fasta_1
-Published_Applications_NA_New -QFMT=fastap
PFIX=oligo.p2n.200scores.rnpbn -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
TS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
ALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
M=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
R=US10821670_@CGN_1_1_62_@runat_07062006_110508_27905 -NCPU=6 -ICPU=3
MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
N_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
APOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

base : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt No.	Score	% Query Match	Length	DB	ID	Description
1	9	2.7	3284	7	US-11-293-697-630	Sequence 630, App
2	8	2.4	2115	7	US-11-217-529-76502	Sequence 76502, A
3	8	2.4	5874	7	US-11-313-450-15	Sequence 15, Appl
4	7	2.1	334	6	US-10-560-723-28	Sequence 28, Appl
5	7	2.1	442	6	US-10-953-349-33510	Sequence 33510, A
6	7	2.1	522	7	US-11-217-529-78298	Sequence 78298, A
7	7	2.1	528	7	US-11-217-529-4334	Sequence 4334, Ap
8	7	2.1	595	6	US-10-953-349-6086	Sequence 6086, Ap
9	7	2.1	819	6	US-10-471-571A-635	Sequence 635, App
10	7	2.1	849	6	US-10-471-571A-5423	Sequence 5423, Ap
c 11	7	2.1	939	6	US-10-953-349-32992	Sequence 32992, A
c 12	7	2.1	975	7	US-11-217-529-79951	Sequence 79951, A
13	7	2.1	1005	6	US-10-953-349-802	Sequence 802, App
14	7	2.1	1035	6	US-10-953-349-8097	Sequence 8097, Ap
c 15	7	2.1	1043	6	US-10-953-349-28829	Sequence 28829, A
c 16	7	2.1	1092	7	US-11-217-529-4663	Sequence 4663, Ap
c 17	7	2.1	1158	7	US-11-217-529-77622	Sequence 77622, A
18	7	2.1	1161	7	US-11-297-134-9	Sequence 9, Appli
c 19	7	2.1	1176	6	US-10-953-349-8850	Sequence 8850, Ap
c 20	7	2.1	1184	6	US-10-953-349-20842	Sequence 20842, A
c 21	7	2.1	1209	7	US-11-217-529-4209	Sequence 4209, Ap
22	7	2.1	1237	6	US-10-953-349-21311	Sequence 21311, A
c 23	7	2.1	1273	6	US-10-953-349-21541	Sequence 21541, A
24	7	2.1	1584	7	US-11-217-529-75662	Sequence 75662, A
c 25	7	2.1	1636	6	US-10-953-349-17465	Sequence 17465, A
26	7	2.1	1651	7	US-11-145-307A-256	Sequence 256, App
c 27	7	2.1	1690	6	US-10-953-349-18501	Sequence 18501, A
28	7	2.1	1717	6	US-10-953-349-33266	Sequence 33266, A
c 29	7	2.1	1728	7	US-11-217-529-78959	Sequence 78959, A
c 30	7	2.1	1737	7	US-11-217-529-81980	Sequence 81980, A
31	7	2.1	1758	7	US-11-217-529-1188	Sequence 1188, Ap
c 32	7	2.1	1956	7	US-11-217-529-76747	Sequence 76747, A
33	7	2.1	2121	7	US-11-217-529-78482	Sequence 78482, A
34	7	2.1	2148	7	US-11-217-529-2300	Sequence 2300, Ap
35	7	2.1	2240	6	US-10-953-349-11671	Sequence 11671, A
c 36	7	2.1	2259	7	US-11-293-697-1478	Sequence 1478, Ap
37	7	2.1	2304	7	US-11-121-154-64	Sequence 64, Appl
c 38	7	2.1	2507	6	US-10-953-349-9838	Sequence 9838, Ap
c 39	7	2.1	2508	7	US-11-293-697-1575	Sequence 1575, Ap
c 40	7	2.1	2616	6	US-10-471-571A-4673	Sequence 4673, Ap
41	7	2.1	2787	6	US-10-471-571A-2597	Sequence 2597, Ap
c 42	7	2.1	2825	7	US-11-293-697-1497	Sequence 1497, Ap
43	7	2.1	2857	6	US-10-196-749-105	Sequence 105, App
c 44	7	2.1	2871	6	US-10-511-455-40	Sequence 40, Appl
c 45	7	2.1	3226	7	US-11-293-697-723	Sequence 723, App
c 46	7	2.1	3624	7	US-11-217-529-3816	Sequence 3816, Ap
c 47	7	2.1	3678	7	US-11-217-529-309	Sequence 309, App
c 48	7	2.1	5934	7	US-11-313-450-13	Sequence 13, Appl
c 49	7	2.1	6371	7	US-11-251-465-8	Sequence 8, Appli
c 50	7	2.1	39536	6	US-10-857-260-27	Sequence 27, Appl
c 51	7	2.1	56580	6	US-10-553-298-1	Sequence 1, Appli
c 52	7	2.1	394191	6	US-10-506-549-3	Sequence 3, Appli
c 53	6	1.8	20	7	US-11-266-409-12	Sequence 12, Appl
54	6	1.8	25	7	US-11-217-529-9246	Sequence 9246, Ap
55	6	1.8	25	7	US-11-217-529-18480	Sequence 18480, A
56	6	1.8	25	7	US-11-217-529-19397	Sequence 19397, A
c 57	6	1.8	25	7	US-11-217-529-31190	Sequence 31190, A
58	6	1.8	25	7	US-11-217-529-36523	Sequence 36523, A
c 59	6	1.8	25	7	US-11-217-529-36968	Sequence 36968, A
c 60	6	1.8	25	7	US-11-217-529-43878	Sequence 43878, A
61	6	1.8	25	7	US-11-217-529-48094	Sequence 48094, A
62	6	1.8	25	7	US-11-217-529-50534	Sequence 50534, A
c 63	6	1.8	25	7	US-11-217-529-71800	Sequence 71800, A
c 64	6	1.8	25	7	US-11-217-529-82993	Sequence 82993, A
65	6	1.8	25	7	US-11-217-529-88008	Sequence 88008, A
66	6	1.8	25	7	US-11-217-529-89000	Sequence 89000, A
67	6	1.8	25	7	US-11-217-529-106446	Sequence 106446,
c 68	6	1.8	25	7	US-11-217-529-107708	Sequence 107708,
c 69	6	1.8	25	7	US-11-217-529-112662	Sequence 112662,
c 70	6	1.8	25	7	US-11-217-529-123888	Sequence 123888,
c 71	6	1.8	25	7	US-11-217-529-134360	Sequence 134360,
72	6	1.8	25	7	US-11-217-529-142444	Sequence 142444,
73	6	1.8	25	7	US-11-217-529-144453	Sequence 144453,
74	6	1.8	72	7	US-11-267-871-456	Sequence 456, App
c 75	6	1.8	72	7	US-11-267-871-456	Sequence 456, App
c 76	6	1.8	177	7	US-11-217-529-79352	Sequence 79352, A
c 77	6	1.8	198	6	US-10-471-571A-5615	Sequence 5615, Ap
78	6	1.8	240	7	US-11-244-678-7	Sequence 7, Appli
c 79	6	1.8	243	7	US-11-217-529-147	Sequence 147, App
80	6	1.8	243	7	US-11-217-529-80845	Sequence 80845, A
81	6	1.8	267	7	US-11-217-529-166793	Sequence 166793,
c 82	6	1.8	273	6	US-10-471-571A-2941	Sequence 2941, Ap

83	6	1.8	279	6	US-10-512-190-1	Sequence 1, Appli
84	6	1.8	294	6	US-10-511-814-9	Sequence 9, Appli
85	6	1.8	294	6	US-10-511-814-10	Sequence 10, Appl
86	6	1.8	294	6	US-10-511-814-12	Sequence 12, Appl
87	6	1.8	294	6	US-10-511-814-13	Sequence 13, Appl
88	6	1.8	297	7	US-11-217-529-81028	Sequence 81028, A
89	6	1.8	303	7	US-11-217-529-5663	Sequence 5663, Ap
90	6	1.8	303	7	US-11-217-529-174215	Sequence 174215,
91	6	1.8	306	7	US-11-217-529-190938	Sequence 190938,
92	6	1.8	306	7	US-11-321-421-87	Sequence 87, Appl
93	6	1.8	309	7	US-11-217-529-81582	Sequence 81582, A
94	6	1.8	312	7	US-11-217-529-75899	Sequence 75899, A
95	6	1.8	315	6	US-10-488-619-794	Sequence 794, App
96	6	1.8	324	7	US-11-217-529-76199	Sequence 76199, A
97	6	1.8	324	7	US-11-023-959A-118	Sequence 118, App
98	6	1.8	332	6	US-10-488-619-375	Sequence 375, App
99	6	1.8	339	7	US-11-217-529-77451	Sequence 77451, A
00	6	1.8	339	7	US-11-217-529-166940	Sequence 166940,
01	6	1.8	348	6	US-10-488-619-499	Sequence 499, App
02	6	1.8	348	7	US-11-217-529-77235	Sequence 77235, A
03	6	1.8	357	7	US-11-217-529-6132	Sequence 6132, Ap
04	6	1.8	365	6	US-10-992-149-2	Sequence 2, Appli
05	6	1.8	369	6	US-10-499-266-11	Sequence 11, Appl
06	6	1.8	379	6	US-10-994-679-63	Sequence 63, Appl
07	6	1.8	386	7	US-11-301-554-442	Sequence 442, App
08	6	1.8	387	7	US-11-217-529-78662	Sequence 78662, A
09	6	1.8	387	7	US-11-217-529-80425	Sequence 80425, A
10	6	1.8	393	7	US-11-217-529-76946	Sequence 76946, A
11	6	1.8	396	7	US-11-217-529-82136	Sequence 82136, A
12	6	1.8	402	7	US-11-217-529-75995	Sequence 75995, A
13	6	1.8	406	7	US-11-301-554-381	Sequence 381, App
14	6	1.8	406	7	US-11-301-554-898	Sequence 898, App
15	6	1.8	420	7	US-11-255-980-6	Sequence 6, Appli
16	6	1.8	423	7	US-11-217-529-3397	Sequence 3397, Ap
17	6	1.8	427	6	US-10-488-619-1587	Sequence 1587, Ap
18	6	1.8	435	7	US-11-217-529-5980	Sequence 5980, Ap
19	6	1.8	436	6	US-10-488-619-552	Sequence 552, App
20	6	1.8	438	6	US-10-488-619-1590	Sequence 1590, Ap
21	6	1.8	441	6	US-10-468-193-6	Sequence 6, Appli
22	6	1.8	444	7	US-11-217-529-82599	Sequence 82599, A
23	6	1.8	447	7	US-11-217-529-166970	Sequence 166970,
24	6	1.8	449	6	US-10-511-937-2873	Sequence 2873, Ap
25	6	1.8	450	6	US-10-471-571A-3305	Sequence 3305, Ap
26	6	1.8	456	6	US-10-488-619-1794	Sequence 1794, Ap
27	6	1.8	461	7	US-11-301-554-965	Sequence 965, App
28	6	1.8	462	6	US-10-473-173-248	Sequence 248, App
29	6	1.8	465	7	US-11-322-999-14	Sequence 14, Appl
30	6	1.8	471	6	US-10-488-619-417	Sequence 417, App
31	6	1.8	471	7	US-11-217-529-5788	Sequence 5788, Ap
32	6	1.8	474	7	US-11-217-529-3216	Sequence 3216, Ap
33	6	1.8	478	6	US-10-505-928-542	Sequence 542, App
34	6	1.8	483	7	US-11-219-563-141	Sequence 141, App
35	6	1.8	483	7	US-11-301-554-1239	Sequence 1239, Ap
36	6	1.8	487	7	US-11-301-554-1263	Sequence 1263, Ap
37	6	1.8	492	7	US-11-301-554-928	Sequence 928, App
38	6	1.8	498	6	US-10-488-619-564	Sequence 564, App
39	6	1.8	498	7	US-11-217-529-5867	Sequence 5867, Ap
40	6	1.8	499	6	US-10-953-349-15009	Sequence 15009, A
41	6	1.8	500	7	US-11-249-305-1	Sequence 1, Appli
42	6	1.8	500	7	US-11-249-305-2	Sequence 2, Appli
43	6	1.8	500	7	US-11-249-305-3	Sequence 3, Appli
44	6	1.8	500	7	US-11-249-305-4	Sequence 4, Appli
45	6	1.8	501	7	US-11-136-524-79	Sequence 79, Appl
46	6	1.8	509	6	US-10-953-349-217	Sequence 217, App
47	6	1.8	510	7	US-11-136-524-37	Sequence 37, Appl
48	6	1.8	510	7	US-11-217-529-2274	Sequence 2274, Ap
49	6	1.8	510	7	US-11-217-529-78451	Sequence 78451, A
50	6	1.8	513	7	US-11-217-529-79024	Sequence 79024, A
51	6	1.8	518	7	US-11-301-554-371	Sequence 371, App
52	6	1.8	518	7	US-11-301-554-1203	Sequence 1203, Ap
53	6	1.8	526	7	US-11-301-554-1218	Sequence 1218, Ap
54	6	1.8	537	6	US-10-471-571A-2883	Sequence 2883, Ap
55	6	1.8	538	6	US-10-488-619-2515	Sequence 2515, Ap
c 156	6	1.8	541	6	US-10-560-723-113	Sequence 113, App
157	6	1.8	543	7	US-11-301-554-956	Sequence 956, App
158	6	1.8	543	7	US-11-217-529-5827	Sequence 5827, Ap
159	6	1.8	549	7	US-11-301-554-359	Sequence 359, App
c 160	6	1.8	555	6	US-10-471-571A-4635	Sequence 4635, Ap
c 161	6	1.8	555	7	US-11-217-529-79490	Sequence 79490, A
162	6	1.8	557	7	US-11-301-554-848	Sequence 848, App
c 163	6	1.8	562	6	US-10-488-619-1255	Sequence 1255, Ap
c 164	6	1.8	564	6	US-10-488-619-1992	Sequence 1992, Ap
c 165	6	1.8	579	6	US-10-473-173-108	Sequence 108, App
166	6	1.8	581	7	US-11-301-951-7	Sequence 7, Appli
167	6	1.8	584	6	US-10-953-349-1733	Sequence 1733, Ap
168	6	1.8	591	6	US-10-488-619-1230	Sequence 1230, Ap
c 169	6	1.8	591	7	US-11-301-554-1122	Sequence 1122, Ap
c 170	6	1.8	593	6	US-10-953-349-25340	Sequence 25340, A
171	6	1.8	594	7	US-11-301-554-1751	Sequence 1751, Ap
172	6	1.8	596	6	US-10-488-619-2778	Sequence 2778, Ap
173	6	1.8	597	6	US-10-488-619-1332	Sequence 1332, Ap
c 174	6	1.8	597	6	US-10-488-619-2832	Sequence 2832, Ap
175	6	1.8	597	6	US-10-471-571A-2843	Sequence 2843, Ap
176	6	1.8	597	7	US-11-217-529-77932	Sequence 77932, A
177	6	1.8	606	6	US-10-953-349-27873	Sequence 27873, A
c 178	6	1.8	607	6	US-10-488-619-1738	Sequence 1738, Ap
c 179	6	1.8	610	6	US-10-488-619-2390	Sequence 2390, Ap
180	6	1.8	615	7	US-11-217-529-2766	Sequence 2766, Ap
181	6	1.8	618	6	US-10-953-349-5623	Sequence 5623, Ap
182	6	1.8	621	7	US-11-217-529-76434	Sequence 76434, A
183	6	1.8	625	6	US-10-953-349-2892	Sequence 2892, Ap
c 184	6	1.8	627	6	US-10-953-349-30134	Sequence 30134, A
c 185	6	1.8	627	6	US-10-471-571A-3259	Sequence 3259, Ap
186	6	1.8	633	6	US-10-953-349-8180	Sequence 8180, Ap
187	6	1.8	633	6	US-10-953-349-28624	Sequence 28624, A
188	6	1.8	634	7	US-11-301-554-23	Sequence 23, Appl
189	6	1.8	635	6	US-10-488-619-2164	Sequence 2164, Ap
c 190	6	1.8	636	6	US-10-953-349-6142	Sequence 6142, Ap
c 191	6	1.8	640	6	US-10-953-349-31246	Sequence 31246, A
c 192	6	1.8	641	6	US-10-488-619-1891	Sequence 1891, Ap
193	6	1.8	642	7	US-11-217-529-2277	Sequence 2277, Ap
194	6	1.8	657	7	US-11-217-529-173805	Sequence 173805,
195	6	1.8	660	7	US-11-217-529-80548	Sequence 80548, A
c 196	6	1.8	663	6	US-10-953-349-3111	Sequence 3111, Ap
c 197	6	1.8	668	6	US-10-953-349-39726	Sequence 39726, A
198	6	1.8	669	6	US-10-488-619-1764	Sequence 1764, Ap
199	6	1.8	669	7	US-11-257-062-37	Sequence 37, Appl
c 200	6	1.8	670	6	US-10-488-619-1464	Sequence 1464, Ap

ALIGNMENTS

RESULT 1
US-11-293-697-630/c
; Sequence 630, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 630
; LENGTH: 3284
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-630

Alignment Scores:

Pred. No.:	7.71	Length:	3284
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0

: Local Similarity: 100.0% Mismatches: 0
cy Match: 2.7% Indels: 0
7 Gaps: 0

10-821-670A-56 (1-328) x US-11-293-697-630 (1-3284)

```
      101 PheLeuLeuIleHisLysLysGluAsp 109
          ||||||||||||||||||||||||||||
     1053 TTTTTACTGATTCACAAAAAGGAAGAC 1027
```

JLT 2
11-217-529-76502
equence 76502, Application US/11217529
iblication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 76502
LENGTH: 2115
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-76502

nment Scores:
i. No.: 54.1 Length: 2115
e: 8.00 Matches: 8
ent Similarity: 100.0% Conservative: 0
: Local Similarity: 100.0% Mismatches: 0
y Match: 2.4% Indels: 0
7 Gaps: 0

10-821-670A-56 (1-328) x US-11-217-529-76502 (1-2115)

```
      241 AsnLeuGlnLeuLysProLeuLys 248
          ||||||||||||||||||||||||
      136 AATTTGCAACTTAAACCACTGAAA 159
```

JLT 3
11-313-450-15/c
equence 15, Application US/11313450
iblication No. US20060110778A1
ENERAL INFORMATION:
APPLICANT: Adorante, Joeseph S.
APPLICANT: Ehring, George R.
ITLE OF INVENTION: High-Throughput Screens For Identifying
ITLE OF INVENTION: Selective Persistent Sodium Channels Channel Blockers
ILE REFERENCE: 17407 CIP (AP)
URRENT APPLICATION NUMBER: US/11/313,450
URRENT FILING DATE: 2005-12-19
RIOR APPLICATION NUMBER: 09/989797
RIOR FILING DATE: 2001-11-20
RIOR APPLICATION NUMBER: 60/252771
RIOR FILING DATE: 2000-11-22
UMBER OF SEQ ID NOS: 41
OFTWARE: FastSEQ for Windows Version 4.0
Q ID NO 15
LENGTH: 5874
TYPE: DNA
ORGANISM: Homo sapiens
11-313-450-15

Alignment Scores:
Pred. No.: 134 Length: 5874
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-56 (1-328) x US-11-313-450-15 (1-5874)

```
Qy          12 SerLeuValLeuLeuAlaProPro 19
               ||||||||||||||||||||||||
Db        1309 TCCCTAGTGCTGCTAGCACCTCCT 1286
```

RESULT 4
US-10-560-723-28
; Sequence 28, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
; APPLICANT: EXONHIT THERAPEUTICALS
; TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: B0213WO
; CURRENT APPLICATION NUMBER: US/10/560,723
; CURRENT FILING DATE: 2005-12-15
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 334
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-560-723-28

Alignment Scores:
Pred. No.: 110 Length: 334
Score: 7.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.1% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-56 (1-328) x US-10-560-723-28 (1-334)

```
Qy         144 TrpLeuThrAlaIleSerThr 150
               ||||||||||||||||||||
Db          27 TGGCTCACTGCAATCTCCACC 47
```

RESULT 5
US-10-953-349-33510/c
; Sequence 33510, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33510
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33510

Alignment Scores:
Pred. No.: 140 Length: 442
Score: 7.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.1% Indels: 0
DB: 6 Gaps: 0

```
0-821-670A-56 (1-328) x US-10-953-349-33510 (1-442)

       14 ValLeuLeuAlaProProLeu 20
          ||||||||||||||||||||
       77 GTGCTCCTTGCTCCTCCTCTT 57

LT 6
1-217-529-78298/c
quence 78298, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 78298
LENGTH: 522
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-78298

nment Scores:
. No.:              163           Length:        522
e:                  7.00          Matches:       7
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            2.1%          Indels:        0
                    7             Gaps:          0

0-821-670A-56 (1-328) x US-11-217-529-78298 (1-522)

       11 PheSerLeuValLeuLeuAla 17
          ||||||||||||||||||||
       44 TTCTCTCTTGTACTATTAGCA 24

LT 7
1-217-529-4334/c
quence 4334, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 4334
LENGTH: 528
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-4334

nment Scores:
. No.:              164           Length:        528
Score:              7.00          Matches:       7
Percent Similarity: 100.0%        Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:        2.1%          Indels:        0
DB:                 7             Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-4334 (1-528)

Qy          12 SerLeuValLeuLeuAlaPro 18
               |||||||||||||||||||
Db         392 TCATTGGTACTGCTAGCTCCG 372

RESULT 8
US-10-953-349-6086/c
; Sequence 6086, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6086
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-6086

Alignment Scores:
Pred. No.:          183           Length:        595
Score:              7.00          Matches:       7
Percent Similarity: 100.0%        Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:        2.1%          Indels:        0
DB:                 6             Gaps:          0

US-10-821-670A-56 (1-328) x US-10-953-349-6086 (1-595)

Qy         154 PheThrValLysSerSerArg 160
               |||||||||||||||||||
Db         354 TTTACTGTGAAGTCTAGTCGT 334

RESULT 9
US-10-471-571A-635/c
; Sequence 635, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 635
;   LENGTH: 819
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-635

Alignment Scores:
Pred. No.:          242           Length:        819
Score:              7.00          Matches:       7
Percent Similarity: 100.0%        Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:        2.1%          Indels:        0
DB:                 6             Gaps:          0
```

10-821-670A-56 (1-328) x US-10-471-571A-635 (1-819)

```
       157 LysSerSerArgGlySerSer 163
           ||||||||||||||||||||
       359 AAATCTTCCCGTGGGTCATCA 339
```

JLT 10
.0-471-571A-5423
equence 5423, Application US/10471571A
ublication No. US20060115490A1
ENERAL INFORMATION:
APPLICANT: CHIRON SpA
ITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
ILE REFERENCE: P026927WO
URRENT APPLICATION NUMBER: US/10/471,571A
URRENT FILING DATE: 2003-09-12
RIOR APPLICATION NUMBER: GB-0107661.1
RIOR FILING DATE: 2001-03-27
UMBER OF SEQ ID NOS: 5642
OFTWARE: SeqWin99, version 1.03
Q ID NO 5423
LENGTH: 849
TYPE: DNA
ORGANISM: Staphylococcus aureus
10-471-571A-5423

nment Scores:

i. No.:	250	Length:	849
e:	7.00	Matches:	7
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	2.1%	Indels:	0
	6	Gaps:	0

10-821-670A-56 (1-328) x US-10-471-571A-5423 (1-849)

```
       121 LysGluSerLysAsnLysIle 127
           ||||||||||||||||||||
       223 AAAGAATCTAAAAATAAGATT 243
```

JLT 11
10-953-349-32992/c
equence 32992, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
ITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
ITLE OF INVENTION: ENCONDED THERBY
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE: 2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 32992
LENGTH: 939
TYPE: DNA
ORGANISM: Zea mays subsp. mays
10-953-349-32992

nment Scores:

i. No.:	273	Length:	939
e:	7.00	Matches:	7
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	2.1%	Indels:	0
	6	Gaps:	0

10-821-670A-56 (1-328) x US-10-953-349-32992 (1-939)

```
       202 AlaAlaGluGluSerLeuPro 208
           ||||||||||||||||||||
       141 GCGGCTGAAGAGAGCCTGCCT 121
```

RESULT 12
US-11-217-529-79951/c
; Sequence 79951, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79951
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79951

Alignment Scores:

Pred. No.:	283	Length:	975
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-79951 (1-975)

```
Qy          11 PheSerLeuValLeuLeuAla 17
               ||||||||||||||||||||
Db         424 TTTTCATTAGTGCTGCTGGCG 404
```

RESULT 13
US-10-953-349-802
; Sequence 802, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 802
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-802

Alignment Scores:

Pred. No.:	290	Length:	1005
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-953-349-802 (1-1005)

```
Qy          96 ValLeuSerHisSerPheLeu 102
               ||||||||||||||||||||
Db         920 GTGTTATCACACTCTTTTCTT 940
```

RESULT 14

```
0-953-349-8097
quence 8097, Application US/10953349
blication No. US20060107345A1
NERAL INFORMATION:
PPLICANT: ALEXANDROV, Nickolai et al.
ITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
ITLE OF INVENTION:  ENCONDED THERBY
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE:  2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 8097
LENGTH: 1035
TYPE: DNA
ORGANISM: Arabidopsis thaliana
0-953-349-8097

nment Scores:
. No.:              298          Length:        1035
e:                  7.00         Matches:       7
ent Similarity:     100.0%       Conservative:  0
 Local Similarity:  100.0%       Mismatches:    0
y Match:            2.1%         Indels:        0
                    6            Gaps:          0

0-821-670A-56 (1-328) x US-10-953-349-8097 (1-1035)

       66 SerGluValLeuGlySerGly 72
          ||||||||||||||||||||
      142 TCTGAAGTCCTTGGAAGCGGC 162

LT 15
0-953-349-28829/c
quence 28829, Application US/10953349
blication No. US20060107345A1
NERAL INFORMATION:
PPLICANT: ALEXANDROV, Nickolai et al.
ITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
ITLE OF INVENTION:  ENCONDED THERBY
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE:  2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 28829
LENGTH: 1043
TYPE: DNA
ORGANISM: Triticum aestivum
0-953-349-28829

nment Scores:
. No.:              300          Length:        1043
e:                  7.00         Matches:       7
ent Similarity:     100.0%       Conservative:  0
 Local Similarity:  100.0%       Mismatches:    0
y Match:            2.1%         Indels:        0
                    6            Gaps:          0

0-821-670A-56 (1-328) x US-10-953-349-28829 (1-1043)

       11 PheSerLeuValLeuLeuAla 17
          ||||||||||||||||||||
      220 TTCTCCTTGGTGCTCTTGGCG 200

LT 16
1-217-529-4663/c
quence 4663, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4663
;   LENGTH: 1092
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4663

Alignment Scores:
Pred. No.:              312          Length:        1092
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.1%         Indels:        0
DB:                     7            Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-4663 (1-1092)

Qy         317 SerSerSerTrpSerAsnTrp 323
               ||||||||||||||||||||||
Db         323 TCCTCCTCTTGGTCAAACTGG 303

RESULT 17
US-11-217-529-77622/c
; Sequence 77622, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77622
;   LENGTH: 1158
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77622

Alignment Scores:
Pred. No.:              329          Length:        1158
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.1%         Indels:        0
DB:                     7            Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-77622 (1-1158)

Qy         317 SerSerSerTrpSerAsnTrp 323
               ||||||||||||||||||||||
Db         398 TCCTCTTCTTGGTCGAATTGG 378

RESULT 18
US-11-297-134-9
; Sequence 9, Application US/11297134
```

iblication No. US20060111297A1
ENERAL INFORMATION:
APPLICANT: Genzyme Corporation
APPLICANT: Roberts, Bruce
ITLE OF INVENTION: BLOOD FACTOR DOMAINS
ILE REFERENCE: 5270C
URRENT APPLICATION NUMBER: US/11/297,134
URRENT FILING DATE: 2005-12-08
RIOR APPLICATION NUMBER: PCT/US2005/018461
RIOR FILING DATE: 2004-06-09
RIOR APPLICATION NUMBER: US 60/477,291
RIOR FILING DATE: 2003-06-09
UMBER OF SEQ ID NOS: 64
OFTWARE: PatentIn version 3.3
Q ID NO 9
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
1-297-134-9

nment Scores:

l. No.:	330	Length:	1161
e:	7.00	Matches:	7
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	2.1%	Indels:	0
	7	Gaps:	0

0-821-670A-56 (1-328) x US-11-297-134-9 (1-1161)

```
      233 IleIleLysProAspProPro 239
          ||||||||||||||||||||
      389 ATCATCAAGCCCGACCCTCCA 409
```

LT 19
0-953-349-8850/c
equence 8850, Application US/10953349
iblication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
ITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
ITLE OF INVENTION: ENCONDED THERBY
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE: 2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 8850
LENGTH: 1176
TYPE: DNA
ORGANISM: Arabidopsis thaliana
0-953-349-8850

nment Scores:

l. No.:	334	Length:	1176
e:	7.00	Matches:	7
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	2.1%	Indels:	0
	6	Gaps:	0

0-821-670A-56 (1-328) x US-10-953-349-8850 (1-1176)

```
      283 AsnArgGluLysLysAspArg 289
          ||||||||||||||||||||
      801 AATCGAGAAAAGAAAGATCGA 781
```

LT 20
0-953-349-20842/c
equence 20842, Application US/10953349
iblication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20842
; LENGTH: 1184
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20842

Alignment Scores:

Pred. No.:	336	Length:	1184
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-953-349-20842 (1-1184)

```
Qy        284 ArgGluLysLysAspArgLeu 290
              |||||||||||||||||||
Db        585 AGAGAGAAAAAGGATAGGTTG 565
```

RESULT 21
US-11-217-529-4209/c
; Sequence 4209, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4209
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4209

Alignment Scores:

Pred. No.:	342	Length:	1209
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-4209 (1-1209)

```
Qy        284 ArgGluLysLysAspArgLeu 290
              |||||||||||||||||||
Db        822 AGAGAAAAAAAAGACCGCCTT 802
```

RESULT 22
US-10-953-349-21311
; Sequence 21311, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

```
ITLE OF INVENTION:  ENCONDED THERBY
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE:  2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 21311
LENGTH: 1237
TYPE: DNA
ORGANISM: Glycine max
0-953-349-21311

nment Scores:
. No.:                349           Length:        1237
e:                    7.00          Matches:       7
ent Similarity:       100.0%        Conservative:  0
 Local Similarity:    100.0%        Mismatches:    0
y Match:              2.1%          Indels:        0
                      6             Gaps:          0

0-821-670A-56 (1-328) x US-10-953-349-21311 (1-1237)

       97 LeuSerHisSerPheLeuLeu 103
          ||||||||||||||||||||
       52 CTTTCTCATTCATTCTTATTA 72

LT 23
0-953-349-21541/c
quence 21541, Application US/10953349
blication No. US20060107345A1
NERAL INFORMATION:
PPLICANT: ALEXANDROV, Nickolai et al.
ITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
ITLE OF INVENTION:  ENCONDED THERBY
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE:  2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 21541
LENGTH: 1273
TYPE: DNA
ORGANISM: Glycine max
0-953-349-21541

nment Scores:
. No.:                358           Length:        1273
e:                    7.00          Matches:       7
ent Similarity:       100.0%        Conservative:  0
 Local Similarity:    100.0%        Mismatches:    0
y Match:              2.1%          Indels:        0
                      6             Gaps:          0

0-821-670A-56 (1-328) x US-10-953-349-21541 (1-1273)

       13 LeuValLeuLeuAlaProPro 19
          ||||||||||||||||||||
      238 TTGGTCCTGCTGGCACCACCA 218

LT 24
1-217-529-75662
quence 75662, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE:  2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75662
;   LENGTH: 1584
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-75662

Alignment Scores:
Pred. No.:                434           Length:        1584
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.1%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-75662 (1-1584)

Qy         213 ValAspAlaIleHisLysLeu 219
               |||||||||||||||||||||
Db        1140 GTGGACGCAATTCATAAGCTA 1160

RESULT 25
US-10-953-349-17465/c
; Sequence 17465, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17465
;   LENGTH: 1636
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-17465

Alignment Scores:
Pred. No.:                447           Length:        1636
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.1%          Indels:        0
DB:                       6             Gaps:          0

US-10-821-670A-56 (1-328) x US-10-953-349-17465 (1-1636)

Qy         226 SerSerPhePheIleArgAsp 232
               |||||||||||||||||||||
Db        1352 TCATCTTTCTTCATAAGAGAT 1332

RESULT 26
US-11-145-307A-256
; Sequence 256, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
```

```
SOFTWARE: PatentIn version 3.1
EQ ID NO 256
LENGTH: 1651
TYPE: DNA
ORGANISM: Homo sapiens
:1-145-307A-256

gnment Scores:
d. No.:                 450             Length:         1651
re:                     7.00            Matches:        7
cent Similarity:        100.0%          Conservative:   0
: Local Similarity:     100.0%          Mismatches:     0
cy Match:               2.1%            Indels:         0
                        7               Gaps:           0

10-821-670A-56 (1-328) x US-11-145-307A-256 (1-1651)

       218 LysLeuLysTyrGluAsnTyr 224
           ||||||||||||||||||||
      1616 AAGTTGAAATATGAAAATTAT 1636

JLT 27
10-953-349-18501/c
equence 18501, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION:  ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE:  2004-09-30
UMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 18501
LENGTH: 1690
TYPE: DNA
ORGANISM: Glycine max
.0-953-349-18501

gnment Scores:
d. No.:                 460             Length:         1690
re:                     7.00            Matches:        7
cent Similarity:        100.0%          Conservative:   0
: Local Similarity:     100.0%          Mismatches:     0
cy Match:               2.1%            Indels:         0
                        6               Gaps:           0

10-821-670A-56 (1-328) x US-10-953-349-18501 (1-1690)

       238 ProProLysAsnLeuGlnLeu 244
           ||||||||||||||||||||
      1257 CCACCTAAAAATCTACAGTTG 1237

JLT 28
10-953-349-33266
equence 33266, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION:  ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE:  2004-09-30
UMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 33266
LENGTH: 1717
TYPE: DNA
ORGANISM: Zea mays subsp. mays
.0-953-349-33266

Alignment Scores:
Pred. No.:              466             Length:         1717
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.1%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-953-349-33266 (1-1717)

Qy         233 IleIleLysProAspProPro 239
               |||||||||||||||||||||
Db         205 ATCATCAAGCCCGACCCTCCC 225

RESULT 29
US-11-217-529-78959/c
; Sequence 78959, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78959
;    LENGTH: 1728
;    TYPE: DNA
;    ORGANISM: Saccharomyces pastorianus
US-11-217-529-78959

Alignment Scores:
Pred. No.:              469             Length:         1728
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.1%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-56 (1-328) x US-11-217-529-78959 (1-1728)

Qy          12 SerLeuValLeuLeuAlaPro 18
               |||||||||||||||||||
Db         122 TCTTTAGTACTGCTTGCCCCG 102

RESULT 30
US-11-217-529-81980/c
; Sequence 81980, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81980
```

```
LENGTH: 1737
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
FEATURE:
NAME/KEY: modified_base
LOCATION: (1678)..(1715)
OTHER INFORMATION: a, c, g, t, unknown, or other
1-217-529-81980

nment Scores:
. No.:                471            Length:        1737
e:                    7.00           Matches:       7
ent Similarity:       100.0%         Conservative:  0
 Local Similarity:    100.0%         Mismatches:    0
y Match:              2.1%           Indels:        0
                      7              Gaps:          0

0-821-670A-56 (1-328) x US-11-217-529-81980 (1-1737)

       66 SerGluValLeuGlySerGly 72
          ||||||||||||||||||||
       30 AGCGAAGTGTTGGGTAGCGGT 10

LT 31
1-217-529-1188
quence 1188, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 1188
LENGTH: 1758
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-1188

nment Scores:
. No.:                476            Length:        1758
e:                    7.00           Matches:       7
ent Similarity:       100.0%         Conservative:  0
 Local Similarity:    100.0%         Mismatches:    0
y Match:              2.1%           Indels:        0
                      7              Gaps:          0

0-821-670A-56 (1-328) x US-11-217-529-1188 (1-1758)

       12 SerLeuValLeuLeuAlaPro 18
          ||||||||||||||||||||
      133 TCATTGGTACTGCTAGCTCCG 153

LT 32
1-217-529-76747/c
quence 76747, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76747
;   LENGTH: 1956
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-76747

Alignment Scores:
Pred. No.:            523            Length:        1956
Score:                7.00           Matches:       7
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          2.1%           Indels:        0
DB:                   7              Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-76747 (1-1956)

Qy         12 SerLeuValLeuLeuAlaPro 18
              ||||||||||||||||||||
Db        130 TCTTTAGTTCTTTTAGCTCCT 110

RESULT 33
US-11-217-529-78482
; Sequence 78482, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78482
;   LENGTH: 2121
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78482

Alignment Scores:
Pred. No.:            562            Length:        2121
Score:                7.00           Matches:       7
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          2.1%           Indels:        0
DB:                   7              Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-78482 (1-2121)

Qy         70 GlySerGlyLysThrLeuThr 76
              ||||||||||||||||||||
Db         85 GGCTCAGGAAAAACGCTAACG 105

RESULT 34
US-11-217-529-2300
; Sequence 2300, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
```

```
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 2300
 LENGTH: 2148
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
.1-217-529-2300

nment Scores:
l. No.:              568          Length:         2148
e:                   7.00         Matches:        7
ent Similarity:      100.0%       Conservative:   0
 Local Similarity:   100.0%       Mismatches:     0
y Match:             2.1%         Indels:         0
                     7            Gaps:           0

0-821-670A-56 (1-328) x US-11-217-529-2300 (1-2148)

        70 GlySerGlyLysThrLeuThr 76
           ||||||||||||||||||||
        85 GGTTCAGGAAAAACGTTGACG 105

JLT 35
10-953-349-11671
equence 11671, Application US/10953349
blication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
ITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
ITLE OF INVENTION:  ENCONDED THERBY
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE:  2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 11671
 LENGTH: 2240
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
.0-953-349-11671

nment Scores:
l. No.:              590          Length:         2240
e:                   7.00         Matches:        7
ent Similarity:      100.0%       Conservative:   0
 Local Similarity:   100.0%       Mismatches:     0
y Match:             2.1%         Indels:         0
                     6            Gaps:           0

.0-821-670A-56 (1-328) x US-10-953-349-11671 (1-2240)

       104 IleHisLysLysGluAspGly 110
           ||||||||||||||||||||
      1054 ATTCATAAGAAAGAAGATGGG 1074

JLT 36
11-293-697-1478/c
equence 1478, Application US/11293697
blication No. US20060105376A1
ENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
ITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1478
;   LENGTH: 2259
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1478

Alignment Scores:
Pred. No.:              594          Length:         2259
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            2.1%         Indels:         0
DB:                     7            Gaps:           0

US-10-821-670A-56 (1-328) x US-11-293-697-1478 (1-2259)

Qy         100 SerPheLeuLeuIleHisLys 106
               ||||||||||||||||||||
Db        1074 AGTTTCCTTTTAATCCATAAG 1054

RESULT 37
US-11-121-154-64
; Sequence 64, Application US/11121154
; Publication No. US20060105914A1
; GENERAL INFORMATION:
;  APPLICANT: TAYLOR, LARRY EDMUND
;  APPLICANT:  WEINER, RONALD M.
;  APPLICANT:  HUTCHESON, STEVEN WAYNE
;  APPLICANT:  EKBORG, NATHAN A.
;  APPLICANT:  HOWARD, MICHAEL
;  TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
;  FILE REFERENCE: 108172-00121
;  CURRENT APPLICATION NUMBER: US/11/121,154
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,971
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 214
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
;   LENGTH: 2304
;   TYPE: DNA
;   ORGANISM: Microbulbifer degradans
US-11-121-154-64

Alignment Scores:
Pred. No.:              605          Length:         2304
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            2.1%         Indels:         0
DB:                     7            Gaps:           0

US-10-821-670A-56 (1-328) x US-11-121-154-64 (1-2304)

Qy         316 TyrSerSerSerTrpSerAsn 322
               ||||||||||||||||||||
Db         202 TACAGTTCATCGTGGAGCAAT 222

RESULT 38
US-10-953-349-9838/c
; Sequence 9838, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
```

```
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE:  2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 9838
LENGTH: 2507
TYPE: DNA
ORGANISM: Arabidopsis thaliana
0-953-349-9838

nment Scores:
. No.:              652          Length:        2507
e:                  7.00         Matches:       7
ent Similarity:     100.0%       Conservative:  0
 Local Similarity:  100.0%       Mismatches:    0
y Match:            2.1%         Indels:        0
                    6            Gaps:          0

0-821-670A-56 (1-328) x US-10-953-349-9838 (1-2507)

       97 LeuSerHisSerPheLeuLeu 103
          ||||||||||||||||||||||
      261 CTTAGCCACAGCTTCCTTCTG 241

LT 39
1-293-697-1575/c
quence 1575, Application US/11293697
blication No. US20060105376A1
NERAL INFORMATION:
PPLICANT: HELIX RESEARCH INSTITUTE
ITLE OF INVENTION: Novel full length cDNA
ILE REFERENCE: H1-A0106
URRENT APPLICATION NUMBER: US/11/293,697
URRENT FILING DATE:  2005-12-05
RIOR APPLICATION NUMBER: US/10/108,260
RIOR FILING DATE: 2002-03-28
UMBER OF SEQ ID NOS: 5458
OFTWARE: PatentIn Ver. 2.1
Q ID NO 1575
LENGTH: 2508
TYPE: DNA
ORGANISM: Homo sapiens
1-293-697-1575

nment Scores:
. No.:              652          Length:        2508
e:                  7.00         Matches:       7
ent Similarity:     100.0%       Conservative:  0
 Local Similarity:  100.0%       Mismatches:    0
y Match:            2.1%         Indels:        0
                    7            Gaps:          0

0-821-670A-56 (1-328) x US-11-293-697-1575 (1-2508)

      225 ThrSerSerPhePheIleArg 231
          |||||||||||||||||||||
     1322 ACCTCGTCATTTTTCATCAGA 1302

LT 40
0-471-571A-4673/c
quence 4673, Application US/10471571A
blication No. US20060115490A1
NERAL INFORMATION:
PPLICANT: CHIRON SpA
ITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
ILE REFERENCE: P026927WO
URRENT APPLICATION NUMBER: US/10/471,571A
URRENT FILING DATE:  2003-09-12
RIOR APPLICATION NUMBER: GB-0107661.1
RIOR FILING DATE: 2001-03-27
UMBER OF SEQ ID NOS: 5642
OFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4673
;   LENGTH: 2616
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-4673

Alignment Scores:
Pred. No.:              677          Length:        2616
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.1%         Indels:        0
DB:                     6            Gaps:          0

US-10-821-670A-56 (1-328) x US-10-471-571A-4673 (1-2616)

Qy        157 LysSerSerArgGlySerSer 163
              ||||||||||||||||||||||
Db       1160 AAATCATCAAGGGGTTCTAGT 1140

RESULT 41
US-10-471-571A-2597
; Sequence 2597, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2597
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-2597

Alignment Scores:
Pred. No.:              716          Length:        2787
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.1%         Indels:        0
DB:                     6            Gaps:          0

US-10-821-670A-56 (1-328) x US-10-471-571A-2597 (1-2787)

Qy         70 GlySerGlyLysThrLeuThr 76
              |||||||||||||||||||||
Db        808 GGAAGTGGTAAGACGTTGACT 828

RESULT 42
US-11-293-697-1497/c
; Sequence 1497, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1497
;   LENGTH: 2825
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1497
```

```
nment Scores:
l. No.:                724              Length:          2825
:e:                    7.00             Matches:         7
:ent Similarity:       100.0%           Conservative:    0
: Local Similarity:    100.0%           Mismatches:      0
:y Match:              2.1%             Indels:          0
                       7                Gaps:            0

:0-821-670A-56 (1-328) x US-11-293-697-1497 (1-2825)

       155 ThrValLysSerSerArgGly 161
           ||||||||||||||||||||
      1956 ACAGTGAAAAGCTCCCGTGGC 1936

JLT 43
:0-196-749-105
equence 105, Application US/10196749
iblication No. US20060094864A1
:NERAL INFORMATION:
\PPLICANT: Baker,Kevin P.
\PPLICANT:  Chen,Jian
\PPLICANT:  Desnoyers,Luc
\PPLICANT:  Goddard,Audrey
\PPLICANT:  Godowski,Paul J.
\PPLICANT:  Gurney,Austin L.
\PPLICANT:  Pan,James
\PPLICANT:  Smith,Victoria
\PPLICANT:  Watanabe,Colin K.
\PPLICANT:  Wood,William I.
\PPLICANT:  Zhang,Zemin
?ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
?ITLE OF INVENTION:  ACIDS ENCODING THE SAME
?ILE REFERENCE: P3430R1C340
:URRENT APPLICATION NUMBER: US/10/196,749
:URRENT FILING DATE:  2002-07-16
?RIOR APPLICATION NUMBER: 10/052586
?RIOR FILING DATE: 2002-01-15
?RIOR APPLICATION NUMBER: 60/059263
?RIOR FILING DATE: 1997-09-18
?RIOR APPLICATION NUMBER: 60/059266
?RIOR FILING DATE: 1997-09-18
?RIOR APPLICATION NUMBER: 60/062250
?RIOR FILING DATE: 1997-10-17
?RIOR APPLICATION NUMBER: 60/063120
?RIOR FILING DATE: 1997-10-24
?RIOR APPLICATION NUMBER: 60/063121
?RIOR FILING DATE: 1997-10-24
?RIOR APPLICATION NUMBER: 60/063486
?RIOR FILING DATE: 1997-10-21
?RIOR APPLICATION NUMBER: 60/063540
?RIOR FILING DATE: 1997-10-28
?RIOR APPLICATION NUMBER: 60/063541
?RIOR FILING DATE: 1997-10-28
?RIOR APPLICATION NUMBER: 60/063544
?RIOR FILING DATE: 1997-10-28
?rior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SQ ID NO 105
 LENGTH: 2857
 TYPE: DNA
 ORGANISM: Homo Sapien
:0-196-749-105

nment Scores:
l. No.:                732              Length:          2857
:e:                    7.00             Matches:         7
:ent Similarity:       100.0%           Conservative:    0
: Local Similarity:    100.0%           Mismatches:      0
:y Match:              2.1%             Indels:          0
                       6                Gaps:            0

.0-821-670A-56 (1-328) x US-10-196-749-105 (1-2857)

Qy          73 LysThrLeuThrIleGlnVal 79
               |||||||||||||||||||
Db        1571 AAGACACTAACAATTCAAGTT 1591

RESULT 44
US-10-511-455-40/c
; Sequence 40, Application US/10511455
; Publication No. US20060088835A1
; GENERAL INFORMATION:
;  APPLICANT: Pickard, Benjamin Simon
;  APPLICANT:  Blackwood, Douglas
;  APPLICANT:  Porteous, David
;  APPLICANT:  Muir, Walter John
;  APPLICANT:  Mors, Ole
;  APPLICANT:  Ewald, Henrik Lykke
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
;  FILE REFERENCE: 9013.63
;  CURRENT APPLICATION NUMBER: US/10/511,455
;  CURRENT FILING DATE:  2004-10-05
;  PRIOR APPLICATION NUMBER: PCT/GB03/001543
;  PRIOR FILING DATE: 2003-04-07
;  PRIOR APPLICATION NUMBER: GB0207902.8
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: GB0207904.4
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: GB0207900.2
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: GB0207901.0
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: GB0227734.1
;  PRIOR FILING DATE: 2002-11-28
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 2871
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-455-40

Alignment Scores:
Pred. No.:             735              Length:          2871
Score:                 7.00             Matches:         7
Percent Similarity:    100.0%           Conservative:    0
Best Local Similarity: 100.0%           Mismatches:      0
Query Match:           2.1%             Indels:          0
DB:                    6                Gaps:            0

US-10-821-670A-56 (1-328) x US-10-511-455-40 (1-2871)

Qy          162 SerSerAspProGlnGlyVal 168
                ||||||||||||||||||||
Db           87 AGCAGCGATCCTCAAGGAGTG 67

RESULT 45
US-11-293-697-723/c
; Sequence 723, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 723
;   LENGTH: 3226
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-723
```

```
nment Scores:
. No.:                815             Length:         3226
e:                    7.00            Matches:        7
ent Similarity:       100.0%          Conservative:   0
 Local Similarity:    100.0%          Mismatches:     0
y Match:              2.1%            Indels:         0
                      7               Gaps:           0

0-821-670A-56 (1-328) x US-11-293-697-723 (1-3226)

      102 LeuLeuIleHisLysLysGlu 108
          ||||||||||||||||||||
     2295 CTACTTATCCATAAAAAGGAA 2275

LT 46
1-217-529-3816/c
quence 3816, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 3816
LENGTH: 3624
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-3816

nment Scores:
. No.:                903             Length:         3624
e:                    7.00            Matches:        7
ent Similarity:       100.0%          Conservative:   0
 Local Similarity:    100.0%          Mismatches:     0
y Match:              2.1%            Indels:         0
                      7               Gaps:           0

0-821-670A-56 (1-328) x US-11-217-529-3816 (1-3624)

      284 ArgGluLysLysAspArgLeu 290
          ||||||||||||||||||||
     2190 AGAGAAAAGAAAGACCGTCTT 2170

LT 47
1-217-529-309/c
quence 309, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
; SEQ ID NO 309
;   LENGTH: 3678
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-309

Alignment Scores:
Pred. No.:            915             Length:         3678
Score:                7.00            Matches:        7
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          2.1%            Indels:         0
DB:                   7               Gaps:           0

US-10-821-670A-56 (1-328) x US-11-217-529-309 (1-3678)

Qy          13 LeuValLeuLeuAlaProPro 19
               |||||||||||||||||||
Db        2602 CTAGTTCTCTTGGCTCCTCCC 2582

RESULT 48
US-11-313-450-13/c
; Sequence 13, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 5934
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-13

Alignment Scores:
Pred. No.:            1.4e+03         Length:         5934
Score:                7.00            Matches:        7
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          2.1%            Indels:         0
DB:                   7               Gaps:           0

US-10-821-670A-56 (1-328) x US-11-313-450-13 (1-5934)

Qy          64 GlnSerSerGluValLeuGly 70
               ||||||||||||||||||||
Db          37 CAAAGCTCTGAGGTCCTGGGG 17

RESULT 49
US-11-251-465-8/c
; Sequence 8, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
;  APPLICANT: Brys, Reginald
;  APPLICANT:  Vandeghinste, Nick
;  APPLICANT:  Tomme, Peter
;  APPLICANT:  Klaassen, Hubertus
;  TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
;  TITLE OF INVENTION:  Same, Useful In The Treatment Of Joint Degenerative And
;  TITLE OF INVENTION:  Inflammatory Diseases
;  FILE REFERENCE: P30,172-A USA
;  CURRENT APPLICATION NUMBER: US/11/251,465
;  CURRENT FILING DATE:  2005-10-14
```

```
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SQ ID NO 8
 LENGTH: 6371
 TYPE: DNA
 ORGANISM: Homo sapiens
11-251-465-8

gnment Scores:
i. No.:                1.49e+03        Length:          6371
ce:                    7.00            Matches:         7
cent Similarity:       100.0%          Conservative:    0
 Local Similarity:     100.0%          Mismatches:      0
cy Match:              2.1%            Indels:          0
                       7               Gaps:            0

10-821-670A-56 (1-328) x US-11-251-465-8 (1-6371)

        64 GlnSerSerGluValLeuGly 70
           ||||||||||||||||||||
        85 CAAAGCTCTGAGGTCCTGGGG 65

JLT 50
10-857-260-27/c
equence 27, Application US/10857260
iblication No. US20060110742A1
ENERAL INFORMATION:
APPLICANT: Lyons, Leslie A.
APPLICANT:  Grahn, Robert
APPLICANT:  Erdman, Carolyn
APPLICANT:  The Regents of the University of California
ITLE OF INVENTION: Carrier Tests for Polycystic Kidney Disease in the Cat
ILE REFERENCE: 023070-146800US
URRENT APPLICATION NUMBER: US/10/857,260
URRENT FILING DATE:  2004-05-28
UMBER OF SEQ ID NOS: 47
OFTWARE: PatentIn Ver. 2.1
SQ ID NO 27
 LENGTH: 39536
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 OTHER INFORMATION: GenBank Accession No. AC145332.28 genomic DNA for
 OTHER INFORMATION: PKD1 39536 bp contig
10-857-260-27

gnment Scores:
i. No.:                7.42e+03        Length:          39536
ce:                    7.00            Matches:         7
cent Similarity:       100.0%          Conservative:    0
 Local Similarity:     100.0%          Mismatches:      0
cy Match:              2.1%            Indels:          0
                       6               Gaps:            0

10-821-670A-56 (1-328) x US-10-857-260-27 (1-39536)

       161 GlySerSerAspProGlnGly 167
           ||||||||||||||||||||
       716 GGGAGCAGCGACCCCCAGGGG 696

JLT 51
10-553-298-1/c
equence 1, Application US/10553298
iblication No. US20060110385A1
ENERAL INFORMATION:
APPLICANT: NeuroNova AG
ITLE OF INVENTION: A Method for Diagnosing and Treating Affective Disorders
ILE REFERENCE: XXX
URRENT APPLICATION NUMBER: US/10/553,298
URRENT FILING DATE:  2005-10-14
UMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 56580
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon1
;   LOCATION: (3000)..(3124)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon2
;   LOCATION: (24841)..(25009)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon3
;   LOCATION: (26134)..(26202)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon4
;   LOCATION: (30958)..(31030)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon5
;   LOCATION: (32481)..(32577)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon6
;   LOCATION: (35416)..(35496)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon7
;   LOCATION: (36113)..(36242)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon8
;   LOCATION: (37541)..(37677)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon9
;   LOCATION: (45470)..(45560)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon10
;   LOCATION: (47229)..(47295)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon11
;   LOCATION: (47380)..(47529)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon12
;   LOCATION: (50438)..(50539)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: exon13
;   LOCATION: (54392)..(54889)
;   OTHER INFORMATION:
US-10-553-298-1

Alignment Scores:
Pred. No.:             1.02e+04        Length:          56580
Score:                 7.00            Matches:         7
Percent Similarity:    100.0%          Conservative:    0
Best Local Similarity: 100.0%          Mismatches:      0
Query Match:           2.1%            Indels:          0
DB:                    6               Gaps:            0

US-10-821-670A-56 (1-328) x US-10-553-298-1 (1-56580)

Qy         65 SerSerGluValLeuGlySer 71
              ||||||||||||||||||||
Db      21521 TCATCTGAGGTCCTGGGTTCG 21501
```

```
LT 52
0-506-549-3/c
quence 3, Application US/10506549
blication No. US20060100417A1
NERAL INFORMATION:
PPLICANT: APPLERA CORPORATION
ITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
ITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
ITLE OF INVENTION:  AND USES THEREOF
ILE REFERENCE: CL001361-US
URRENT APPLICATION NUMBER: US/10/506,549
URRENT FILING DATE:  2004-09-03
RIOR APPLICATION NUMBER: 60/361,343
RIOR FILING DATE: 2002-03-05
UMBER OF SEQ ID NOS: 4
OFTWARE: FastSEQ for Windows Version 4.0
Q ID NO 3
LENGTH: 394191
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(394191)
OTHER INFORMATION: n = A,T,C or G
0-506-549-3

nment Scores:
. No.:              5.41e+04        Length:         394191
e:                  7.00            Matches:        7
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            2.1%            Indels:         0
                    6               Gaps:           0

0-821-670A-56 (1-328) x US-10-506-549-3 (1-394191)

      144 TrpLeuThrAlaIleSerThr 150
          ||||||||||||||||||||
   331384 TGGCTCACTGCAATCTCCACC 331364

LT 53
1-266-409-12/c
quence 12, Application US/11266409
blication No. US20060093578A1
NERAL INFORMATION:
PPLICANT: SUZUMURA, AKIO
ITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
ILE REFERENCE: 279847US40
URRENT APPLICATION NUMBER: US/11/266,409
URRENT FILING DATE:  2005-11-04
RIOR APPLICATION NUMBER: US 60/624,851
RIOR FILING DATE: 2004-11-04
UMBER OF SEQ ID NOS: 22
OFTWARE: PatentIn version 3.3
Q ID NO 12
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
1-266-409-12

nment Scores:
. No.:              94              Length:         20
e:                  6.00            Matches:        6
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            1.8%            Indels:         0
                    7               Gaps:           0

0-821-670A-56 (1-328) x US-11-266-409-12 (1-20)

      266 ProHisSerTyrPheSer 271
          ||||||||||||||||||
Db         20 CCCCATTCCTACTTCTCC 3

RESULT 54
US-11-217-529-9246
; Sequence 9246, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9246
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-9246

Alignment Scores:
Pred. No.:              115             Length:         25
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            1.8%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-56 (1-328) x US-11-217-529-9246 (1-25)

Qy         158 SerSerArgGlySerSer 163
               ||||||||||||||||||
Db           8 TCATCGAGAGGCAGCAGT 25

RESULT 55
US-11-217-529-18480
; Sequence 18480, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18480
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-18480

Alignment Scores:
Pred. No.:              115             Length:         25
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            1.8%            Indels:         0
```

7 Gaps: 0

.0-821-670A-56 (1-328) x US-11-217-529-18480 (1-25)

204 GluGluSerLeuProIle 209
||||||||||||||||||||
2 GAGGAATCGTTGCCTATC 19

JLT 56
l1-217-529-19397
equence 19397, Application US/11217529
iblication No. US20060099612A1
ENERAL INFORMATION:
\PPLICANT: SUNTORY LIMITED
\PPLICANT: NAKAO, YOSHIHIRO
\PPLICANT: NAKAMURA, NORIHISA
\PPLICANT: KODAMA, YUKIKO
\PPLICANT: FUJIMURA, TOMOKO
\PPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 19397
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
l1-217-529-19397

nment Scores:

i. No.:	115	Length:	25
e:	6.00	Matches:	6
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	1.8%	Indels:	0
	7	Gaps:	0

.0-821-670A-56 (1-328) x US-11-217-529-19397 (1-25)

11 PheSerLeuValLeuLeu 16
||||||||||||||||||||
8 TTTTCACTGGTTCTCTTG 25

JLT 57
l1-217-529-31190/c
equence 31190, Application US/11217529
iblication No. US20060099612A1
ENERAL INFORMATION:
\PPLICANT: SUNTORY LIMITED
\PPLICANT: NAKAO, YOSHIHIRO
\PPLICANT: NAKAMURA, NORIHISA
\PPLICANT: KODAMA, YUKIKO
\PPLICANT: FUJIMURA, TOMOKO
\PPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 31190
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
l1-217-529-31190

nment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-31190 (1-25)

Qy 67 GluValLeuGlySerGly 72
||||||||||||||||||||
Db 22 GAAGTATTAGGTTCAGGG 5

RESULT 58
US-11-217-529-36523
; Sequence 36523, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36523
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-36523

Alignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-36523 (1-25)

Qy 31 TyrValValGluLeuAsp 36
||||||||||||||||||||
Db 2 TACGTCGTGGAGTTAGAT 19

RESULT 59
US-11-217-529-36968/c
; Sequence 36968, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36968
; LENGTH: 25

```
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-36968

nment Scores:
. No.:              115           Length:        25
e:                  6.00          Matches:       6
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            1.8%          Indels:        0
                    7             Gaps:          0

0-821-670A-56 (1-328) x US-11-217-529-36968 (1-25)

      147 AlaIleSerThrAspLeu 152
          ||||||||||||||||||
       22 GCTATTAGTACAGATCTG 5

LT 60
1-217-529-43878/c
quence 43878, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 43878
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-43878

nment Scores:
. No.:              115           Length:        25
e:                  6.00          Matches:       6
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            1.8%          Indels:        0
                    7             Gaps:          0

0-821-670A-56 (1-328) x US-11-217-529-43878 (1-25)

      158 SerSerArgGlySerSer 163
          ||||||||||||||||||
       21 TCTTCAAGAGGTTCGTCT 4

LT 61
1-217-529-48094
quence 48094, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48094
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-48094

Alignment Scores:
Pred. No.:              115           Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            1.8%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-48094 (1-25)

Qy         113 SerThrAspIleLeuArg 118
               |||||||||||||||||||
Db           2 AGTACGGATATTTTAAGG 19

RESULT 62
US-11-217-529-50534
; Sequence 50534, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50534
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-50534

Alignment Scores:
Pred. No.:              115           Length:        25
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            1.8%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-50534 (1-25)

Qy          80 LysGluPheAlaAspAla 85
               |||||||||||||||||||
Db           6 AAGGAGTTCGCGGACGCA 23

RESULT 63
US-11-217-529-71800/c
; Sequence 71800, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
```

ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 71800
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-71800

nment Scores:

. No.:	115	Length:	25
e:	6.00	Matches:	6
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	1.8%	Indels:	0
	7	Gaps:	0

0-821-670A-56 (1-328) x US-11-217-529-71800 (1-25)

```
        44 GluMetValValLeuThr 49
           ||||||||||||||||||
        18 GAGATGGTGGTACTGACC 1
```

LT 64
1-217-529-82993/c
equence 82993, Application US/11217529
blication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 82993
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-82993

nment Scores:

. No.:	115	Length:	25
e:	6.00	Matches:	6
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	1.8%	Indels:	0
	7	Gaps:	0

0-821-670A-56 (1-328) x US-11-217-529-82993 (1-25)

```
        93 GlyGlyGluValLeuSer 98
           ||||||||||||||||||
        20 GGTGGAGAAGTGCTATCT 3
```

LT 65
1-217-529-88008
equence 88008, Application US/11217529
blication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-88008

Alignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-88008 (1-25)

```
Qy        242 LeuGlnLeuLysProLeu 247
              ||||||||||||||||||
Db          2 CTGCAGCTCAAACCTCTG 19
```

RESULT 66
US-11-217-529-89000
; Sequence 89000, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89000
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-89000

Alignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-89000 (1-25)

```
Qy         12 SerLeuValLeuLeuAla 17
              ||||||||||||||||||
Db          5 TCCCTTGTCCTACTGGCT 22
```

RESULT 67

```
1-217-529-106446
quence 106446, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 106446
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-106446

nment Scores:
. No.:                115          Length:        25
e:                    6.00         Matches:       6
ent Similarity:       100.0%       Conservative:  0
 Local Similarity:    100.0%       Mismatches:    0
y Match:              1.8%         Indels:        0
                      7            Gaps:          0

0-821-670A-56 (1-328) x US-11-217-529-106446 (1-25)

       73 LysThrLeuThrIleGln 78
          |||||||||||||||||
        3 AAGACGCTAACGATCCAG 20

LT 68
1-217-529-107708/c
quence 107708, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 107708
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-107708

nment Scores:
. No.:                115          Length:        25
e:                    6.00         Matches:       6
ent Similarity:       100.0%       Conservative:  0
 Local Similarity:    100.0%       Mismatches:    0
y Match:              1.8%         Indels:        0
                      7            Gaps:          0

0-821-670A-56 (1-328) x US-11-217-529-107708 (1-25)

Qy         295 ThrSerAlaLysValVal 300
               |||||||||||||||||
Db          22 ACGTCGGCAAAAGTTGTC 5

RESULT 69
US-11-217-529-112662/c
; Sequence 112662, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112662
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-112662

Alignment Scores:
Pred. No.:                115          Length:        25
Score:                    6.00         Matches:       6
Percent Similarity:       100.0%       Conservative:  0
Best Local Similarity:    100.0%       Mismatches:    0
Query Match:              1.8%         Indels:        0
DB:                       7            Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-112662 (1-25)

Qy         292 ValAspLysThrSerAla 297
               ||||||||||||||||||
Db          24 GTCGACAAAACCAGCGCA 7

RESULT 70
US-11-217-529-123888/c
; Sequence 123888, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123888
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-123888

Alignment Scores:
Pred. No.:                115          Length:        25
Score:                    6.00         Matches:       6
Percent Similarity:       100.0%       Conservative:  0
Best Local Similarity:    100.0%       Mismatches:    0
```

y Match:	1.8%	Indels:	0
	7	Gaps:	0

10-821-670A-56 (1-328) x US-11-217-529-123888 (1-25)

```
       279 GlnGlyLysAsnAsnArg 284
           |||||||||||||||||
        24 CAAGGAAAGAACAATCGA 7
```

JLT 71
11-217-529-134360/c
equence 134360, Application US/11217529
iblication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 134360
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-134360

nment Scores:

l. No.:	115	Length:	25
e:	6.00	Matches:	6
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	1.8%	Indels:	0
	7	Gaps:	0

10-821-670A-56 (1-328) x US-11-217-529-134360 (1-25)

```
        12 SerLeuValLeuLeuAla 17
           |||||||||||||||||
        24 TCATTAGTGCTGCTGGCG 7
```

JLT 72
11-217-529-142444
equence 142444, Application US/11217529
iblication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 142444
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-142444

Alignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-142444 (1-25)

```
Qy         65 SerSerGluValLeuGly 70
              |||||||||||||||||||
Db          3 TCTTCGGAAGTACTGGGC 20
```

RESULT 73
US-11-217-529-144453
; Sequence 144453, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 144453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-144453

Alignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-144453 (1-25)

```
Qy        158 SerSerArgGlySerSer 163
              |||||||||||||||||||
Db          5 TCTAGTCGAGGGTCTTCA 22
```

RESULT 74
US-11-267-871-456
; Sequence 456, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 456

```
LENGTH: 72
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
1-267-871-456

nment Scores:
. No.:              292           Length:        72
e:                  6.00          Matches:       6
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            1.8%          Indels:        0
                    7             Gaps:          0

0-821-670A-56 (1-328) x US-11-267-871-456 (1-72)

      158 SerSerArgGlySerSer 163
          ||||||||||||||||||
       13 TCCAGTCGTGGATCGAGC 30

LT 75
1-267-871-456/c
quence 456, Application US/11267871
blication No. US20060094655A1
NERAL INFORMATION:
PPLICANT: Guyon, Thierry
PPLICANT:  Borrelly, Gilles
PPLICANT:  Drittanti, Lila
PPLICANT:  Vega, Manuel
ITLE OF INVENTION: MODIFIED GROWTH HORMONES
ILE REFERENCE: 17109-015001/925
URRENT APPLICATION NUMBER: US/11/267,871
URRENT FILING DATE:  2005-11-03
RIOR APPLICATION NUMBER: 60/706,697
RIOR FILING DATE: 2005-08-08
RIOR APPLICATION NUMBER: 60/625,652
RIOR FILING DATE: 2004-11-04
UMBER OF SEQ ID NOS: 719
OFTWARE: FastSEQ for Windows Version 4.0
Q ID NO 456
LENGTH: 72
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
1-267-871-456

nment Scores:
. No.:              292           Length:        72
e:                  6.00          Matches:       6
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            1.8%          Indels:        0
                    7             Gaps:          0

0-821-670A-56 (1-328) x US-11-267-871-456 (1-72)

      158 SerSerArgGlySerSer 163
          ||||||||||||||||||
       60 TCCAGTCGTGGATCGAGC 43

LT 76
1-217-529-79352/c
quence 79352, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79352
;   LENGTH: 177
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79352

Alignment Scores:
Pred. No.:              647           Length:        177
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            1.8%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-79352 (1-177)

Qy        246 ProLeuLysAsnSerArg 251
              |||||||||||||||||
Db        119 CCCTTGAAAAATTCTAGA 102

RESULT 77
US-10-471-571A-5615/c
; Sequence 5615, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5615
;   LENGTH: 198
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-5615

Alignment Scores:
Pred. No.:              715           Length:        198
Score:                  6.00          Matches:       6
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            1.8%          Indels:        0
DB:                     6             Gaps:          0

US-10-821-670A-56 (1-328) x US-10-471-571A-5615 (1-198)

Qy        102 LeuLeuIleHisLysLys 107
              ||||||||||||||||||
Db        154 TTACTAATACATAAAAAA 137

RESULT 78
US-11-244-678-7
; Sequence 7, Application US/11244678
; Publication No. US20060099206A1
; GENERAL INFORMATION:
;  APPLICANT: Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark
;  APPLICANT:  Laken, Haley A.
;  APPLICANT:  Rouse, Jason
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMPROVING
;  TITLE OF INVENTION:  RECOMBINANT PROTEIN PRODUCTION
```

FILE REFERENCE: 16158-052001
CURRENT APPLICATION NUMBER: US/11/244,678
CURRENT FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/616,474
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SQ ID NO 7
LENGTH: 240
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated oligonucleotide
11-244-678-7

gnment Scores:

d. No.:	847	Length:	240
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	1.8%	Indels:	0
	7	Gaps:	0

10-821-670A-56 (1-328) x US-11-244-678-7 (1-240)

```
       275 GlyValGlnValGlnGly 280
           |||||||||||||||||
         6 GGAGTACAAGTGCAAGGT 23
```

SULT 79
11-217-529-147/c
equence 147, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SQ ID NO 147
LENGTH: 243
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-147

gnment Scores:

d. No.:	857	Length:	243
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	1.8%	Indels:	0
	7	Gaps:	0

10-821-670A-56 (1-328) x US-11-217-529-147 (1-243)

```
       283 AsnArgGluLysLysAsp 288
           |||||||||||||||||
       198 AATCGTGAGAAAAAAGAC 181
```

SULT 80
11-217-529-80845
equence 80845, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80845
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80845

Alignment Scores:

Pred. No.:	857	Length:	243
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-80845 (1-243)

```
Qy        158 SerSerArgGlySerSer 163
              |||||||||||||||||
Db         37 TCTAGTCGAGGGTCTTCA 54
```

RESULT 81
US-11-217-529-166793
; Sequence 166793, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166793
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166793

Alignment Scores:

Pred. No.:	931	Length:	267
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-166793 (1-267)

```
Qy        171 GlyAlaAlaThrLeuSer 176
              |||||||||||||||||
Db        241 GGTGCTGCAACTTTATCC 258
```

```
LT 82
0-471-571A-2941/c
quence 2941, Application US/10471571A
blication No. US20060115490A1
NERAL INFORMATION:
PPLICANT: CHIRON SpA
ITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
ILE REFERENCE: P026927WO
URRENT APPLICATION NUMBER: US/10/471,571A
URRENT FILING DATE:  2003-09-12
RIOR APPLICATION NUMBER: GB-0107661.1
RIOR FILING DATE: 2001-03-27
UMBER OF SEQ ID NOS: 5642
OFTWARE: SeqWin99, version 1.03
Q ID NO 2941
LENGTH: 273
TYPE: DNA
ORGANISM: Staphylococcus aureus
0-471-571A-2941

nment Scores:
. No.:              950           Length:         273
e:                  6.00          Matches:        6
ent Similarity:     100.0%        Conservative:   0
 Local Similarity:  100.0%        Mismatches:     0
y Match:            1.8%          Indels:         0
                    6             Gaps:           0

0-821-670A-56 (1-328) x US-10-471-571A-2941 (1-273)

       17 AlaProProLeuMetAla 22
          ||||||||||||||||||
      155 GCACCACCACTGATGGCA 138

LT 83
0-512-190-1/c
quence 1, Application US/10512190
blication No. US20060099219A1
NERAL INFORMATION:
PPLICANT: Hallez, Sophie
PPLICANT:  Burny, Arsene
PPLICANT:  Jacquet, Alain
PPLICANT:  Bollen, Alex
ITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION
ITLE OF INVENTION:  COMPRISING IT AND ITS PREPARATION PROCESS
ILE REFERENCE: 9997.50USWO
URRENT APPLICATION NUMBER: US/10/512,190
URRENT FILING DATE:  2004-10-22
RIOR APPLICATION NUMBER: PCT/BE03/000073
RIOR FILING DATE: 2003-04-24
RIOR APPLICATION NUMBER: US 60/410,461
RIOR FILING DATE: 2002-09-13
RIOR APPLICATION NUMBER: FR 0205173
RIOR FILING DATE: 2002-04-24
RIOR APPLICATION NUMBER: FR 0304170
RIOR FILING DATE: 2003-04-03
UMBER OF SEQ ID NOS: 9
OFTWARE: PatentIn version 3.3
Q ID NO 1
LENGTH: 279
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Mutated (recombinant) HPV-16 E7
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(279)
0-512-190-1

nment Scores:
. No.:              968           Length:         279
e:                  6.00          Matches:        6
ent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%    Mismatches:     0
Query Match:            1.8%      Indels:         0
DB:                     6         Gaps:           0

US-10-821-670A-56 (1-328) x US-10-512-190-1 (1-279)

Qy        197 GlySerAlaCysProAla 202
              ||||||||||||||||||
Db        122 GGTTCTGCTTGTCCAGCT 105

RESULT 84
US-10-511-814-9/c
; Sequence 9, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
;  APPLICANT: McCance, Dennis
;  APPLICANT:  Westbrook, III, Thomas F.
;  TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
;  FILE REFERENCE: 21108.0016U2
;  CURRENT APPLICATION NUMBER: US/10/511,814
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US03/12667
;  PRIOR FILING DATE: 2003-04-21
;  PRIOR APPLICATION NUMBER: 60/374,245
;  PRIOR FILING DATE: 2002-04-19
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: Synthetic Construct
US-10-511-814-9

Alignment Scores:
Pred. No.:              1.01e+03      Length:         294
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            1.8%          Indels:         0
DB:                     6             Gaps:           0

US-10-821-670A-56 (1-328) x US-10-511-814-9 (1-294)

Qy        197 GlySerAlaCysProAla 202
              ||||||||||||||||||
Db        140 GGTTCTGCTTGTCCAGCT 123

RESULT 85
US-10-511-814-10/c
; Sequence 10, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
;  APPLICANT: McCance, Dennis
;  APPLICANT:  Westbrook, III, Thomas F.
;  TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
;  FILE REFERENCE: 21108.0016U2
;  CURRENT APPLICATION NUMBER: US/10/511,814
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US03/12667
;  PRIOR FILING DATE: 2003-04-21
;  PRIOR APPLICATION NUMBER: 60/374,245
;  PRIOR FILING DATE: 2002-04-19
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
```

OTHER INFORMATION: Synthetic Construct
10-511-814-10

gnment Scores:
d. No.: 1.01e+03 Length: 294
ce: 6.00 Matches: 6
cent Similarity: 100.0% Conservative: 0
: Local Similarity: 100.0% Mismatches: 0
cy Match: 1.8% Indels: 0
6 Gaps: 0

10-821-670A-56 (1-328) x US-10-511-814-10 (1-294)

197 GlySerAlaCysProAla 202
||||||||||||||||||
140 GGTTCTGCTTGTCCAGCT 123

JLT 86
10-511-814-12/c
equence 12, Application US/10511814
ublication No. US20060088472A1
ENERAL INFORMATION:
APPLICANT: McCance, Dennis
APPLICANT: Westbrook, III, Thomas F.
TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
FILE REFERENCE: 21108.0016U2
URRENT APPLICATION NUMBER: US/10/511,814
URRENT FILING DATE: 2004-10-19
RIOR APPLICATION NUMBER: PCT/US03/12667
RIOR FILING DATE: 2003-04-21
RIOR APPLICATION NUMBER: 60/374,245
RIOR FILING DATE: 2002-04-19
UMBER OF SEQ ID NOS: 21
OFTWARE: FastSEQ for Windows Version 4.0
Q ID NO 12
LENGTH: 294
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =
OTHER INFORMATION: Synthetic Construct
10-511-814-12

gnment Scores:
d. No.: 1.01e+03 Length: 294
ce: 6.00 Matches: 6
cent Similarity: 100.0% Conservative: 0
: Local Similarity: 100.0% Mismatches: 0
cy Match: 1.8% Indels: 0
6 Gaps: 0

10-821-670A-56 (1-328) x US-10-511-814-12 (1-294)

197 GlySerAlaCysProAla 202
||||||||||||||||||
140 GGTTCTGCTTGTCCAGCT 123

JLT 87
10-511-814-13/c
equence 13, Application US/10511814
ublication No. US20060088472A1
ENERAL INFORMATION:
APPLICANT: McCance, Dennis
APPLICANT: Westbrook, III, Thomas F.
TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
FILE REFERENCE: 21108.0016U2
URRENT APPLICATION NUMBER: US/10/511,814
URRENT FILING DATE: 2004-10-19
RIOR APPLICATION NUMBER: PCT/US03/12667
RIOR FILING DATE: 2003-04-21
RIOR APPLICATION NUMBER: 60/374,245
RIOR FILING DATE: 2002-04-19
UMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-511-814-13

Alignment Scores:
Pred. No.: 1.01e+03 Length: 294
Score: 6.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 1.8% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-56 (1-328) x US-10-511-814-13 (1-294)

Qy 197 GlySerAlaCysProAla 202
||||||||||||||||||
Db 140 GGTTCTGCTTGTCCAGCT 123

RESULT 88
US-11-217-529-81028
; Sequence 81028, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81028
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81028

Alignment Scores:
Pred. No.: 1.02e+03 Length: 297
Score: 6.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 1.8% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-56 (1-328) x US-11-217-529-81028 (1-297)

Qy 117 LeuArgGluGlnLysGlu 122
||||||||||||||||||
Db 79 TTAAGAGAGCAGAAGGAA 96

RESULT 89
US-11-217-529-5663
; Sequence 5663, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO

```
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 5663
LENGTH: 303
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-5663

nment Scores:
. No.:              1.04e+03       Length:         303
e:                  6.00           Matches:        6
ent Similarity:     100.0%         Conservative:   0
 Local Similarity:  100.0%         Mismatches:     0
y Match:            1.8%           Indels:         0
                    7              Gaps:           0

0-821-670A-56 (1-328) x US-11-217-529-5663 (1-303)

        8 IleAlaTrpPheSerLeu 13
          ||||||||||||||||||
       37 ATCGCCTGGTTTTCCCTG 54

LT 90
1-217-529-174215
quence 174215, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
PPLICANT: SUNTORY LIMITED
PPLICANT:  NAKAO, YOSHIHIRO
PPLICANT:  NAKAMURA, NORIHISA
PPLICANT:  KODAMA, YUKIKO
PPLICANT:  FUJIMURA, TOMOKO
PPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE:  2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
Q ID NO 174215
LENGTH: 303
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-174215

nment Scores:
. No.:              1.04e+03       Length:         303
e:                  6.00           Matches:        6
ent Similarity:     100.0%         Conservative:   0
 Local Similarity:  100.0%         Mismatches:     0
y Match:            1.8%           Indels:         0
                    7              Gaps:           0

0-821-670A-56 (1-328) x US-11-217-529-174215 (1-303)

       15 LeuLeuAlaProProLeu 20
          ||||||||||||||||||
      142 CTTTTAGCTCCACCTTTA 159

LT 91
1-217-529-190938
quence 190938, Application US/11217529
blication No. US20060099612A1
NERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190938
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190938

Alignment Scores:
Pred. No.:              1.05e+03       Length:         306
Score:                  6.00           Matches:        6
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            1.8%           Indels:         0
DB:                     7              Gaps:           0

US-10-821-670A-56 (1-328) x US-11-217-529-190938 (1-306)

Qy         281 LysAsnAsnArgGluLys 286
               |||||||||||||||||
Db         139 AAAAACAATCGTGAAAAG 156

RESULT 92
US-11-321-421-87
; Sequence 87, Application US/11321421
; Publication No. US20060115496A1
; GENERAL INFORMATION:
;  APPLICANT: Milhausen, Michael James
;  TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
;  FILE REFERENCE: TX-1-C2-1
;  CURRENT APPLICATION NUMBER: US/11/321,421
;  CURRENT FILING DATE:  2005-12-29
;  PRIOR APPLICATION NUMBER: 09/216,393
;  PRIOR FILING DATE: 1998-12-18
;  PRIOR APPLICATION NUMBER: 08/994,825
;  PRIOR FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 366
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Toxoplasma gondii
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(306)
;   OTHER INFORMATION:
US-11-321-421-87

Alignment Scores:
Pred. No.:              1.05e+03       Length:         306
Score:                  6.00           Matches:        6
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            1.8%           Indels:         0
DB:                     7              Gaps:           0

US-10-821-670A-56 (1-328) x US-11-321-421-87 (1-306)

Qy          39 ProAspAlaProGlyGlu 44
               |||||||||||||||||
Db         204 CCTGACGCCCCAGGAGAG 221
```

JLT 93
11-217-529-81582
equence 81582, Application US/11217529
iblication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
EQ ID NO 81582
LENGTH: 309
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-81582

gnment Scores:

d. No.:	1.06e+03	Length:	309
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	1.8%	Indels:	0
	7	Gaps:	0

10-821-670A-56 (1-328) x US-11-217-529-81582 (1-309)

```
          8 IleAlaTrpPheSerLeu 13
            |||||||||||||||||||
         37 ATTGCCTGGTTCTCCCTG 54
```

JLT 94
11-217-529-75899
equence 75899, Application US/11217529
iblication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
OFTWARE: PatentIn version 3.3
EQ ID NO 75899
LENGTH: 312
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-75899

gnment Scores:

d. No.:	1.07e+03	Length:	312
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	1.8%	Indels:	0
	7	Gaps:	0

US-10-821-670A-56 (1-328) x US-11-217-529-75899 (1-312)

```
Qy         12 SerLeuValLeuLeuAla 17
              |||||||||||||||||
Db        169 TCCCTTGTCCTACTGGCT 186
```

RESULT 95
US-10-488-619-794
; Sequence 794, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 794
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(315)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-794

Alignment Scores:

Pred. No.:	1.08e+03	Length:	315
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x US-10-488-619-794 (1-315)

```
Qy         14 ValLeuLeuAlaProPro 19
              ||||||||||||||||||
Db         27 GTCCTCCTTGCTCCACCC 44
```

RESULT 96
US-11-217-529-76199
; Sequence 76199, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76199
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76199

Alignment Scores:

Pred. No.:	1.1e+03	Length:	324
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0

```
y Match:            1.8%          Indels:        0
                    7             Gaps:          0

0-821-670A-56 (1-328) x US-11-217-529-76199 (1-324)

      172 AlaAlaThrLeuSerAla 177
          |||||||||||||||||||
       37 GCAGCTACGCTGAGCGCA 54

LT 97
1-023-959A-118
quence 118, Application US/11023959A
blication No. US20060106203A1
NERAL INFORMATION:
PPLICANT: Winter, Greg
ITLE OF INVENTION: Ligand
ILE REFERENCE: 8039/2142
URRENT APPLICATION NUMBER: US/11/023,959A
URRENT FILING DATE:  2004-12-28
RIOR APPLICATION NUMBER: PCT/GB03/002804
RIOR FILING DATE: 2003-06-30
UMBER OF SEQ ID NOS: 187
OFTWARE: PatentIn version 3.3
Q ID NO 118
LENGTH: 324
TYPE: DNA
ORGANISM: Homo sapiens
1-023-959A-118

nment Scores:
. No.:              1.1e+03       Length:        324
e:                  6.00          Matches:       6
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            1.8%          Indels:        0
                    7             Gaps:          0

0-821-670A-56 (1-328) x US-11-023-959A-118 (1-324)

       11 PheSerLeuValLeuLeu 16
          |||||||||||||||||||
       75 TTCAGTCTCGTATTGCTT 92

LT 98
0-488-619-375/c
quence 375, Application US/10488619
blication No. US20060099578A1
NERAL INFORMATION:
PPLICANT: Greenlee, Winner and Sullivan, P.C.
ITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
ITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
ILE REFERENCE: 98-01 WO
URRENT APPLICATION NUMBER: US/10/488,619
URRENT FILING DATE:  2004-03-01
UMBER OF SEQ ID NOS: 3040
OFTWARE: PatentIn version 3.1
Q ID NO 375
LENGTH: 332
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(332)
OTHER INFORMATION: n is g, c, a or t
0-488-619-375

nment Scores:
. No.:              1.13e+03      Length:        332
e:                  6.00          Matches:       6
ent Similarity:     100.0%        Conservative:  0
 Local Similarity:  100.0%        Mismatches:    0
y Match:            1.8%          Indels:        0
                    6             Gaps:          0

US-10-821-670A-56 (1-328) x US-10-488-619-375 (1-332)

Qy          11 PheSerLeuValLeuLeu 16
               ||||||||||||||||||
Db         289 TTTTCTTTGGTCTTGCTC 272

RESULT 99
US-11-217-529-77451/c
; Sequence 77451, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77451
;   LENGTH: 339
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77451

Alignment Scores:
Pred. No.:          1.15e+03      Length:        339
Score:              6.00          Matches:       6
Percent Similarity: 100.0%        Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:        1.8%          Indels:        0
DB:                 7             Gaps:          0

US-10-821-670A-56 (1-328) x US-11-217-529-77451 (1-339)

Qy          15 LeuLeuAlaProProLeu 20
               ||||||||||||||||||
Db         224 CTATTAGCGCCCCCTTTA 207

RESULT 100
US-11-217-529-166940/c
; Sequence 166940, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166940
;   LENGTH: 339
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (186)..(210)
;   OTHER INFORMATION: a, c, g, t, unknown, or other
```

l1-217-529-166940

gnment Scores:

i. No.:	1.15e+03	Length:	339
ce:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
: Local Similarity:	100.0%	Mismatches:	0
cy Match:	1.8%	Indels:	0
	7	Gaps:	0

l0-821-670A-56 (1-328) x US-11-217-529-166940 (1-339)

```
        97 LeuSerHisSerPheLeu 102
           ||||||||||||||||||
       297 CTTAGTCATTCTTTTCTT 280
```

rch completed: June 10, 2006, 02:19:43
time : 153.354 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

nucleic - nucleic search, using sw model

on: June 10, 2006, 03:13:25 ; Search time 247.137 Seconds
(without alignments)
15525.205 Million cell updates/sec

le: US-10-821-670A-83
fect score: 60
ience: 1 ctgcagtggtggcggtggcg.....acccctactccatccccggg 60

cing table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

ched: 6366136 seqs, 31973710525 residues

al number of hits satisfying chosen parameters: 12732272

imum DB seq length: 0
imum DB seq length: 2000000000

:-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ilt No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	60	2	AR595989	AR595989 Sequence
2	60	100.0	60	2	AR595990	AR595990 Sequence
3	60	100.0	1533	2	AR595959	AR595959 Sequence
4	60	100.0	1533	2	AR595960	AR595960 Sequence
5	60	100.0	1599	2	AR595956	AR595956 Sequence
6	60	100.0	1599	2	AR595957	AR595957 Sequence
7	59	98.3	1533	2	AR595973	AR595973 Sequence
8	59	98.3	1533	2	AR595974	AR595974 Sequence
9	59	98.3	1599	2	AR595971	AR595971 Sequence
10	59	98.3	1599	2	AR595972	AR595972 Sequence
11	32.8	54.7	1626	8	AF401989	AF401989 Synthetic
12	30.4	50.7	3352	2	CQ585665	CQ585665 Sequence
13	30.4	50.7	4343	2	CQ581862	CQ581862 Sequence
14	30.4	50.7	4877	13	AY051978	AY051978 Drosophil
15	30.4	50.7	6727	2	CQ581861	CQ581861 Sequence
16	30.4	50.7	83141	13	AC005115	AC005115 Drosophil
17	30.4	50.7	178190	13	AC092241	AC092241 Drosophil
18	30.4	50.7	180968	12	AC019702	AC019702 Drosophil
c 19	30.4	50.7	256684	13	AE003631	AE003631 Drosophil
c 20	29.2	48.7	1194	6	AF020305	AF020305 Mus muscu
c 21	29.2	48.7	1244	6	AF041842	AF041842 Mus muscu
c 22	29.2	48.7	1867	6	AB008833	AB008833 Mus muscu
c 23	29.2	48.7	1878	2	BD195078	BD195078 Ret ligan
c 24	29.2	48.7	1878	2	AR452067	AR452067 Sequence
c 25	29.2	48.7	1878	2	AR642125	AR642125 Sequence
c 26	29.2	48.7	1884	6	AF051766	AF051766 Mus muscu
c 27	29.2	48.7	1889	2	BD195079	BD195079 Ret ligan
c 28	29.2	48.7	1889	2	AR452068	AR452068 Sequence
c 29	29.2	48.7	1889	2	AR642126	AR642126 Sequence
c 30	29.2	48.7	1911	6	AF036163	AF036163 Mus muscu
c 31	29.2	48.7	1932	6	MMTRNR3	Y15110 Mus musculu
c 32	29.2	48.7	1935	2	BD137007	BD137007 GFR alpha
c 33	29.2	48.7	2006	6	BC066202	BC066202 Mus muscu
c 34	29.2	48.7	168661	12	AC145591	AC145591 Mus muscu
35	28.8	48.0	86603	12	AP007885	AP007885 Lotus cor
c 36	28.6	47.7	576	2	CQ522261	CQ522261 Sequence
37	28.6	47.7	46849	5	AC113358	AC113358 Homo sapi
38	28.6	47.7	145435	5	AC011419	AC011419 Homo sapi
39	28.2	47.0	1080	2	AR316602	AR316602 Sequence
40	28.2	47.0	1086	2	AR316599	AR316599 Sequence
c 41	27.4	45.7	164845	12	AC121528	AC121528 Mus muscu
c 42	27.4	45.7	196651	6	AL845360	AL845360 Mouse DNA
43	27.2	45.3	189519	12	CT025730	CT025730 Drosophil
c 44	27.2	45.3	259160	12	AC112027	AC112027 Rattus no
45	27.2	45.3	321034	12	AC133998	AC133998 Rattus no

ALIGNMENTS

RESULT 1
AR595989
LOCUS AR595989 60 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 83 from patent US 6818444.
ACCESSION AR595989
VERSION AR595989.1 GI:56646970
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 60)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 83 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .60
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 60; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60

RESULT 2
AR595990/c
LOCUS AR595990 60 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 84 from patent US 6818444.
ACCESSION AR595990
VERSION AR595990.1 GI:56646971
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 60)

```
THORS   Wonderling,R.S. and Boroughs,K.L.
TLE     Canine and feline proteins, nucleic acid molecules and uses thereof
URNAL   Patent: US 6818444-A 84 16-NOV-2004;
        Heska Corporation; Fort Collins, CO
URES            Location/Qualifiers
 source         1. .60
                /organism="unknown"
                /mol_type="genomic DNA"
IN

ery Match           100.0%;  Score 60;  DB 2;  Length 60;
st Local Similarity  100.0%;  Pred. No. 9.3e-14;
tches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       60 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1


LT 3
5959
S       AR595959                1533 bp    DNA     linear   PAT 15-DEC-2004
NITION  Sequence 43 from patent US 6818444.
SSION   AR595959
ION     AR595959.1  GI:56646940
ORDS    .
CE      Unknown.
GANISM  Unknown.
        Unclassified.
RENCE   1  (bases 1 to 1533)
THORS   Wonderling,R.S. and Boroughs,K.L.
TLE     Canine and feline proteins, nucleic acid molecules and uses thereof
URNAL   Patent: US 6818444-A 43 16-NOV-2004;
        Heska Corporation; Fort Collins, CO
URES            Location/Qualifiers
 source         1. .1533
                /organism="unknown"
                /mol_type="genomic DNA"
IN

ery Match           100.0%;  Score 60;  DB 2;  Length 1533;
st Local Similarity  100.0%;  Pred. No. 1.7e-13;
tches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     915 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974


LT 4
5960/c
S       AR595960                1533 bp    DNA     linear   PAT 15-DEC-2004
NITION  Sequence 45 from patent US 6818444.
SSION   AR595960
ION     AR595960.1  GI:56646941
ORDS    .
CE      Unknown.
GANISM  Unknown.
        Unclassified.
RENCE   1  (bases 1 to 1533)
THORS   Wonderling,R.S. and Boroughs,K.L.
TLE     Canine and feline proteins, nucleic acid molecules and uses thereof
URNAL   Patent: US 6818444-A 45 16-NOV-2004;
        Heska Corporation; Fort Collins, CO
URES            Location/Qualifiers
 source         1. .1533
                /organism="unknown"
                /mol_type="genomic DNA"
IN

ery Match           100.0%;  Score 60;  DB 2;  Length 1533;
st Local Similarity  100.0%;  Pred. No. 1.7e-13;
tches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 5
AR595956
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .1599
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 60;  DB 2;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-13;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040


RESULT 6
AR595957/c
LOCUS       AR595957                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .1599
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 60;  DB 2;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-13;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 7
AR595973
LOCUS       AR595973                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
```

RCE Unknown.
RGANISM Unknown.
Unclassified.
ERENCE 1 (bases 1 to 1533)
JTHORS Wonderling,R.S. and Boroughs,K.L.
ITLE Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL Patent: US 6818444-A 66 16-NOV-2004;
Heska Corporation; Fort Collins, CO
TURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
IN

iery Match 98.3%; Score 59; DB 2; Length 1533;
est Local Similarity 100.0%; Pred. No. 4.5e-13;
atches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
916 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974

ULT 8
95974/c
US AR595974 1533 bp DNA linear PAT 15-DEC-2004
INITION Sequence 68 from patent US 6818444.
ESSION AR595974
SION AR595974.1 GI:56646955
WORDS .
RCE Unknown.
RGANISM Unknown.
Unclassified.
ERENCE 1 (bases 1 to 1533)
JTHORS Wonderling,R.S. and Boroughs,K.L.
ITLE Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL Patent: US 6818444-A 68 16-NOV-2004;
Heska Corporation; Fort Collins, CO
TURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
IN

iery Match 98.3%; Score 59; DB 2; Length 1533;
est Local Similarity 100.0%; Pred. No. 4.5e-13;
atches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560

ULT 9
95971
US AR595971 1599 bp DNA linear PAT 15-DEC-2004
INITION Sequence 61 from patent US 6818444.
ESSION AR595971
SION AR595971.1 GI:56646952
WORDS .
RCE Unknown.
RGANISM Unknown.
Unclassified.
ERENCE 1 (bases 1 to 1599)
JTHORS Wonderling,R.S. and Boroughs,K.L.
ITLE Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL Patent: US 6818444-A 61 16-NOV-2004;
Heska Corporation; Fort Collins, CO
TURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
IN

Query Match 98.3%; Score 59; DB 2; Length 1599;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 982 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040

RESULT 10
AR595972/c
LOCUS AR595972 1599 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 63 from patent US 6818444.
ACCESSION AR595972
VERSION AR595972.1 GI:56646953
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 63 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 98.3%; Score 59; DB 2; Length 1599;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560

RESULT 11
AF401989
LOCUS AF401989 1626 bp mRNA linear SYN 14-FEB-2002
DEFINITION Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION AF401989
VERSION AF401989.1 GI:18656516
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1626)
AUTHORS McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L., Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D., Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
TITLE Production of biologically active equine interleukin 12 through expression of p35, p40 and single chain IL-12 in mammalian and baculovirus expression systems
JOURNAL Equine Vet. J. 33 (7), 693-698 (2001)
PUBMED 11770992
REFERENCE 2 (bases 1 to 1626)
AUTHORS McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A., Argyle,D.J., Onions,D.E. and Nicolson,L.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES Location/Qualifiers
source 1. .1626
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
CDS 1. .1626
/note="derived from Equus caballus; N-terminal p40 subunit linked by (Gly4Ser)3 linker to signal-peptide deleted p35

```
                subunit"
                /codon_start=1
                /transl_table=11
                /product="single chain interleukin-12"
                /protein_id="AAL77817.1"
                /db_xref="GI:18656517"
                /translation="MGHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
                MVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHL
                LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
                QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCSGGGGS
                GGGGSGGGGSRNLPTATPGPGMFQCLNHSQNLLRTVSNTLQKARQTLEFYSCTSEEID
                HEDITKDKSSTVAACLPLELAPNESCLASREISFITNGSCLTPGKASSMMTLCLSSIY
                EDLKMYQVEFKAMNAKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETVPQKPSLEGL
                DFYKTKVKLCILLHAFRIRAVTINRMMGYLNAS"
 primer_bind    1. .14
 misc_feature   15. .987
                /note="interleukin-12 p40 sequence"
 misc_feature   988. .1032
                /note="linker"
 misc_feature   1033. .1611
                /note="interleukin-12 p35 sequence"
 primer_bind    complement(1612. .1626)
IN

ery Match            54.7%;  Score 32.8;  DB 8;  Length 1626;
st Local Similarity  71.7%;  Pred. No. 0.049;
tches   43;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          | |  ||||   ||||||||||||||||||| ||| | || ||  | || |||  ||| ||
     1005 CGGTGGTGGATCCGGTGGCGGCGGATCTAGGAACCTCCCCACAGCCACACCAGGCCCAGG 1064


LT 12
5665
S       CQ585665               3352 bp    DNA     linear   PAT 02-FEB-2004
NITION  Sequence 13423 from Patent WO0171042.
SSION   CQ585665
ION     CQ585665.1  GI:41645756
ORDS    .
CE      Drosophila sp.
GANISM  Drosophila sp.
        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
        Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
        Ephydroidea; Drosophilidae; Drosophila.
RENCE   1
THORS   Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
TLE     Detection kits, such as nucleic acid arrays, for detecting the
        expression of 10,000 or more Drosophila genes and uses thereof
URNAL   Patent: WO 0171042-A 13423 27-SEP-2001;
        PE Corporation (NY) (US)
URES            Location/Qualifiers
 source         1. .3352
                /organism="Drosophila sp."
                /mol_type="unassigned DNA"
                /db_xref="taxon:7242"
IN

ery Match            50.7%;  Score 30.4;  DB 2;  Length 3352;
st Local Similarity  71.4%;  Pred. No. 0.57;
tches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

        2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
          |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
      285 TGCAGTGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 340


LT 13
1862/c
S       CQ581862               4343 bp    DNA     linear   PAT 02-FEB-2004
NITION  Sequence 9620 from Patent WO0171042.

ACCESSION   CQ581862
VERSION     CQ581862.1  GI:41643221
KEYWORDS    .
SOURCE      Drosophila sp.
  ORGANISM  Drosophila sp.
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1
  AUTHORS   Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
  TITLE     Detection kits, such as nucleic acid arrays, for detecting the
            expression of 10,000 or more Drosophila genes and uses thereof
  JOURNAL   Patent: WO 0171042-A 9620 27-SEP-2001;
            PE Corporation (NY) (US)
FEATURES            Location/Qualifiers
     source         1. .4343
                    /organism="Drosophila sp."
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:7242"
ORIGIN

  Query Match           50.7%;  Score 30.4;  DB 2;  Length 4343;
  Best Local Similarity 71.4%;  Pred. No. 0.6;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        244 TGCAGTGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 189


RESULT 14
AY051978/c
LOCUS       AY051978               4877 bp    mRNA    linear   INV 27-AUG-2001
DEFINITION  Drosophila melanogaster LD44770 full length cDNA.
ACCESSION   AY051978
VERSION     AY051978.1  GI:15292266
KEYWORDS    FLI_CDNA.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 4877)
  AUTHORS   Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
            Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
            Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,
            Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K.,
            Yu,C., Lewis,S.E., Rubin,G.M. and Celniker,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
            Lawrence Berkeley National Laboratory, One Cyclotron Road,
            Berkeley, CA 94720, USA
COMMENT     Sequence submitted by:
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory
            Berkeley, CA 94720
            This clone was sequenced as part of a high-throughput process to
            sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
            Science 2000). The sequence has been subjected to integrity checks
            for sequence accuracy, presence of a polyA tail and contiguity
            within 100 kb in the genome. Thus we believe the sequence to
            reflect accurately this particular cDNA clone.  However, there are
            artifacts associated with the generation of cDNA clones that may
            have not been detected in our initial analyses such as internal
            priming, priming from contaminating genomic DNA, retained introns
            due to reverse transcription of unspliced precursor RNAs, and
            reverse transcriptase errors that result in single base changes.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our Web site
            (http://fruitfly.berkeley.edu) or send email to
            cdna@fruitfly.berkeley.edu.
FEATURES            Location/Qualifiers
     source         1. .4877
```

```
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /strain="y; cn bw sp"
                     /db_xref="taxon:7227"
                     /map="32D4-32D4"
     gene            1. .4877
                     /gene="CG4751"
                     /note="alignment with genomic scaffold AE003631"
                     /db_xref="FLYBASE:FBgn0032348"
     CDS             105. .4343
                     /gene="CG4751"
                     /note="Longest ORF"
                     /codon_start=1
                     /product="LD44770p"
                     /protein_id="AAK93402.1"
                     /db_xref="GI:15292267"
                     /db_xref="FLYBASE:FBgn0032348"
                     /translation="MENGVEHGVDESGENQVLSSSDGEGDCDGDGEVEGEVLQPPPPP
                     PLQITNDCVGEGVQAEEGERAPATTGAVDVTPDPGPPPTDGAAPVAILEDNMCDKDVD
                     SDAGDEDNDDETKENYEGFNGTGRTVTLQTLMAANVLQPGLGLMTIEYLGQKFVGDLL
                     ADGKIKSHETETIFLTPSAWAMHCKRIINPDKKSGCGWASVKYKGKKLDAYKNTYLRK
                     CALQKETPLDDCELDAERKTDTPEIVVKRTVFAHNTVSNRNVVHDANMLIESVPFTSV
                     GKLQPFLITVNSSALLLADFHCHLTVREVCGYLGGTWDMNTHTLSITKTYPCRSTRFD
                     RQRAGEVERDIQKMMIQDQLLLVGWYHSHPKFQAEPTLRDCDAQLDYQIKMRGASDLT
                     YTPCVSLIISPYYDENPTLESVVKCIWIVPPNENRQSMEYGRPMLMQYSVLPDKEIPE
                     EVRSEIQLCVDYYSQYRSEMVKFRNIYNNDVTYNEKLKNTLYPKFPSKQSDKALWNWI
                     CAVLDCEQEDDFIPPKTIKIIDNDDLEVKEEDKPVVLMDLSGDVKINPPKEEQFSEAM
                     GGLEDSGRKAEEESNAQAEQKASELKVMSLQEQLCMPSGLNMNPVRMLSPLATPNPTS
                     LPPVLPNLGAPVLPATPSQLLPPQVPAVTAPPAITPAVTTSALTSALNASPRDSPITI
                     QSNSASPAKFEVPVRASPSPAKSDTSSHASTSRTRNSPAPSPGKFSVSDIARNSPSIT
                     PNKYEAAAAAALVPPAAACLPTANDLMAASLAQLAGQLPPNFLQGDLAALFQQQRKDYG
                     SSSLNQLAAAAAKVGGSKQSNASASSGLNDPNVAAAVAAYSNSFNMPLPTGVGIGGSG
                     NSNAHSSSKSKSERSSKSSSSSSSSSNSSSTSNSYKTKLMKELDELKNDPLKMSELIRS
                     PEYAALLLQQAEALGATTLGTLGFGSDYSYLTGAGLGVPAANALTGGQSSNSSSSKSS
                     KSSPAAAAAAALSADYNNLIQASKLLGYDSYMQQSKQSNDLNAFLQQQMAVAAASIPP
                     PPQTASSGSSNSSSSKKQQQLQQQQHQQQQQQQQQQAAAQADYTALLQTYTKLFDPNN
                     QFAAAMSSNKHMAGAHNELSALLSSGVGVGGGASGGGSKQKQKDIQSDMLNQLLQLEK
                     QDSEIKALLYRQNKAAADLDALFATPSGAVVGAGSSANAMKSGSSAGNSGVSGMSSPS
                     SLSNQAAYYNALAQEKMQDYAAFFQQQHGKYGIPDPLSKTTLAANNMFMTPSALFKIQ
                     QESLSAMMMKPPKSTTPSSARTRESSASPALERLTPTKSASSGGSGGGGSNSNSGGKY
                     NFSAVDLAISSVPSNTPSPAPSDGSSGSSHRRPSPDIGRLYGELAPPGALLGSGGVPK
                     KRMEFASVADLAAPPPAKMPKNNMGDDILNLSHD"
GIN

iery Match            50.7%;  Score 30.4;  DB 13;  Length 4877;
est Local Similarity  71.4%;  Pred. No. 0.61;
itches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
            ||||||||  |||||  |||||||||  |  ||  |  ||  ||  ||  ||  |  ||  ||  ||
        244 TGCAGTGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 189


JLT 15
31861
JS       CQ581861               6727 bp    DNA     linear   PAT 02-FEB-2004
INITION  Sequence 9619 from Patent WO0171042.
ESSION   CQ581861
SION     CQ581861.1  GI:41643220
WORDS    .
RCE      Drosophila sp.
RGANISM  Drosophila sp.
         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
         Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
         Ephydroidea; Drosophilidae; Drosophila.
ERENCE   1
UTHORS   Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
ITLE     Detection kits, such as nucleic acid arrays, for detecting the
         expression of 10,000 or more Drosophila genes and uses thereof
OURNAL   Patent: WO 0171042-A 9619 27-SEP-2001;
         PE Corporation (NY) (US)
TURES             Location/Qualifiers
  source          1. .6727
                     /organism="Drosophila sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:7242"
ORIGIN

  Query Match            50.7%;  Score 30.4;  DB 2;  Length 6727;
  Best Local Similarity  71.4%;  Pred. No. 0.65;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              ||||||||  |||||  |||||||||  |  ||  |  ||  ||  ||  ||  |  ||  ||  ||
Db       5484 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 5539


Search completed: June 10, 2006, 15:46:24
Job time : 250.137 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

nucleic - nucleic search, using sw model

on: June 10, 2006, 03:13:22 ; Search time 44.3224 Seconds
(without alignments)
9438.451 Million cell updates/sec

le: US-10-821-670A-83
fect score: 60
ience: 1 ctgcagtggtggcggtggcg.....acccctactccatccccggg 60

ring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

rched: 5244920 seqs, 3486124231 residues

al number of hits satisfying chosen parameters: 10489840

imum DB seq length: 0
imum DB seq length: 2000000000

:-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	60	100.0	60	6	ABK98983	Abk98983 Feline se
	2	60	100.0	60	6	ABK98984	Abk98984 Feline an
	3	60	100.0	60	14	ADV34734	Adv34734 Feline IL
	4	60	100.0	60	14	ADV34733	Adv34733 Feline IL
	5	60	100.0	1533	6	ABK98954	Abk98954 Feline in
	6	60	100.0	1533	6	ABK98953	Abk98953 Feline in
	7	60	100.0	1533	14	ADV34697	Adv34697 Feline si
	8	60	100.0	1533	14	ADV34695	Adv34695 Feline si
	9	60	100.0	1599	6	ABK98950	Abk98950 Feline in
	10	60	100.0	1599	6	ABK98951	Abk98951 Feline in
	11	60	100.0	1599	14	ADV34691	Adv34691 Feline si
	12	60	100.0	1599	14	ADV34693	Adv34693 Feline si
	13	59	98.3	1533	6	ABK98967	Abk98967 Canine in
	14	59	98.3	1533	6	ABK98968	Abk98968 Canine in
	15	59	98.3	1533	14	ADV34718	Adv34718 Canine si
	16	59	98.3	1533	14	ADV34716	Adv34716 Canine si
	17	59	98.3	1599	6	ABK98965	Abk98965 Canine in
	18	59	98.3	1599	6	ABK98966	Abk98966 Canine in
c	19	59	98.3	1599	14	ADV34715	Adv34715 Canine si
	20	59	98.3	1599	14	ADV34713	Adv34713 Canine si
	21	42.4	70.7	11453	10	ADG25152	Adg25152 Vector pS
	22	42.4	70.7	11569	10	ADG25150	Adg25150 Vector pA
	23	33	55.0	33	2	AAT35197	Aat35197 (Gly6)Ser
	24	30.4	50.7	3352	4	ABL10788	Abl10788 Drosophil
c	25	30.4	50.7	4343	4	ABL08253	Abl08253 Drosophil
	26	30.4	50.7	6727	4	ABL08252	Abl08252 Drosophil
	27	29.2	48.7	42	6	AAL44013	Aal44013 Reproduct
c	28	29.2	48.7	1878	2	AAV00256	Aav00256 Mouse Ret
c	29	29.2	48.7	1878	12	ADJ58706	Adj58706 Murine re
c	30	29.2	48.7	1878	14	ADY53842	Ady53842 Partial m
c	31	29.2	48.7	1878	14	ADZ00206	Adz00206 Mouse Ret
c	32	29.2	48.7	1889	2	AAV00249	Aav00249 Mouse Ret
c	33	29.2	48.7	1889	12	ADJ58708	Adj58708 Murine re
c	34	29.2	48.7	1889	14	ADY53844	Ady53844 Mouse ret
c	35	29.2	48.7	1889	14	ADZ00208	Adz00208 Mouse Ret
c	36	29.2	48.7	1935	3	AAZ29100	Aaz29100 Murine GF
c	37	28.6	47.7	576	5	ABV54109	Abv54109 Human pro
	38	28.2	47.0	1080	2	AAZ21160	Aaz21160 Artificia
	39	28.2	47.0	1086	2	AAZ21157	Aaz21157 Artificia
c	40	28	46.7	42	6	AAL44012	Aal44012 Reproduct
	41	27.6	46.0	8608	6	AAD31548	Aad31548 pIRES-hB7
	42	27.6	46.0	8623	6	AAD31547	Aad31547 pIRES-hB7
	43	27.6	46.0	8629	6	AAD31552	Aad31552 pIRES-IL1
	44	27.6	46.0	8638	6	AAD31549	Aad31549 pIRES-hB7
	45	27.6	46.0	8644	6	AAD31551	Aad31551 pIRES-IL1

ALIGNMENTS

RESULT 1
ABK98983
ID ABK98983 standard; DNA; 60 BP.
XX
AC ABK98983;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline sense linker DNA sequence.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; PCR; primer;
KW ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 8; Page 28; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain

proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline PCR primer that was used in the methods of the invention

Sequence 60 BP; 10 A; 20 C; 19 G; 11 T; 0 U; 0 Other;

ery Match 100.0%; Score 60; DB 6; Length 60;
st Local Similarity 100.0%; Pred. No. 5.9e-12;
tches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
```

LT 2
8984/c
ABK98984 standard; DNA; 60 BP.

ABK98984;

21-OCT-2002 (first entry)

Feline antisense linker DNA sequence.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; PCR; primer; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 3; Page 28; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline PCR primer that was used in the methods of the invention

XX
SQ Sequence 60 BP; 11 A; 19 C; 20 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.9e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1
```

RESULT 3
ADV34734/c
ID ADV34734 standard; DNA; 60 BP.
XX
AC ADV34734;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline IL-12p35 and p40 cDNAs linking antisense linker.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ss.
XX
OS Unidentified.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 84; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline interleukin-12p35 and p40 encoding cDNAs
CC linking sense linker.
XX
SQ Sequence 60 BP; 11 A; 19 C; 20 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 60; DB 14; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.9e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1
```

RESULT 4
ADV34733
ID ADV34733 standard; DNA; 60 BP.
XX

ADV34733;

24-FEB-2005 (first entry)

Feline IL-12p35 and p40 cDNAs linking sense linker.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ss.

Unidentified.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Claim 26; SEQ ID NO 83; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline interleukin-12p35 and p40 encoding cDNAs linking sense linker.

Sequence 60 BP; 10 A; 20 C; 19 G; 11 T; 0 U; 0 Other;

ıery Match 100.0%; Score 60; DB 14; Length 60;
ɜst Local Similarity 100.0%; Pred. No. 5.9e-12;
ıtches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
```

JLT 5
)8954/c
ABK98954 standard; cDNA; 1533 BP.

ABK98954;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12-1533 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 66-67; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Query Match 100.0%; Score 60; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560
```

RESULT 6
ABK98953
ID ABK98953 standard; cDNA; 1533 BP.
XX
AC ABK98953;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 63-64; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

```
ery Match             100.0%;  Score 60;  DB 6;  Length 1533;
st Local Similarity   100.0%;  Pred. No. 1.1e-11;
tches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      915 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974
```

LT 7
4697/c
ADV34697 standard; DNA; 1533 BP.

ADV34697;

24-FEB-2005 (first entry)

Feline single chain IL-12 complementary DNA, nFeIL-12 1533.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Felis catus.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 3; SEQ ID NO 45; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12 complementary DNA.

Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 60;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560
```

RESULT 8
ADV34695
ID ADV34695 standard; cDNA; 1533 BP.
XX
AC ADV34695;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 1. .1533
FT /*tag= a
FT /product= "PFeIL-12 511 protein"
FT /partial
FT /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34696.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 60;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      915 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974
```

JLT 9
98950
ABK98950 standard; cDNA; 1599 BP.

ABK98950;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12-1599 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69306.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 58-60; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

```
iery Match            100.0%;  Score 60;  DB 6;  Length 1599;
est Local Similarity   100.0%;  Pred. No. 1.1e-11;
atches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      981 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040
```

JLT 10
98951/c
ABK98951 standard; cDNA; 1599 BP.

AC ABK98951;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 61-62; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

```
  Query Match            100.0%;  Score 60;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560
```

RESULT 11
ADV34691
ID ADV34691 standard; cDNA; 1599 BP.
XX
AC ADV34691;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX

```
Key             Location/Qualifiers
CDS             1. .1599
                /*tag= a
                /product= "PFeIL-12p533 protein"
                /partial
                /note= "No stop codon"

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS,  Boroughs KL;

WPI; 2005-020565/02.
P-PSDB; ADV34692.

New nucleic acid molecule comprising a sequence encoding a feline p35 or
p40 subunit protein and a nucleic acid linker, useful in preparing a
vaccine against infectious diseases in feline animals.

Claim 24; SEQ ID NO 38; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40
subunit protein and their encoding nucleic acid molecules and a nucleic
acid linker. The invention also provides the feline caspase (casp)-1,
feline IL-18 single chain and canine IL-12 single chain proteins and
their nucleic acid molecules. The nucleic acid molecule is useful in
preparing a vaccine against infectious diseases in feline animals. The
present sequence is the feline single chain IL-12 protein encoding cDNA.

Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

ery Match            100.0%;  Score 60;  DB 14;  Length 1599;
st Local Similarity  100.0%;  Pred. No. 1.1e-11;
tches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      981 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040


LT 12
4693/c
 ADV34693 standard; DNA; 1599 BP.

 ADV34693;

 24-FEB-2005  (first entry)

 Feline single chain IL-12 complementary DNA, nFeIL-12 1599.

 DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
 infectious disease; antimicrobial; ds.

 Felis catus.

 US2004248261-A1.

 09-DEC-2004.

 09-APR-2004; 2004US-00821670.

 04-AUG-2000; 2000US-0223016P.
 27-JUL-2001; 2001US-00917265.

 PA   (WOND/) WONDERLING R S.
 PA   (BORO/) BOROUGHS K L.
 XX
 PI   Wonderling RS,  Boroughs KL;
 XX
 DR   WPI; 2005-020565/02.
 XX
 PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
 PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
 PT   vaccine against infectious diseases in feline animals.
 XX
 PS   Example 3; SEQ ID NO 40; 103pp; English.
 XX
 CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
 CC   subunit protein and their encoding nucleic acid molecules and a nucleic
 CC   acid linker. The invention also provides the feline caspase (casp)-1,
 CC   feline IL-18 single chain and canine IL-12 single chain proteins and
 CC   their nucleic acid molecules. The nucleic acid molecule is useful in
 CC   preparing a vaccine against infectious diseases in feline animals. The
 CC   present sequence is the feline single chain IL-12 complementary DNA.
 XX
 SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

   Query Match            100.0%;  Score 60;  DB 14;  Length 1599;
   Best Local Similarity  100.0%;  Pred. No. 1.1e-11;
   Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

 Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 13
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69314.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 83-85; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
```

proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

ıery Match 98.3%; Score 59; DB 6; Length 1533;
ɜst Local Similarity 100.0%; Pred. No. 2.5e-11;
ıtches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
        2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      916 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974
```

JLT 14
98968/c
ABK98968 standard; cDNA; 1533 BP.

ABK98968;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12-1533 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 86-87; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Query Match 98.3%; Score 59; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560
```

RESULT 15
ADV34718/c
ID ADV34718 standard; DNA; 1533 BP.
XX
AC ADV34718;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 68; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Query Match 98.3%; Score 59; DB 14; Length 1533;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560
```

Search completed: June 10, 2006, 04:50:59
Job time : 46.3224 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

nucleic - nucleic search, using sw model

on: June 10, 2006, 03:16:38 ; Search time 350.396 Seconds
(without alignments)
9575.336 Million cell updates/sec

le: US-10-821-670A-83
fect score: 60
uence: 1 ctgcagtggtggcggtggcg.....acccctactccatccccggg 60

ring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

rched: 48236798 seqs, 27959665780 residues

al number of hits satisfying chosen parameters: 96473596

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	% Query Match	Length	DB	ID	Description
1	31	51.7	389	2	BI372699	BI372699 RE59742.5
2	31	51.7	590	2	BI372718	BI372718 RE59764.5
3	30.4	50.7	475	1	AI546686	AI546686 SD10406.5
4	30.4	50.7	484	1	AI511787	AI511787 LD43310.5
5	30.4	50.7	526	1	AI512758	AI512758 LD44770.5
6	30.4	50.7	544	1	AA949039	AA949039 LD27781.5
7	30.4	50.7	558	1	AI541995	AI541995 SD07995.5
8	30.4	50.7	610	2	BI638233	BI638233 SD20467.5
9	30.4	50.7	622	1	AA735618	AA735618 LD21627.5
10	29.2	48.7	442	1	AA049894	AA049894 mj11d08.r
11	29.2	48.7	499	11	AZ758753	AZ758753 1M0550L21
12	29.2	48.7	600	2	BI987608	BI987608 3203-65 M
13	29.2	48.7	740	5	CK782042	CK782042 UI-M-HJ0-
14	29.2	48.7	1919	6	AK046542	AK046542 Mus muscu
15	28.8	48.0	591	14	AG222152	AG222152 Lotus cor
16	28.6	47.7	586	5	CF121277	CF121277 UI-HF-CB0
17	28.6	47.7	856	5	CK151523	CK151523 FGAS03409
18	28.4	47.3	240	14	AB082403	AB082403 Drosophil
19	28	46.7	472	1	AJ845249	AJ845249 AJ845249
20	28	46.7	480	13	CW460629	CW460629 fsbb001f2
21	28	46.7	598	13	CW288787	CW288787 104_767_1
22	28	46.7	659	13	CW201644	CW201644 104_627_1
c 23	28	46.7	681	13	CW201645	CW201645 104_627_1
24	28	46.7	750	2	BG583687	BG583687 EST485440
25	28	46.7	754	13	CW438124	CW438124 fsbb001f1
c 26	27.8	46.3	260	1	AA940899	AA940899 LD23227.5
27	27.8	46.3	1101	14	CNS00HE3	AL073368 Drosophil
c 28	27.6	46.0	747	7	BE892594	BE892594 601433403
c 29	27.4	45.7	977	6	CNS08HN3	BX012283 Single re
30	27.2	45.3	192	8	CV388598	CV388598 QV1-NN017
31	27.2	45.3	451	11	BZ244441	BZ244441 CH230-362
32	27.2	45.3	637	11	BH268535	BH268535 CH230-122
33	27.2	45.3	1459	12	BZ572910	BZ572910 msh2_2855
34	27	45.0	628	4	CA610835	CA610835 wr1.pk012
c 35	26.8	44.7	384	5	CD180715	CD180715 MS1-0027T
c 36	26.8	44.7	384	5	CD181150	CD181150 MS1-0027T
37	26.8	44.7	420	4	CD110886	CD110886 ME1-0020T
c 38	26.8	44.7	458	4	CD096251	CD096251 ME1-0007T
c 39	26.8	44.7	458	4	CD096276	CD096276 ME1-0007T
40	26.8	44.7	507	4	CA250030	CA250030 SCRUFL111
41	26.8	44.7	517	1	AI119674	AI119674 uf05g11.y
c 42	26.8	44.7	1101	14	CNS00H7Y	AL073046 Drosophil
43	26.6	44.3	383	12	CG859544	CG859544 ZMMBBc026
c 44	26.6	44.3	395	11	AQ131072	AQ131072 HS_3034_A
45	26.6	44.3	526	2	BJ519662	BJ519662 BJ519662

ALIGNMENTS

RESULT 1
BI372699/c
LOCUS BI372699 389 bp mRNA linear EST 01-AUG-2001
DEFINITION RE59742.5prime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone RE59742 5 similar to CG4751: FBan0004751 GO:[] located on: 2L 32D4-32D4;: 05/16/2001, mRNA sequence.
ACCESSION BI372699
VERSION BI372699.1 GI:15068727
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 389)
AUTHORS Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin,G.M.
TITLE BDGP/HHMI RE Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003631: arm:2L [10950468,11211850]
estimated-cyto:32D2-32F1: 05/16/2001
Plate: RE.597 row: D column: 6
High quality sequence stop: 331.
FEATURES Location/Qualifiers
source 1. .389
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE59742"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"

/lab_host="DH5-alpha TonA"
/clone_lib="RE Drosophila melanogaster normalized Embryo pFlc-1"
/note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

IN

ery Match 51.7%; Score 31; DB 2; Length 389;
st Local Similarity 71.4%; Pred. No. 7.4;
tches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
||||||||| ||||| |||||||| | || | || || || || | || || ||
264 TGCAGTGGCGGCGGCGGCGGCGGCTNCAGCACCTCCCCCTCCACTTCACCGTCACC 209

LT 2
2718/c
S BI372718 590 bp mRNA linear EST 01-AUG-2001
NITION RE59764.5prime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone RE59764 5 similar to CG4751: FBan0004751 GO:[] located on: 2L 32D4-32D4;: 05/16/2001, mRNA sequence.
SSION BI372718
ION BI372718.1 GI:15068746
ORDS EST.
CE Drosophila melanogaster (fruit fly)
GANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
RENCE 1 (bases 1 to 590)
THORS Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin,G.M.
TLE BDGP/HHMI RE Drosophila EST Project
URNAL Unpublished (2001)
ENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003631: arm:2L [10950468,11211850]
estimated-cyto:32D2-32F1: 05/16/2001
Plate: RE.597 row: F column: 4
High quality sequence stop: 466.
URES Location/Qualifiers
source 1. .590
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE59764"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
/clone_lib="RE Drosophila melanogaster normalized Embryo pFlc-1"
/note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

IN

ery Match 51.7%; Score 31; DB 2; Length 590;
st Local Similarity 71.4%; Pred. No. 7.6;
tches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
||||||||| ||||| |||||||| | || | || || || || | || || ||
Db 264 TGCAGTGGCGGCGGCGGCGGCGGNTGCAGCACCTCCCCCTCCACTTCACCGTCACC 209

RESULT 3
AI546686/c
LOCUS AI546686 475 bp mRNA linear EST 19-APR-2001
DEFINITION SD10406.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD10406 5prime, mRNA sequence.
ACCESSION AI546686
VERSION AI546686.1 GI:4464059
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 475)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC005115
Plate: 104 row: A column: 6
High quality sequence stop: 405.
FEATURES Location/Qualifiers
source 1. .475
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="SD10406"
/lab_host="DH5-alpha"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell culture pOT2"
/note="Vector: pOT2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
ORIGIN

Query Match 50.7%; Score 30.4; DB 1; Length 475;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
||||||||| ||||| |||||||| | || | || || || || | || || ||
Db 214 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 159

RESULT 4
AI511787/c
LOCUS AI511787 484 bp mRNA linear EST 19-APR-2001
DEFINITION LD43310.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD43310 5prime, mRNA sequence.
ACCESSION AI511787
VERSION AI511787.1 GI:4421205
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 484)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.
TITLE BDGP/HHMI Drosophila EST Project

```
)URNAL   Unpublished (2001)
1ENT     Contact: Stapleton, M.
         BDGP
         Lawrence Berkeley National Lab
         One Cyclotron Rd, Berkeley, CA 94720, USA
         Fax: 510 486 6798
         Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
         hit genomic sequence AC005115
         Plate: 433  row: A  column: 10
         High quality sequence stop: 424.
TURES            Location/Qualifiers
  source         1. .484
                 /organism="Drosophila melanogaster"
                 /mol_type="mRNA"
                 /db_xref="taxon:7227"
                 /clone="LD43310"
                 /sex="male and female"
                 /dev_stage="0 to 24 hours mixed stage embryonic"
                 /lab_host="XL1 Blue"
                 /clone_lib="LD Drosophila melanogaster embryo pOT2"
                 /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                 XhoI; Sized fractionated cDNAs were directly ligated into
                 pOT2. "
IN

iery Match            50.7%;  Score 30.4;  DB 1;  Length 484;
est Local Similarity  71.4%;  Pred. No. 12;
atches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
            |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
        223 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 168


JLT 5
l2758/c
JS       AI512758                526 bp    mRNA    linear   EST 02-DEC-2003
INITION  LD44770.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
         melanogaster cDNA clone LD44770 5 similar to CG4751: FBan0004751
         GO:[] located on: 2L 32D4-32D4;: 08/13/2002, mRNA sequence.
SSION    AI512758
SION     AI512758.2  GI:13770030
WORDS    EST.
RCE      Drosophila melanogaster (fruit fly)
RGANISM  Drosophila melanogaster
         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
         Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
         Ephydroidea; Drosophilidae; Drosophila.
ERENCE   1  (bases 1 to 526)
UTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
         Lewis,S. and Rubin,G.M.
ITLE     BDGP/HHMI Drosophila EST Project
OURNAL   Unpublished (2001)
MENT     On Mar 16, 1999 this sequence version replaced gi:4422176.
         Other_ESTs: LD44770.3prime
         Contact: Stapleton, M.
         BDGP
         Lawrence Berkeley National Lab
         One Cyclotron Rd, Berkeley, CA 94720, USA
         Fax: 510 486 6798
         Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
         hit genomic AE003631: arm:2L [10950468,11211850]
         estimated-cyto:32D2-32F1: 04/10/2001
         Plate: LD.447  row: F  column: 10
         High quality sequence stop: 457
         POLYA=No.
TURES            Location/Qualifiers
  source         1. .526
                 /organism="Drosophila melanogaster"
                 /mol_type="mRNA"
                 /db_xref="taxon:7227"
                 /clone="LD44770"
                 /sex="male and female"
                 /dev_stage="0 to 24 hours mixed stage embryonic"
                 /lab_host="XL1 Blue"
                 /clone_lib="LD Drosophila melanogaster embryo pOT2"
                 /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                 XhoI; Sized fractionated cDNAs were directly ligated into
                 pOT2. "
ORIGIN

  Query Match            50.7%;  Score 30.4;  DB 1;  Length 526;
  Best Local Similarity  71.4%;  Pred. No. 12;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        244 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 189


RESULT 6
AA949039/c
LOCUS       AA949039                544 bp    mRNA    linear   EST 19-APR-2001
DEFINITION  LD27781.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
            melanogaster cDNA clone LD27781 5prime, mRNA sequence.
ACCESSION   AA949039
VERSION     AA949039.1  GI:3110948
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 544)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 277  row: G  column: 9
            High quality sequence stop: 455.
FEATURES             Location/Qualifiers
     source          1. .544
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="LD27781"
                     /sex="male and female"
                     /dev_stage="0 to 24 hours mixed stage embryonic"
                     /lab_host="XL1 Blue"
                     /clone_lib="LD Drosophila melanogaster embryo pOT2"
                     /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2. "
ORIGIN

  Query Match            50.7%;  Score 30.4;  DB 1;  Length 544;
  Best Local Similarity  71.4%;  Pred. No. 12;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        220 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 165


RESULT 7
AI541995/c
LOCUS       AI541995                558 bp    mRNA    linear   EST 19-APR-2001
DEFINITION  SD07995.5prime SD Drosophila melanogaster Schneider L2 cell culture
            pOT2 Drosophila melanogaster cDNA clone SD07995 5prime, mRNA
            sequence.
```

```
SSION   AI541995
ION     AI541995.1  GI:4459368
ORDS    EST.
CE      Drosophila melanogaster (fruit fly)
GANISM  Drosophila melanogaster
        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
        Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
        Ephydroidea; Drosophilidae; Drosophila.
RENCE   1  (bases 1 to 558)
THORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
        Lewis,S. and Rubin,G.M.
TLE     BDGP/HHMI Drosophila EST Project
URNAL   Unpublished (2001)
ENT     Contact: Stapleton, M.
        BDGP
        Lawrence Berkeley National Lab
        One Cyclotron Rd, Berkeley, CA 94720, USA
        Fax: 510 486 6798
        Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
        hit genomic sequence AC005115
        Plate: 79  row: H  column: 11
        High quality sequence stop: 418.
URES            Location/Qualifiers
 source         1. .558
                /organism="Drosophila melanogaster"
                /mol_type="mRNA"
                /db_xref="taxon:7227"
                /clone="SD07995"
                /lab_host="DH5-alpha"
                /clone_lib="SD Drosophila melanogaster Schneider L2 cell
                culture pOT2"
                /note="Vector: pOT2; Site_1: EcoRI; Site_2: Xho1; Sized
                fractionated cDNAs were directly ligated into pOT2.
                Plasmid cDNA library."
IN

ery Match             50.7%;  Score 30.4;  DB 1;  Length 558;
st Local Similarity   71.4%;  Pred. No. 12;
tches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

        2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
          ||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
      214 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 159


LT 8
8233/c
S       BI638233                610 bp    mRNA    linear   EST 10-SEP-2001
NITION  SD20467.5prime SD Drosophila melanogaster Schneider L2 cell culture
        pOT2 Drosophila melanogaster cDNA clone SD20467 5 similar to
        CG4751: FBan0004751 GO:[] located on: 2L 32D4-32D4;: 05/19/2001,
        mRNA sequence.
SSION   BI638233
ION     BI638233.1  GI:15540443
ORDS    EST.
CE      Drosophila melanogaster (fruit fly)
GANISM  Drosophila melanogaster
        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
        Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
        Ephydroidea; Drosophilidae; Drosophila.
RENCE   1  (bases 1 to 610)
THORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
        Lewis,S. and Rubin,G.M.
TLE     BDGP/HHMI Drosophila EST Project
URNAL   Unpublished (2001)
ENT     Contact: Stapleton, M.
        BDGP
        Lawrence Berkeley National Lab
        One Cyclotron Rd, Berkeley, CA 94720, USA
        Fax: 510 486 6798
        Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
        hit genomic AE003631: arm:2L [10950468,11211850]
        estimated-cyto:32D2-32F1: 05/19/2001
        Plate: SD.204  row: F  column: 7
        High quality sequence stop: 609.
FEATURES        Location/Qualifiers
     source     1. .610
                /organism="Drosophila melanogaster"
                /mol_type="mRNA"
                /db_xref="taxon:7227"
                /clone="SD20467"
                /lab_host="DH5-alpha"
                /clone_lib="SD Drosophila melanogaster Schneider L2 cell
                culture pOT2"
                /note="Vector: pOT2; Site_1: EcoRI; Site_2: Xho1; Sized
                fractionated cDNAs were directly ligated into pOT2.
                Plasmid cDNA library."
ORIGIN

  Query Match           50.7%;  Score 30.4;  DB 2;  Length 610;
  Best Local Similarity   71.4%;  Pred. No. 12;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              ||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        214 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 159


RESULT 9
AA735618/c
LOCUS       AA735618                622 bp    mRNA    linear   EST 23-APR-2001
DEFINITION  LD21627.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
            melanogaster cDNA clone LD21627 5 similar to CG4751: FBan0004751
            located on: 2L 32D4-32D4;: 04/10/2001, mRNA sequence.
ACCESSION   AA735618
VERSION     AA735618.2  GI:13767408
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 622)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     On Jan 9, 1998 this sequence version replaced gi:2761548.
            Other_ESTs: LD21627.3prime
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003631: arm:2L [10950468,11211850]
            estimated-cyto:32D2-32F1: 04/10/2001
            Plate: LD.216  row: C  column: 3
            High quality sequence stop: 554
            POLYA=No.
FEATURES            Location/Qualifiers
     source         1. .622
                    /organism="Drosophila melanogaster"
                    /mol_type="mRNA"
                    /db_xref="taxon:7227"
                    /clone="LD21627"
                    /sex="male and female"
                    /dev_stage="0 to 24 hours mixed stage embryonic"
                    /lab_host="XL1 Blue"
                    /clone_lib="LD Drosophila melanogaster embryo pOT2"
                    /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                    XhoI; Sized fractionated cDNAs were directly ligated into
                    pOT2. "
ORIGIN

  Query Match           50.7%;  Score 30.4;  DB 1;  Length 622;
```

```
est Local Similarity   71.4%;  Pred. No. 12;
atches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCCTACTCCATCCCC 57
            |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
        223 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 168


JLT 10
49894/c
JS        AA049894                 442 bp    mRNA    linear   EST 30-DEC-1996
INITION   mj11d08.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
          clone IMAGE:475791 5', mRNA sequence.
ESSION    AA049894
SION      AA049894.1  GI:1755226
WORDS     EST.
RCE       Mus musculus (house mouse)
RGANISM   Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE    1  (bases 1 to 442)
UTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
          Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
          Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
          Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
          Waterston,R.
ITLE      The WashU-HHMI Mouse EST Project
OURNAL    Unpublished (1996)
MENT      On Dec 30, 1996 this sequence version replaced gi:1529566.
          Contact: Marra M/Mouse EST Project
          WashU-HHMI Mouse EST Project
          Washington University School of MedicineP
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: mouseest@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          MGI:286535
          Seq primer: -28M13 rev2 from Amersham
          High quality sequence stop: 405.
TURES               Location/Qualifiers
  source            1. .442
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:475791"
                    /sex="unknown"
                    /tissue_type="embryo"
                    /dev_stage="13.5-14.5dpc total fetus"
                    /lab_host="DH10B"
                    /clone_lib="Soares mouse embryo NbME13.5 14.5"
                    /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                    1st strand cDNA was primed with a Not I - oligo(dT) primer
                    [5'
                    TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTTT
                    T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                    14.5dpc embryos [total RNA provided by  Minoru Ko, Wayne
                    State Univ., from 2 ]; double-stranded cDNA was ligated to
                    Eco RI adaptors (Pharmacia), digested with Not I and
                    cloned into the Not I and Eco RI sites of the modified
                    pT7T3 vector. Library went through one round of
                    normalization, and was constructed by Bento Soares and
                    M.Fatima Bonaldo.  "
GIN

uery Match             48.7%;  Score 29.2;  DB 1;  Length 442;
est Local Similarity   69.0%;  Pred. No. 31;
atches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
```

```
            |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        107 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 50


RESULT 11
AZ758753
LOCUS       AZ758753                 499 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0550L21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0550L21 R, genomic survey sequence.
ACCESSION   AZ758753
VERSION     AZ758753.1  GI:12864893
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0550  row: L  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 499.
FEATURES            Location/Qualifiers
     source         1. .499
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0550L21"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
ORIGIN

  Query Match             48.7%;  Score 29.2;  DB 11;  Length 499;
  Best Local Similarity   69.0%;  Pred. No. 31;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;
```

```
        3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
      122 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 179


LT 12
7608/c
S       BI987608                 600 bp    mRNA    linear   EST 20-DEC-2001
NITION  3203-65 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
        mRNA sequence.
SSION   BI987608
'ION    BI987608.1  GI:17958576
ORDS    EST.
CE      Mus musculus (house mouse)
GANISM  Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
        Sciurognathi; Muroidea; Muridae; Murinae; Mus.
RENCE   1  (bases 1 to 600)
'THORS  Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
        White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
TLE     Gene expression in the developing mouse retina by EST sequencing
        and microarray analysis
URNAL   Nucleic Acids Res. 29 (24), 4983-4993 (2001)
UBMED   11812828
'ENT    Contact: Klein WH
        Department of Biochemistry and Molecular Biology
        University of Texas M.D. Anderson Cancer Center
        Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
        Tel: 713 792 3646
        Fax: 713 790 0329.
URES            Location/Qualifiers
 source         1. .600
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /tissue_type="neural retina"
                /dev_stage="embryonic day 14.5 post-fertilization"
                /clone_lib="Mouse E14.5 retina lambda ZAP II Library"
'IN

ery Match            48.7%;  Score 29.2;  DB 2;  Length 600;
st Local Similarity  69.0%;  Pred. No. 32;
tches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

        3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
      443 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 386


LT 13
2042/c
S       CK782042                 740 bp    mRNA    linear   EST 23-FEB-2004
NITION  UI-M-HJ0-cmi-e-21-0-UI.r1 NIH_BMAP_HJ0 Mus musculus cDNA clone
        IMAGE:30626324 5', mRNA sequence.
SSION   CK782042
ION     CK782042.1  GI:42747720
ORDS    EST.
'CE     Mus musculus (house mouse)
'GANISM Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
        Sciurognathi; Muroidea; Muridae; Murinae; Mus.
RENCE   1  (bases 1 to 740)
'THORS  NIH-MGC http://mgc.nci.nih.gov/.
TLE     National Institutes of Health, Mammalian Gene Collection (MGC)
URNAL   Unpublished (1999)
'ENT    Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: Dr. James Lin University of Iowa
         cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
         cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
         DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
         Clone Distribution: Distribution information can be found at
        http://genome.uiowa.edu/distribution/mousefl.html
         This clone was contributed by the Brain Molecular Anatomy Project
        (BMAP)
        Seq primer: pYX-5.
FEATURES        Location/Qualifiers
     source     1. .740
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6"
                /db_xref="taxon:10090"
                /clone="IMAGE:30626324"
                /tissue_type="Upper Head"
                /dev_stage="9.5 and 10.5 dpc"
                /lab_host="DH10B (T1 phage resistant)"
                /clone_lib="NIH_BMAP_HJ0"
                /note="Organ: Head; Vector: pYX-Asc; Site_1: EcoR I;
                Site_2: Not I; The library was constructed according
                Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                1996. Denatured RNA was size fractionated on a 1% agarose
                gel.First strand cDNA synthesis was primed with oligo-dT
                primer containing a Not I site .Double strand cDNA was
                size selected according to mRNA size fraction ,ligated
                with EcoR I adaptor , digested with NotI and then cloned
                directionally into pYX-Asc vector . The library tag
                sequence located between the Not I site and the polyA tail
                is CGAACTGAAT. This library was created for the University
                Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                Developing Mouse Nervous System', supported by National
                Institute of Mental Health (NIMH)."
ORIGIN

  Query Match            48.7%;  Score 29.2;  DB 5;  Length 740;
  Best Local Similarity  69.0%;  Pred. No. 32;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        499 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 442


RESULT 14
AK046542/c
LOCUS       AK046542                 1919 bp    mRNA    linear   HTC 02-SEP-2005
DEFINITION  Mus musculus adult male adrenal gland cDNA, RIKEN full-length
            enriched library, clone:B330033O18 product:glial cell line derived
            neurotrophic factor family receptor alpha 3, full insert sequence.
ACCESSION   AK046542
VERSION     AK046542.1  GI:26338184
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
```

```
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  ITLE      RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  OURNAL    Genome Res. 10 (11), 1757-1771 (2000)
  UBMED     11076861
  ERENCE    4
  UTHORS    The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  ITLE      Functional annotation of a full-length mouse cDNA collection
  OURNAL    Nature 409, 685-690 (2001)
  ERENCE    5
  UTHORS    The FANTOM Consortium, the RIKEN Genome Exploration Research Group
            Phase I and II Team.
  ITLE      Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  OURNAL    Nature 420, 563-573 (2002)
  ERENCE    6
  UTHORS    RIKEN Genome Exploration Research Group, Genome Science Group
            (Genome Network Core Team) and the FANTOM Consortium.
  ITLE      Antisense Transcription in the Mammalian Transcriptome
  OURNAL    Science 309, 1564-1566 (2005)
  ERENCE    7
  UTHORS    The FANTOM Consortium, Riken Genome Exploration Research Group and
            Genome Science Group (Genome Network Project Core Group).
  ITLE      The Transcriptional Landscape of the Mammalian Genome
  OURNAL    Science 309, 1559-1563 (2005)
  ERENCE    8  (bases 1 to 1919)
  UTHORS    Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  ITLE      Direct Submission
  OURNAL    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
  ENT       cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
  TURES                 Location/Qualifiers
     source             1. .1919
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="FANTOM_DB:B330033O18"
                        /db_xref="taxon:10090"
                        /clone="B330033O18"
                        /sex="male"
                        /tissue_type="adrenal gland"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="adult"
     CDS                95. .1288
                        /note="unnamed protein product; glial cell line derived
                        neurotrophic factor family receptor alpha 3
                        (MGD|MGI:1201403 GB|NM_010280, evidence: BLASTN, 99%,
                        match=1867)
                        putative"
                        /codon_start=1
                        /protein_id="BAC32778.1"
                        /db_xref="GI:26338185"
                        /translation="MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQA
                        RKKCEANPACKAAYQHLGSCTCSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHR
                        RMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCL
                        KFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCA
                        PEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILG
                        TCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQ
                        NPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSILPLIL
                        LQTLW"
     polyA_signal       1900. .1905
                        /note="putative"
     polyA_site         1919
                        /note="putative"
  ORIGIN

    Query Match             48.7%;  Score 29.2;  DB 6;  Length 1919;
    Best Local Similarity   69.0%;  Pred. No. 34;
    Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

  Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
                |||| ||||||| |||| |||||||     | | ||||  ||| ||  || | | | ||
  Db        673 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 616


  RESULT 15
  AG222152/c
  LOCUS       AG222152                 591 bp    DNA     linear   GSS 19-JUL-2003
  DEFINITION  Lotus corniculatus var. japonicus DNA, clone:LjB06103_r, genomic
              survey sequence.
  ACCESSION   AG222152
  VERSION     AG222152.1  GI:26529105
  KEYWORDS    GSS.
  SOURCE      Lotus corniculatus var. japonicus (Lotus japonicus)
    ORGANISM  Lotus corniculatus var. japonicus
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
              Lotus.
  REFERENCE   1
    AUTHORS   Sato,S., Nakamura,Y. and Tabata,S.
    TITLE     Lotus japonicus BAC End sequences
    JOURNAL   Published Only in Database (2002)
  REFERENCE   2  (bases 1 to 591)
    AUTHORS   Sato,S.
    TITLE     Direct Submission
    JOURNAL   Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
              The First Laboratory for Plant Gene Research; 2-6-7
              Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
              (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
              Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
  FEATURES              Location/Qualifiers
       source           1. .591
                        /organism="Lotus corniculatus var. japonicus"
                        /mol_type="genomic DNA"
                        /strain="Miyakojima MG-20"
                        /variety="japonicus"
                        /db_xref="taxon:34305"
                        /clone="LjB06103_r"
                        /clone_lib="genomic BAC library"
                        /note="VECTOR:pBeloBAC11
                        synonym: Lotus japonicus"
  ORIGIN

    Query Match             48.0%;  Score 28.8;  DB 14;  Length 591;
    Best Local Similarity   69.6%;  Pred. No. 43;
    Matches   39;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

  Qy          5 AGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
                | || ||| ||||| | |||||||||| |||| | ||| | |||   ||   |||
  Db        463 ACTGATGGTGGTGGGTGTGGATCTAGAATCTTGGCCACCACCACTAATTCTAAGGG 408
```

ch completed: June 10, 2006, 17:40:22
time : 353.396 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

ucleic - nucleic search, using sw model

on: June 10, 2006, 04:51:14 ; Search time 12.952 Seconds
(without alignments)
8667.862 Million cell updates/sec

le: US-10-821-670A-83
fect score: 60
ience: 1 ctgcagtggtggcggtggcg.....acccctactccatccccggg 60

ring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

rched: 1403666 seqs, 935554401 residues

al number of hits satisfying chosen parameters: 2807332

imum DB seq length: 0
imum DB seq length: 2000000000

:-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ılt No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	60	3	US-09-917-265A-83	Sequence 83, Appl
2	60	100.0	60	3	US-09-917-265A-84	Sequence 84, Appl
3	60	100.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
4	60	100.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
5	60	100.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
6	60	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
7	59	98.3	1533	3	US-09-917-265A-66	Sequence 66, Appl
8	59	98.3	1533	3	US-09-917-265A-68	Sequence 68, Appl
9	59	98.3	1599	3	US-09-917-265A-61	Sequence 61, Appl
10	59	98.3	1599	3	US-09-917-265A-63	Sequence 63, Appl
11	29.2	48.7	1878	3	US-09-187-906-14	Sequence 14, Appl
12	29.2	48.7	1878	3	US-09-489-407-14	Sequence 14, Appl
13	29.2	48.7	1889	3	US-09-187-906-16	Sequence 16, Appl
14	29.2	48.7	1889	3	US-09-489-407-16	Sequence 16, Appl
15	29.2	48.7	1935	5	US-09-272-835D-4	Sequence 4, Appli
16	28.2	47.0	1080	3	US-09-646-028-39	Sequence 39, Appl
17	28.2	47.0	1086	3	US-09-646-028-36	Sequence 36, Appl
18	25.4	42.3	69	2	US-08-373-190-12	Sequence 12, Appl
19	25.4	42.3	69	3	US-08-350-215-11	Sequence 11, Appl
20	25.4	42.3	70	2	US-08-438-190A-11	Sequence 11, Appl
21	25.4	42.3	70	3	US-09-287-145A-11	Sequence 11, Appl
22	25.4	42.3	70	3	US-09-556-111-11	Sequence 11, Appl
23	25.4	42.3	3015	3	US-09-248-796A-4016	Sequence 4016, Ap
24	25.2	42.0	1005	3	US-09-646-028-41	Sequence 41, Appl
25	25.2	42.0	1020	3	US-09-646-028-47	Sequence 47, Appl
26	25.2	42.0	1047	3	US-09-646-028-44	Sequence 44, Appl
c 27	24.8	41.3	1785	3	US-09-732-357B-1	Sequence 1, Appli
c 28	24.8	41.3	1807	3	US-09-949-002-111	Sequence 111, App
c 29	24.8	41.3	1807	3	US-09-949-002-218	Sequence 218, App
c 30	24.8	41.3	1840	3	US-09-807-200-1	Sequence 1, Appli
c 31	24.8	41.3	1847	3	US-09-999-833A-235	Sequence 235, App
c 32	24.8	41.3	1847	3	US-10-020-445A-235	Sequence 235, App
c 33	24.8	41.3	1847	4	US-09-978-189-235	Sequence 235, App
c 34	24.8	41.3	1847	4	US-10-017-085A-235	Sequence 235, App
c 35	24.8	41.3	1847	5	US-10-145-129A-235	Sequence 235, App
c 36	24.8	41.3	1847	5	US-10-013-929A-235	Sequence 235, App
c 37	24.8	41.3	1847	5	US-10-013-917A-235	Sequence 235, App
c 38	24.8	41.3	9880	3	US-09-949-002-683	Sequence 683, App
c 39	24.8	41.3	9881	3	US-09-949-002-790	Sequence 790, App
40	24.6	41.0	748	2	US-08-235-838-10	Sequence 10, Appl
41	24.6	41.0	748	2	US-08-465-473B-10	Sequence 10, Appl
42	24.6	41.0	748	4	US-09-596-774-3	Sequence 3, Appli
43	24.6	41.0	2012	2	US-08-235-838-15	Sequence 15, Appl
44	24.6	41.0	2012	2	US-08-465-473B-15	Sequence 15, Appl
c 45	24.2	40.3	527	3	US-09-621-976-3819	Sequence 3819, Ap

ALIGNMENTS

RESULT 1
US-09-917-265A-83
; Sequence 83, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-917-265A-83

Query Match 100.0%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60

RESULT 2
US-09-917-265A-84/c
; Sequence 84, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016

RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 84
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Primer
9-917-265A-84

ery Match 100.0%; Score 60; DB 3; Length 60;
st Local Similarity 100.0%; Pred. No. 1.7e-12;
tches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       60 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1
```

LT 3
9-917-265A-43
quence 43, Application US/09917265A
tent No. 6818444
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT: Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION: THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE: 2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 43
LENGTH: 1533
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
9-917-265A-43

ery Match 100.0%; Score 60; DB 3; Length 1533;
st Local Similarity 100.0%; Pred. No. 3.6e-12;
tches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      915 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974
```

LT 4
9-917-265A-45/c
quence 45, Application US/09917265A
tent No. 6818444
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT: Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION: THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE: 2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 45
LENGTH: 1533
TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-45

Query Match 100.0%; Score 60; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560
```

RESULT 5
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Query Match 100.0%; Score 60; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040
```

RESULT 6
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-40

Query Match 100.0%; Score 60; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


JLT 7
)9-917-265A-66
equence 66, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 66
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1533)
)9-917-265A-66

iery Match             98.3%;  Score 59;  DB 3;  Length 1533;
est Local Similarity   100.0%;  Pred. No. 8.3e-12;
atches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        916 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974


JLT 8
)9-917-265A-68/c
equence 68, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265A
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 68
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Canis familiaris
)9-917-265A-68

iery Match             98.3%;  Score 59;  DB 3;  Length 1533;
est Local Similarity   100.0%;  Pred. No. 8.3e-12;
atches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


JLT 9
)9-917-265A-61
equence 61, Application US/09917265A
atent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;    LENGTH: 1599
;    TYPE: DNA
;    ORGANISM: Canis familiaris
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)..(1599)
US-09-917-265A-61

  Query Match             98.3%;  Score 59;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-12;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040


RESULT 10
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;    LENGTH: 1599
;    TYPE: DNA
;    ORGANISM: Canis familiaris
US-09-917-265A-63

  Query Match             98.3%;  Score 59;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-12;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 11
US-09-187-906-14/c
; Sequence 14, Application US/09187906
; Patent No. 6677135
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
;    TITLE OF INVENTION:  and Renal Growth
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Biogen, Inc.
;      STREET:  14 Cambridge Center
```

```
   CITY:  Cambridge
   STATE:  MA
   COUNTRY:  USA
   ZIP:  02142
 COMPUTER READABLE FORM:
   MEDIUM TYPE:  Floppy disk
   COMPUTER:  IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:  PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/09/187,906
   FILING DATE:
   CLASSIFICATION:
 PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  PCT/US97/07726
   FILING DATE:  07-MAY-97
   APPLICATION NUMBER:  US 60/017,427
   FILING DATE:  08-MAY-96
 PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  US 60/019,300
   FILING DATE:  07-JUN-96
 PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  US 60/021,859
   FILING DATE:  16-JUL-96
 PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  US 60/043,533
   FILING DATE:  10-APR-97
 ATTORNEY/AGENT INFORMATION:
   NAME:  Kaplan, Warren A.
   REGISTRATION NUMBER:  34,199
   REFERENCE/DOCKET NUMBER:  A008 PCT CIP
 TELECOMMUNICATION INFORMATION:
   TELEPHONE:  617-679-2400
   TELEFAX:  617-679-2838
NFORMATION FOR SEQ ID NO:  14:
 SEQUENCE CHARACTERISTICS:
   LENGTH:  1878 base pairs
   TYPE:  nucleic acid
   STRANDEDNESS:  single
   TOPOLOGY:  linear
 MOLECULE TYPE:  cDNA
 FEATURE:
   NAME/KEY:  CDS
   LOCATION:  205..1242
9-187-906-14

ery Match            48.7%;  Score 29.2;  DB 3;  Length 1878;
st Local Similarity   69.0%;  Pred. No. 0.57;
tches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

        3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
      630 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 573


LT 12
9-489-407-14/c
quence 14, Application US/09489407
tent No. 6861509
ENERAL INFORMATION:
 APPLICANT:  BIOGEN, INC.
 TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
 TITLE OF INVENTION:  and Renal Growth
 NUMBER OF SEQUENCES:  21
 CORRESPONDENCE ADDRESS:
   ADDRESSEE:  Biogen, Inc.
   STREET:  14 Cambridge Center
   CITY:  Cambridge
   STATE:  MA
   COUNTRY:  USA
   ZIP:  02142
 COMPUTER READABLE FORM:
   MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/489,407
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US97/07726
;      FILING DATE:  07-MAY-97
;      APPLICATION NUMBER:  US 60/017,427
;      FILING DATE:  08-MAY-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/019,300
;      FILING DATE:  07-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/021,859
;      FILING DATE:  16-JUL-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/043,533
;      FILING DATE:  10-APR-97
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kaplan, Warren A.
;      REGISTRATION NUMBER:  34,199
;      REFERENCE/DOCKET NUMBER:  A008 PCT CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-679-2400
;      TELEFAX:  617-679-2838
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1878 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  205..1242
US-09-489-407-14

  Query Match            48.7%;  Score 29.2;  DB 3;  Length 1878;
  Best Local Similarity   69.0%;  Pred. No. 0.57;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        630 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 573


RESULT 13
US-09-187-906-16/c
; Sequence 16, Application US/09187906
; Patent No. 6677135
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
;    TITLE OF INVENTION:  and Renal Growth
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Biogen, Inc.
;      STREET:  14 Cambridge Center
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02142
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/187,906
;      FILING DATE:
```

```
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/US97/07726
    FILING DATE:  07-MAY-97
    APPLICATION NUMBER:  US 60/017,427
    FILING DATE:  08-MAY-96
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 60/019,300
    FILING DATE:  07-JUN-96
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 60/021,859
    FILING DATE:  16-JUL-96
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 60/043,533
    FILING DATE:  10-APR-97
  ATTORNEY/AGENT INFORMATION:
    NAME:  Kaplan, Warren A.
    REGISTRATION NUMBER:  34,199
    REFERENCE/DOCKET NUMBER:  A008 PCT CIP
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  617-679-2400
    TELEFAX:  617-679-2838
INFORMATION FOR SEQ ID NO:  16:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1889 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  41..1231
09-187-906-16

uery Match             48.7%;  Score 29.2;  DB 3;  Length 1889;
est Local Similarity   69.0%;  Pred. No. 0.57;
atches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
            |||| ||||||| |||| |||||||     | | ||||  ||| ||  || | | | ||
        619 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 562


ULT 14
09-489-407-16/c
equence 16, Application US/09489407
atent No. 6861509
ENERAL INFORMATION:
  APPLICANT:  BIOGEN, INC.
  TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
  TITLE OF INVENTION:  and Renal Growth
  NUMBER OF SEQUENCES:  21
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Biogen, Inc.
    STREET:  14 Cambridge Center
    CITY:  Cambridge
    STATE:  MA
    COUNTRY:  USA
    ZIP:  02142
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/489,407
    FILING DATE:
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/US97/07726
    FILING DATE:  07-MAY-97
    APPLICATION NUMBER:  US 60/017,427
    FILING DATE:  08-MAY-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/019,300
;     FILING DATE:  07-JUN-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/021,859
;     FILING DATE:  16-JUL-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/043,533
;     FILING DATE:  10-APR-97
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Kaplan, Warren A.
;     REGISTRATION NUMBER:  34,199
;     REFERENCE/DOCKET NUMBER:  A008 PCT CIP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-679-2400
;     TELEFAX:  617-679-2838
; INFORMATION FOR SEQ ID NO:  16:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1889 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  41..1231
US-09-489-407-16

  Query Match             48.7%;  Score 29.2;  DB 3;  Length 1889;
  Best Local Similarity   69.0%;  Pred. No. 0.57;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||     | | ||||  ||| ||  || | | | ||
Db        619 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 562


RESULT 15
US-09-272-835D-4/c
; Sequence 4, Application US/09272835D
; Patent No. 7026138
; GENERAL INFORMATION:
;  APPLICANT: De Sauvage, Frederic J.
;  APPLICANT:  Klein, Richard D.
;  APPLICANT:  Rosenthal, Arnon
;  APPLICANT:  Phillips, Heidi S.
;  TITLE OF INVENTION: GFRALPHA3 AND ITS USES
;  FILE REFERENCE: GENENT.065A
;  CURRENT APPLICATION NUMBER: US/09/272,835D
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER: 60/079,124
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 60/081,569
;  PRIOR FILING DATE: 1998-04-13
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 1935
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-272-835D-4

  Query Match             48.7%;  Score 29.2;  DB 5;  Length 1935;
  Best Local Similarity   69.0%;  Pred. No. 0.57;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||     | | ||||  ||| ||  || | | | ||
Db        667 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 610


Search completed: June 10, 2006, 18:08:47
Job time : 13.952 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

nucleic - nucleic search, using sw model

on: June 10, 2006, 07:19:28 ; Search time 68.4044 Seconds
(without alignments)
10777.934 Million cell updates/sec

le: US-10-821-670A-83
fect score: 60
ience: 1 ctgcagtggtggcggtggcg.....acccctactccatccccggg 60

cing table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

ched: 18892170 seqs, 6143817638 residues

al number of hits satisfying chosen parameters: 37784340

imum DB seq length: 0
imum DB seq length: 2000000000

:-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ılt No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	60	3	US-09-917-265-83	Sequence 83, Appl
2	60	100.0	60	3	US-09-917-265-84	Sequence 84, Appl
3	60	100.0	60	9	US-10-821-670-83	Sequence 83, Appl
4	60	100.0	60	9	US-10-821-670-84	Sequence 84, Appl
5	60	100.0	1533	3	US-09-917-265-43	Sequence 43, Appl
6	60	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
7	60	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
8	60	100.0	1533	9	US-10-821-670-45	Sequence 45, Appl
9	60	100.0	1599	3	US-09-917-265-38	Sequence 38, Appl
10	60	100.0	1599	3	US-09-917-265-40	Sequence 40, Appl
11	60	100.0	1599	9	US-10-821-670-38	Sequence 38, Appl
12	60	100.0	1599	9	US-10-821-670-40	Sequence 40, Appl
13	59	98.3	1533	3	US-09-917-265-66	Sequence 66, Appl
14	59	98.3	1533	3	US-09-917-265-68	Sequence 68, Appl
15	59	98.3	1533	9	US-10-821-670-66	Sequence 66, Appl
16	59	98.3	1533	9	US-10-821-670-68	Sequence 68, Appl
17	59	98.3	1599	3	US-09-917-265-61	Sequence 61, Appl
c 18	59	98.3	1599	3	US-09-917-265-63	Sequence 63, Appl
19	59	98.3	1599	9	US-10-821-670-61	Sequence 61, Appl
c 20	59	98.3	1599	9	US-10-821-670-63	Sequence 63, Appl
21	42.4	70.7	11453	10	US-10-511-237-3	Sequence 3, Appli
22	42.4	70.7	11569	10	US-10-511-237-1	Sequence 1, Appli
23	30.4	50.7	3352	13	US-11-097-143-13423	Sequence 13423, A
c 24	30.4	50.7	4343	13	US-11-097-143-9620	Sequence 9620, Ap
25	30.4	50.7	6727	13	US-11-097-143-9619	Sequence 9619, Ap
c 26	29.2	48.7	1878	10	US-10-668-936-14	Sequence 14, Appl
c 27	29.2	48.7	1889	10	US-10-668-936-16	Sequence 16, Appl
c 28	29.2	48.7	1935	10	US-10-621-855-4	Sequence 4, Appli
c 29	28.6	47.7	576	9	US-10-357-930-54128	Sequence 54128, A
30	28.2	47.0	1080	7	US-10-335-394-39	Sequence 39, Appl
31	28.2	47.0	1086	7	US-10-335-394-36	Sequence 36, Appl
32	27.6	46.0	8608	3	US-09-828-825-7	Sequence 7, Appli
33	27.6	46.0	8623	3	US-09-828-825-5	Sequence 5, Appli
34	27.6	46.0	8629	3	US-09-828-825-15	Sequence 15, Appl
35	27.6	46.0	8638	3	US-09-828-825-9	Sequence 9, Appli
36	27.6	46.0	8644	3	US-09-828-825-13	Sequence 13, Appl
37	27.6	46.0	8659	3	US-09-828-825-11	Sequence 11, Appl
38	27	45.0	387	8	US-10-437-963-100784	Sequence 100784,
39	26.6	44.3	375	12	US-10-301-480-43357	Sequence 43357, A
40	26.6	44.3	375	12	US-10-301-480-656766	Sequence 656766,
c 41	26.6	44.3	406	6	US-10-027-632-182782	Sequence 182782,
c 42	26.6	44.3	406	7	US-10-027-632-182782	Sequence 182782,
c 43	26.2	43.7	409	9	US-10-357-930-3531	Sequence 3531, Ap
c 44	26.2	43.7	412	9	US-10-357-930-33856	Sequence 33856, A
c 45	26.2	43.7	412	9	US-10-357-930-42746	Sequence 42746, A

ALIGNMENTS

RESULT 1
US-09-917-265-83
; Sequence 83, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-917-265-83

Query Match 100.0%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60

RESULT 2
US-09-917-265-84/c
; Sequence 84, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE

ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265
URRENT FILING DATE: 2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 109
OFTWARE: PatentIn version 3.1
Q ID NO 84
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Primer
9-917-265-84

ery Match 100.0%; Score 60; DB 3; Length 60;
st Local Similarity 100.0%; Pred. No. 2.1e-12;
tches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       60 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1
```

LT 3
0-821-670-83
quence 83, Application US/10821670
blication No. US20040248261A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT: Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION: THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE: 2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 83
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Primer
0-821-670-83

ery Match 100.0%; Score 60; DB 9; Length 60;
st Local Similarity 100.0%; Pred. No. 2.1e-12;
tches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
```

LT 4
0-821-670-84/c
quence 84, Application US/10821670
blication No. US20040248261A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT: Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION: THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE: 2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2

; SEQ ID NO 84
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-10-821-670-84

Query Match 100.0%; Score 60; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1
```

RESULT 5
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-43

Query Match 100.0%; Score 60; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 2.5e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        915 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974
```

RESULT 6
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-45

Query Match 100.0%; Score 60; DB 3; Length 1533;

```
est Local Similarity   100.0%;  Pred. No. 2.5e-12;
atches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


ULT 7
10-821-670-43
equence 43, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 43
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1533)
10-821-670-43

uery Match             100.0%;  Score 60;  DB 9;  Length 1533;
est Local Similarity   100.0%;  Pred. No. 2.5e-12;
atches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        915 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974


ULT 8
10-821-670-45/c
equence 45, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 45
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Felis catus
10-821-670-45

uery Match             100.0%;  Score 60;  DB 9;  Length 1533;
est Local Similarity   100.0%;  Pred. No. 2.5e-12;
atches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 9
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             100.0%;  Score 60;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-12;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040


RESULT 10
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match             100.0%;  Score 60;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-12;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 11
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
```

```
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 38
LENGTH: 1599
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
0-821-670-38

ery Match             100.0%;  Score 60;  DB 9;  Length 1599;
st Local Similarity   100.0%;  Pred. No. 2.5e-12;
tches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      981 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040


LT 12
0-821-670-40/c
quence 40, Application US/10821670
blication No. US20040248261A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
ITLE OF INVENTION:  THEREOF
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/10/821,670
URRENT FILING DATE:  2004-04-09
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 111
OFTWARE: PatentIn version 3.2
Q ID NO 40
LENGTH: 1599
TYPE: DNA
ORGANISM: Felis catus
0-821-670-40

ery Match             100.0%;  Score 60;  DB 9;  Length 1599;
st Local Similarity   100.0%;  Pred. No. 2.5e-12;
tches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

        1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


LT 13
9-917-265-66
quence 66, Application US/09917265
tent No. US20020052030A1
NERAL INFORMATION:
PPLICANT: Wonderling, Ramani S.
PPLICANT:  Boroughs, Karen L.
ITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
ILE REFERENCE: IM-5
URRENT APPLICATION NUMBER: US/09/917,265
URRENT FILING DATE:  2001-07-27
RIOR APPLICATION NUMBER: 60/223,016
RIOR FILING DATE: 2000-08-04
UMBER OF SEQ ID NOS: 109
OFTWARE: PatentIn version 3.1
Q ID NO 66
LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             98.3%;  Score 59;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 6e-12;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974


RESULT 14
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             98.3%;  Score 59;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 6e-12;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 15
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

  Query Match             98.3%;  Score 59;  DB 9;  Length 1533;
```

est Local Similarity 100.0%; Pred. No. 6e-12;
atches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        916 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974
```

rch completed: June 10, 2006, 18:16:42
time : 68.4044 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

ucleic - nucleic search, using sw model

on: June 10, 2006, 15:46:40 ; Search time 1.04011 Seconds
(without alignments)
7321.729 Million cell updates/sec

le: US-10-821-670A-83
fect score: 60
ience: 1 ctgcagtggtggcggtggcg.....accctactccatccccggg 60

ring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

rched: 253354 seqs, 63461778 residues

al number of hits satisfying chosen parameters: 506708

imum DB seq length: 0
imum DB seq length: 2000000000

:-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt No.	Score	% Query Match	Length	DB	ID	Description
1	23.4	39.0	981	6	US-10-953-349-30329	Sequence 30329, A
2	22.2	37.0	4899	7	US-11-217-529-4664	Sequence 4664, Ap
3	22	36.7	843	6	US-10-861-934-7	Sequence 7, Appli
4	22	36.7	924	6	US-10-861-934-33	Sequence 33, Appl
5	22	36.7	924	6	US-10-861-934-34	Sequence 34, Appl
6	22	36.7	924	6	US-10-861-934-35	Sequence 35, Appl
7	22	36.7	1909	6	US-10-511-937-409	Sequence 409, App
8	22	36.7	2196	7	US-11-293-697-1239	Sequence 1239, Ap
9	22	36.7	2432	6	US-10-861-934-29	Sequence 29, Appl
10	22	36.7	3597	6	US-10-505-928-651	Sequence 651, App
11	22	36.7	3597	6	US-10-511-937-2802	Sequence 2802, Ap
12	21.8	36.3	733	6	US-10-539-402-66	Sequence 66, Appl
13	21.8	36.3	740	6	US-10-539-402-44	Sequence 44, Appl
14	21.8	36.3	873	7	US-11-154-103-36	Sequence 36, Appl
15	21.8	36.3	1349	6	US-10-953-349-31650	Sequence 31650, A
16	21.6	36.0	370	6	US-10-473-173-277	Sequence 277, App
17	21.6	36.0	756	7	US-11-330-353-17	Sequence 17, Appl
18	21.6	36.0	1476	6	US-10-953-349-6684	Sequence 6684, Ap
19	21.4	35.7	1233	6	US-10-953-349-25579	Sequence 25579, A
20	21.4	35.7	2310	7	US-11-217-529-2824	Sequence 2824, Ap
21	21.2	35.3	551	6	US-10-953-349-26465	Sequence 26465, A
22	21.2	35.3	1032	7	US-11-217-529-174305	Sequence 174305,
23	21.2	35.3	1249	6	US-10-953-349-27946	Sequence 27946, A
24	21.2	35.3	1731	6	US-10-953-349-23745	Sequence 23745, A
25	21.2	35.3	1987	7	US-11-293-697-1783	Sequence 1783, Ap
c 26	21.2	35.3	2008	7	US-11-293-697-1217	Sequence 1217, Ap
27	21	35.0	444	6	US-10-953-349-29453	Sequence 29453, A
28	21	35.0	2692	6	US-10-196-749-225	Sequence 225, App
c 29	20.8	34.7	552	6	US-10-488-619-1053	Sequence 1053, Ap
30	20.8	34.7	1323	6	US-10-953-349-9783	Sequence 9783, Ap
31	20.8	34.7	1451	6	US-10-953-349-31780	Sequence 31780, A
32	20.8	34.7	2358	7	US-11-293-697-932	Sequence 932, App
c 33	20.8	34.7	2445	7	US-11-293-697-848	Sequence 848, App
c 34	20.8	34.7	2816	7	US-11-293-697-1772	Sequence 1772, Ap
35	20.8	34.7	3487	7	US-11-145-307A-255	Sequence 255, App
36	20.8	34.7	38187	6	US-10-857-260-31	Sequence 31, Appl
37	20.6	34.3	697	6	US-10-953-349-38410	Sequence 38410, A
38	20.6	34.3	1172	6	US-10-953-349-40050	Sequence 40050, A
c 39	20.6	34.3	1539	6	US-10-953-349-23883	Sequence 23883, A
c 40	20.6	34.3	1645	6	US-10-953-349-31610	Sequence 31610, A
c 41	20.6	34.3	2621	7	US-11-293-697-1407	Sequence 1407, Ap
c 42	20.6	34.3	3003	7	US-11-293-697-2442	Sequence 2442, Ap
c 43	20.6	34.3	3044	6	US-10-480-962-31	Sequence 31, Appl
c 44	20.6	34.3	4011	7	US-11-106-014-91	Sequence 91, Appl
c 45	20.4	34.0	231	7	US-11-217-529-174331	Sequence 174331,

ALIGNMENTS

RESULT 1
US-10-953-349-30329/c
; Sequence 30329, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30329
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-30329

Query Match 39.0%; Score 23.4; DB 6; Length 981;
Best Local Similarity 81.8%; Pred. No. 4.3;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy         12 GCGGTGGCGGCGGATCTAGAAACTTGCCAACCC 44
              ||||||| |||| || |||| | |||||||||
Db        749 GCGGTGGTCGCGGCTCGAGAATCCTGCCAACCC 717
```

RESULT 2
US-11-217-529-4664/c
; Sequence 4664, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4664

```
LENGTH: 4899
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
1-217-529-4664

ery Match             37.0%;  Score 22.2;  DB 7;  Length 4899;
st Local Similarity   69.8%;  Pred. No. 17;
tches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

        3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCC 45
          || ||||||| ||||| |  | ||| |||  ||||   | |||
      403 GCGGTGGTGGTGGTGGTGCGGAATCCAGATCCTTGTTGAACCC 361


LT 3
0-861-934-7/c
quence 7, Application US/10861934
blication No. US20060089491A2
GENERAL INFORMATION:
     APPLICANT: Nagata, Shigikazu
                Suda, Takashi
                Takahashi, Tomoniro
                Nakamura, Norio
     TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
                         Encoding the Same
     NUMBER OF SEQUENCES: 103
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Birch, Stewart, Kolasch & Birch
          STREET: P.O. Box 747
          CITY: Falls Church
          STATE: Virginia
          COUNTRY: USA
          ZIP: 22040-0747
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/10/861,934
          FILING DATE: 07-Jun-2004
          CLASSIFICATION: 530
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: US/08/683,703
          FILING DATE: 07-JUL-1996
     ATTORNEY/AGENT INFORMATION:
          NAME: Murphy Jr., Gerald M.
          REGISTRATION NUMBER: 28,977
          REFERENCE/DOCKET NUMBER: 1110-163P
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: 703-205-8000
          TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 843 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: Not Relevant
          TOPOLOGY: Not Relevant
     MOLECULE TYPE: cDNA to mRNA
     HYPOTHETICAL: NO
     ANTI-SENSE: NO
     ORIGINAL SOURCE:
          ORGANISM: Human
          TISSUE TYPE: T lymphocyte
     FEATURE:
          NAME/KEY:  CDS
          LOCATION:  1..843
     SEQUENCE DESCRIPTION: SEQ ID NO: 7:
0-861-934-7

ery Match             36.7%;  Score 22;  DB 6;  Length 843;
st Local Similarity   83.3%;  Pred. No. 13;
tches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAA 32
              |||||||||||| |||||||||  | | |
Db        190 GCAGTGGTGGCGGCGGCGGCGGAGGTGGTA 161


RESULT 4
US-10-861-934-33
; Sequence 33, Application US/10861934
; Publication No. US20060089491A2
;   GENERAL INFORMATION:
;        APPLICANT: Nagata, Shigikazu
;                   Suda, Takashi
;                   Takahashi, Tomoniro
;                   Nakamura, Norio
;        TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
;                            Encoding the Same
;        NUMBER OF SEQUENCES: 103
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Birch, Stewart, Kolasch & Birch
;             STREET: P.O. Box 747
;             CITY: Falls Church
;             STATE: Virginia
;             COUNTRY: USA
;             ZIP: 22040-0747
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/861,934
;             FILING DATE: 07-Jun-2004
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/683,703
;             FILING DATE: 07-JUL-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Murphy Jr., Gerald M.
;             REGISTRATION NUMBER: 28,977
;             REFERENCE/DOCKET NUMBER: 1110-163P
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-205-8000
;             TELEFAX: 703-205-8050
;   INFORMATION FOR SEQ ID NO: 33:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 924 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        HYPOTHETICAL: NO
;        ANTI-SENSE: YES
;        ORIGINAL SOURCE:
;             ORGANISM: human
;        SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-861-934-33

  Query Match             36.7%;  Score 22;  DB 6;  Length 924;
  Best Local Similarity   83.3%;  Pred. No. 14;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAA 32
              |||||||||||| |||||||||  | | |
Db        676 GCAGTGGTGGCGGCGGCGGCGGAGGTGGTA 705


RESULT 5
US-10-861-934-34
; Sequence 34, Application US/10861934
; Publication No. US20060089491A2
;   GENERAL INFORMATION:
```

```
      APPLICANT: Nagata, Shigikazu
                 Suda, Takashi
                 Takahashi, Tomoniro
                 Nakamura, Norio
      TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
                          Encoding the Same
      NUMBER OF SEQUENCES: 103
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Birch, Stewart, Kolasch & Birch
           STREET: P.O. Box 747
           CITY: Falls Church
           STATE: Virginia
           COUNTRY: USA
           ZIP: 22040-0747
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/10/861,934
           FILING DATE: 07-Jun-2004
           CLASSIFICATION: 530
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: US/08/683,703
           FILING DATE: 07-JUL-1996
      ATTORNEY/AGENT INFORMATION:
           NAME: Murphy Jr., Gerald M.
           REGISTRATION NUMBER: 28,977
           REFERENCE/DOCKET NUMBER: 1110-163P
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: 703-205-8000
           TELEFAX: 703-205-8050
 INFORMATION FOR SEQ ID NO: 34:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 924 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
           DESCRIPTION: /desc = "RNA"
      HYPOTHETICAL: NO
      ANTI-SENSE: YES
      ORIGINAL SOURCE:
           ORGANISM: human
      SEQUENCE DESCRIPTION: SEQ ID NO: 34:
10-861-934-34

iery Match             36.7%;  Score 22;  DB 6;  Length 924;
est Local Similarity   73.3%;  Pred. No. 14;
atches   22;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAA 32
            ||||:||:||||| |||||||||  : | |
        676 GCAGUGGUGGCGGCGGCGGCGGAGGUGGUA 705


JLT 6
10-861-934-35/c
equence 35, Application US/10861934
ublication No. US20060089491A2
 GENERAL INFORMATION:
      APPLICANT: Nagata, Shigikazu
                 Suda, Takashi
                 Takahashi, Tomoniro
                 Nakamura, Norio
      TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
                          Encoding the Same
      NUMBER OF SEQUENCES: 103
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Birch, Stewart, Kolasch & Birch
           STREET: P.O. Box 747
           CITY: Falls Church
           STATE: Virginia
           COUNTRY: USA
           ZIP: 22040-0747
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/10/861,934
           FILING DATE: 07-Jun-2004
           CLASSIFICATION: 530
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: US/08/683,703
           FILING DATE: 07-JUL-1996
      ATTORNEY/AGENT INFORMATION:
           NAME: Murphy Jr., Gerald M.
           REGISTRATION NUMBER: 28,977
           REFERENCE/DOCKET NUMBER: 1110-163P
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: 703-205-8000
           TELEFAX: 703-205-8050
   INFORMATION FOR SEQ ID NO: 35:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 924 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: Not Relevant
           TOPOLOGY: Not Relevant
      MOLECULE TYPE: cDNA
      HYPOTHETICAL: NO
      ANTI-SENSE: NO
      FEATURE:
           NAME/KEY:  5'UTR
           LOCATION:  1..59
      FEATURE:
           NAME/KEY:  3'UTR
           LOCATION:  906..924
      FEATURE:
           NAME/KEY:  -
           LOCATION:  1..924
           OTHER INFORMATION:  /note= "pBH-hFL1"
      SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-861-934-35

  Query Match             36.7%;  Score 22;  DB 6;  Length 924;
  Best Local Similarity   83.3%;  Pred. No. 14;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAA 32
              |||||||||||| |||||||||  | | |
Db        249 GCAGTGGTGGCGGCGGCGGCGGAGGTGGTA 220


RESULT 7
US-10-511-937-409/c
; Sequence 409, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
```

```
RIOR APPLICATION NUMBER: US 10/131,831
RIOR FILING DATE: 2002-04-24
RIOR APPLICATION NUMBER: US 10/325,899
RIOR FILING DATE: 2002-12-20
UMBER OF SEQ ID NOS: 3117
OFTWARE: PatentIn version 3.2
Q ID NO 409
LENGTH: 1909
TYPE: DNA
ORGANISM: Homo sapiens
0-511-937-409

ery Match             36.7%;  Score 22;  DB 6;  Length 1909;
st Local Similarity   83.3%;  Pred. No. 16;
tches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

        3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAA 32
          |||||||||||| |||||||||  | | |
      347 GCAGTGGTGGCGGCGGCGGCGGAGGTGGTA 318


LT 8
1-293-697-1239/c
quence 1239, Application US/11293697
blication No. US20060105376A1
NERAL INFORMATION:
PPLICANT: HELIX RESEARCH INSTITUTE
ITLE OF INVENTION: Novel full length cDNA
ILE REFERENCE: H1-A0106
URRENT APPLICATION NUMBER: US/11/293,697
URRENT FILING DATE:  2005-12-05
RIOR APPLICATION NUMBER: US/10/108,260
RIOR FILING DATE: 2002-03-28
UMBER OF SEQ ID NOS: 5458
OFTWARE: PatentIn Ver. 2.1
Q ID NO 1239
LENGTH: 2196
TYPE: DNA
ORGANISM: Homo sapiens
1-293-697-1239

ery Match             36.7%;  Score 22;  DB 7;  Length 2196;
st Local Similarity   63.0%;  Pred. No. 17;
tches   34;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

        6 GTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGG 59
          ||||||| |||||||| ||   | |   ||      ||  ||  |||||  ||||
      320 GTGGTGGTGGTGGCGGTGGTGGTGGTCCCTCAGGTACATCTCATCCATGTCCGG 267


LT 9
0-861-934-29/c
quence 29, Application US/10861934
blication No. US20060089491A2
GENERAL INFORMATION:
     APPLICANT: Nagata, Shigikazu
                Suda, Takashi
                Takahashi, Tomoniro
                Nakamura, Norio
     TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
                         Encoding the Same
     NUMBER OF SEQUENCES: 103
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Birch, Stewart, Kolasch & Birch
          STREET: P.O. Box 747
          CITY: Falls Church
          STATE: Virginia
          COUNTRY: USA
          ZIP: 22040-0747
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/861,934
;            FILING DATE: 07-Jun-2004
;            CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/683,703
;            FILING DATE: 07-JUL-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Murphy Jr., Gerald M.
;            REGISTRATION NUMBER: 28,977
;            REFERENCE/DOCKET NUMBER: 1110-163P
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 703-205-8000
;            TELEFAX: 703-205-8050
;   INFORMATION FOR SEQ ID NO: 29:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2432 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: Not Relevant
;            TOPOLOGY: Not Relevant
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;            ORGANISM: human
;       IMMEDIATE SOURCE:
;            CLONE: LambdaFL5
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  join(496..843, 982..1027, 1213..1269, 1716..2107)
;            OTHER INFORMATION:  /label= Figs_16-18
;       SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-861-934-29

  Query Match             36.7%;  Score 22;  DB 6;  Length 2432;
  Best Local Similarity   83.3%;  Pred. No. 17;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAA 32
              |||||||||||| |||||||||  | | |
Db        685 GCAGTGGTGGCGGCGGCGGCGGAGGTGGTA 656


RESULT 10
US-10-505-928-651
; Sequence 651, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 651
;   LENGTH: 3597
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-651

  Query Match             36.7%;  Score 22;  DB 6;  Length 3597;
  Best Local Similarity   63.0%;  Pred. No. 19;
  Matches   34;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          4 CAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              ||||  | || ||||| || | | | || ||  | |  | ||  || || ||||
Db       2395 CAGTCCTTGCTGTGGCTGCTGCTGTGGAGACAGGTCCTCGCCCCCTACAACCCC 2448
```

JLT 11
10-511-937-2802
equence 2802, Application US/10511937
iblication No. US20060088836A1
ENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
ITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
ITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
ILE REFERENCE: 506612000104
URRENT APPLICATION NUMBER: US/10/511,937
URRENT FILING DATE: 2004-10-19
RIOR APPLICATION NUMBER: PCT/US2003/012946
RIOR FILING DATE: 2003-04-24
RIOR APPLICATION NUMBER: US 10/131,831
RIOR FILING DATE: 2002-04-24
RIOR APPLICATION NUMBER: US 10/325,899
RIOR FILING DATE: 2002-12-20
UMBER OF SEQ ID NOS: 3117
OFTWARE: PatentIn version 3.2
Q ID NO 2802
LENGTH: 3597
TYPE: DNA
ORGANISM: Homo sapiens
10-511-937-2802

iery Match 36.7%; Score 22; DB 6; Length 3597;
est Local Similarity 63.0%; Pred. No. 19;
atches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

```
          4 CAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
            ||||  | || ||||| || | | | || ||  | |  | ||  || || ||||
       2395 CAGTCCTTGCTGTGGCTGCTGCTGTGGAGACAGGTCCTCGCCCCCTACAACCCC 2448
```

JLT 12
10-539-402-66
equence 66, Application US/10539402
iblication No. US20060115477A1
ENERAL INFORMATION:
APPLICANT: Xerion Pharmaceuticals AG
APPLICANT: Tufts University
ITLE OF INVENTION: Neuropilin-1 Inhibitor
ILE REFERENCE: XE12EPC
URRENT APPLICATION NUMBER: US/10/539,402
URRENT FILING DATE: 2005-06-17
RIOR APPLICATION NUMBER: US 60/435,893
RIOR FILING DATE: 2002-12-20
RIOR APPLICATION NUMBER: EP 03000615
RIOR FILING DATE: 2003-01-15
UMBER OF SEQ ID NOS: 108
OFTWARE: PatentIn version 3.1
Q ID NO 66
LENGTH: 733
TYPE: DNA
ORGANISM: human
10-539-402-66

iery Match 36.3%; Score 21.8; DB 6; Length 733;
est Local Similarity 61.4%; Pred. No. 15;
atches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
            | |  ||||  |||| || ||||||||     | |  |   ||||   |||| ||| |
        374 CGGAGGTGGCAGCGGCGGTGGCGGATCGGACATCCAGATGACCCAGTCTCCTTCCAC 430
```

RESULT 13
US-10-539-402-44
; Sequence 44, Application US/10539402
; Publication No. US20060115477A1
; GENERAL INFORMATION:
; APPLICANT: Xerion Pharmaceuticals AG
; APPLICANT: Tufts University
; TITLE OF INVENTION: Neuropilin-1 Inhibitor
; FILE REFERENCE: XE12EPC
; CURRENT APPLICATION NUMBER: US/10/539,402
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 60/435,893
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: EP 03000615
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 740
; TYPE: DNA
; ORGANISM: human
US-10-539-402-44

Query Match 36.3%; Score 21.8; DB 6; Length 740;
Best Local Similarity 61.4%; Pred. No. 15;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              | |  ||||  |||| || ||||||||     | |  |   ||||   |||| ||| |
Db        381 CGGAGGTGGCAGCGGCGGTGGCGGATCGGACATCCAGATGACCCAGTCTCCTTCCAC 437
```

RESULT 14
US-11-154-103-36
; Sequence 36, Application US/11154103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-36

Query Match 36.3%; Score 21.8; DB 7; Length 873;
Best Local Similarity 61.4%; Pred. No. 16;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              | |  ||||    || || ||||||||   ||   |||  || |   |||||||| |
Db        453 CGGAGGTGGCTCTGGCGGTGGCGGATCGGAAATTGTGCTGACTCAGTCTCCATCCTC 509
```

RESULT 15
US-10-953-349-31650/c
; Sequence 31650, Application US/10953349
; Publication No. US20060107345A1

NERAL INFORMATION:
PPLICANT: ALEXANDROV, Nickolai et al.
ITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
ITLE OF INVENTION: ENCONDED THERBY
ILE REFERENCE: 2750-1579PUS2
URRENT APPLICATION NUMBER: US/10/953,349
URRENT FILING DATE: 2004-09-30
UMBER OF SEQ ID NOS: 40252
OFTWARE: PatentIn version 3.3
Q ID NO 31650
LENGTH: 1349
TYPE: DNA
ORGANISM: Triticum aestivum
0-953-349-31650

ery Match 36.3%; Score 21.8; DB 6; Length 1349;
st Local Similarity 61.4%; Pred. No. 18;
tches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
        3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGG 59
          ||||| ||||  || | |||||| |  |       |||| | ||  ||||  || | |
      352 GCAGTCGTGGAAGTAGAGGCGGAGCATGCCCGCCGCCACCGCCACCTCCTGCCGCAG 296
```

ch completed: June 10, 2006, 18:19:00
time : 2.04011 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

on: June 10, 2006, 00:20:47 ; Search time 4020.2 Seconds
(without alignments)
6843.525 Million cell updates/sec

le: US-10-821-670A-56
fect score: 1757
uence: 1 MHPQQLVIAWFSLVLLAPPL.....VQARDRYYSSSWSNWASVSC 328

ring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

rched: 48236798 seqs, 27959665780 residues

al number of hits satisfying chosen parameters: 96473596

imum DB seq length: 0
imum DB seq length: 2000000000

:-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

nand line parameters:
DEL=frame+_p2n.model -DEV=xlp
/abss/ABSSWEB_spool/US10821670/runat_07062006_110104_26172/app_query.fasta_1
=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
ITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
CALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
TFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
ER=US10821670_@CGN_1_1_27300_@runat_07062006_110104_26172 -NCPU=6 -ICPU=3
MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
N_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
APOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

abase : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt No.	Score	% Query Match	Length	DB	ID	Description
1	1176.5	67.0	1839	6	AK162981	AK162981 Mus muscu
2	1163.5	66.2	2908	6	AK155593	AK155593 Mus muscu
3	1111.5	63.3	735	5	CD559605	CD559605 AGENCOURT
4	1111.5	63.3	756	5	CK130264	CK130264 AGENCOURT
5	1098.5	62.5	747	5	CD559607	CD559607 AGENCOURT
6	1084	61.7	772	5	CD559604	CD559604 AGENCOURT
7	981.5	55.9	745	5	CD559602	CD559602 AGENCOURT
c 8	961	54.7	785	5	CD559448	CD559448 AGENCOURT
c 9	959.5	54.6	736	5	CD559453	CD559453 AGENCOURT
c 10	956.5	54.4	772	5	CD559450	CD559450 AGENCOURT
c 11	951.5	54.2	762	5	CD559451	CD559451 AGENCOURT
c 12	902.5	51.4	766	5	CD559449	CD559449 AGENCOURT
c 13	894.5	50.9	754	5	CD559452	CD559452 AGENCOURT
c 14	820	46.7	725	5	CD559454	CD559454 AGENCOURT
15	781	44.5	724	5	CD559603	CD559603 AGENCOURT
16	776.5	44.2	1042	5	CD559606	CD559606 AGENCOURT
17	759.5	43.2	649	5	CJ134671	CJ134671 CJ134671
18	580.5	33.0	475	7	BF704417	BF704417 MI-P-E6-a
19	506.5	28.8	417	8	CO949904	CO949904 UMC-pd12c
20	461	26.2	387	4	BY167742	BY167742 BY167742
21	452	25.7	432	4	BY154173	BY154173 BY154173
22	425	24.2	423	4	BY218447	BY218447 BY218447
23	412	23.4	375	4	BY222535	BY222535 BY222535
24	406	23.1	346	4	BY164658	BY164658 BY164658
25	394	22.4	355	4	BY221814	BY221814 BY221814
26	378	21.5	535	11	AZ441303	AZ441303 1M0232M24
27	365	20.8	700	12	CE093997	CE093997 tigr-gss-
c 28	351	20.0	569	11	AZ853726	AZ853726 2M0157M01
29	346.5	19.7	252	10	DV799576	DV799576 est_t_tru
30	277	15.8	666	4	BY749553	BY749553 BY749553
c 31	229.5	13.1	812	10	DT349218	DT349218 JGI_CAAX1
32	192.5	11.0	755	10	DV591060	DV591060 AGENCOURT
33	191.5	10.9	748	10	DV593962	DV593962 AGENCOURT
34	189	10.8	705	8	CX261472	CX261472 1314997 N
35	184	10.5	1277	14	DQ037702	DQ037702 Homo sapi
36	182.5	10.4	2548	6	AK046337	AK046337 Mus muscu
37	182	10.4	1277	14	DQ037703	DQ037703 Pan trogl
38	181.5	10.3	1118	14	AY403646	AY403646 Mus muscu
39	181.5	10.3	1881	6	AK137026	AK137026 Mus muscu
40	180.5	10.3	2373	6	AK141197	AK141197 Mus muscu
41	180	10.2	850	3	BU291084	BU291084 603603708
42	177.5	10.1	709	4	CA344594	CA344594 675030 NC
c 43	177	10.1	665	4	CA062264	CA062264 ssalrgb52
c 44	177	10.1	689	10	DW558518	DW558518 EST_ssal_
45	176	10.0	1008	4	BX364435	BX364435 BX364435

ALIGNMENTS

RESULT 1
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

URNAL Genome Res. 10 (11), 1757-1771 (2000)

UBMED 11076861

RENCE 4

THORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

NSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TLE Functional annotation of a full-length mouse cDNA collection

URNAL Nature 409 (6821), 685-690 (2001)

UBMED 11217851

RENCE 5

THORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

NSRTM FANTOM Consortium

TLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

URNAL Nature 420 (6915), 563-573 (2002)

UBMED 12466851

RENCE 6

THORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

```
  source          1. .1839
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="FANTOM_DB:A430014H12"
                  /db_xref="taxon:10090"
                  /clone="A430014H12"
                  /tissue_type="thymus"
                  /clone_lib="RIKEN full-length enriched mouse cDNA library"
                  /dev_stage="0 day neonate"
  CDS             58. .1065
                  /note="unnamed protein product; interleukin 12b
                  (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%,
                  match=1816)
                  putative"
                  /codon_start=1
                  /protein_id="BAE37146.1"
                  /db_xref="GI:74188062"
                  /translation="MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGE
                  TVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHL
                  LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
                  DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
                  ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                  KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
                  S"
GIN

gnment Scores:
d. No.:                1.62e-120      Length:          1839
re:                    1176.50        Matches:         225
cent Similarity:       78.0%          Conservative:    37
: Local Similarity:    67.0%          Mismatches:      61
ry Match:              67.0%          Indels:          13
                       6              Gaps:            4

10-821-670A-56 (1-328) x AK162981 (1-1839)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            |||   ||||||:::|||   |||:::|||||||:::::|||||||||      ||||||
         58 ATGTGTCCTCAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTC 117

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||:::|||||||||||||||:::|||||||||||||||:::||||||   ||||||
        118 ATGGCCATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGAT 177

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||   |||   |||||||||:::|||||||||||||||||||||||||||
        178 GCCCCTGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 237

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||          |||:::|||||||||||||||||||||||||||||||
        238 ACCTCAGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAA 297

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||   |||||||||||||||||||||||||||||||||||||   ||||||||||||
        298 GAGTTTCTAGATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCA 357

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
               ||||||:::|||||||||||||:::|||||||||||||||:::||||||
        358 CATCTGCTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA--------- 408

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            |||       |||||||||   ||||||||||||||||||||   ||||||||||||||||||
        409 AAAAATTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTC 468

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||   ||||||          :::   ||||||||||||   :::||||||||||
        469 ACGTGCTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAGC 528

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
               |||   |||   :::   ||||||||||||   |||:::||||||||||||||||||
        529 AGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTC 588

        Qy      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                    :::|||   ||||||||:::||||||:::|||   |||||||||          |||
        Db      589 ACACTGGACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGC 648

        Qy      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                    |||   |||||||||:::|||||||||||:::   ::::::|||       :::   |||
        Db      649 CCAACTGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAA 708

        Qy      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
                    ||||||||||:::::|||||||||||||||||||||||||||||||||||||||||||
        Db      709 TATGAGAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAG 768

        Qy      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
                    |||||||||:::|||||||||||||||||||:::   ||||||||||||||||||||||
        Db      769 AACTTGCAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCT 825

        Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                    |||:::|||||||||||||||||||||||||||||||   |||   |||::::::|||
        Db      826 GACTCCTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGC 885

        Qy      281 LysAsnAsnArgGluLys----------------------LysAspArgLeuSerVal 292
                    |||       :::   |||                      |||          |||
        Db      886 AAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGTA 945

        Qy      293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
                    :::|||||||||   :::|||   |||   |||          :::   ||||||||:::
        Db      946 GAGAAGACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAG 1002

        Qy      313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
                    ||||||||||:::||||||   |||   ||||||   |||   |||
        Db     1003 GATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1050

RESULT 2
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
```

Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

NSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TLE Functional annotation of a full-length mouse cDNA collection

URNAL Nature 409 (6821), 685-690 (2001)

UBMED 11217851

RENCE 5

THORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

NSRTM FANTOM Consortium

TLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

URNAL Nature 420 (6915), 563-573 (2002)

UBMED 12466851

RENCE 6

THORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 2908)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2908
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:F730005O03"
/db_xref="taxon:10090"
/clone="F730005O03"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"

```
  misc_feature    1. .2908
                  /note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence:
                  BLASTN, 99%, match=1807)
                  putative"
GIN

gnment Scores:
d. No.:               9.28e-119      Length:        2908
re:                   1163.50        Matches:       225
cent Similarity:      77.7%          Conservative:  37
t Local Similarity:   66.8%          Mismatches:    61
ry Match:             66.2%          Indels:        14
                      6              Gaps:          4

10-821-670A-56 (1-328) x AK155593 (1-2908)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            |||   ||||||:::|||   |||:::||||||:::::|||||||||      ||||||
        461 ATGTGTCCTCAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTC 520

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||:::|||||||||||||||:::|||||||||||||||:::||||||   ||||||
        521 ATGGCCATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGAT 580

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||   |||   |||||||||:::|||||||||||||||||||||||||||
        581 GCCCCTGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 640

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||          |||:::|||||||||||||||||||||||   ||||||
        641 ACCTCAGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAA 700

         81 GluPheAlaAspAlaGlyGln-TyrThrCysHisLysGlyGlyGluValLeuSerHisSe 100
            ||||||   ||||||||||| ||||||||||||||||||||||   ||||||||||||
        701 GAGTTTCTAGATGCTGGCCAGCTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTC 760

        100 rPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGl 120
            |   ||||||:::|||||||||||||:::|||||||||||||||:::||||||
        761 ACATCTGCTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA-------- 812

        120 nLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPh 140
             |||       |||||||||   |||||||||||||||||||   ||||||||||||||||
        813 -AAAAATTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTT 871

        140 eThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerAr 160
            |||||||   ||||||          :::   ||||||||||||   :::||||||||||
        872 CACGTGCTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAG 931

        160 gGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVa 180
             |||   |||   :::   ||||||||||||   |||:::||||||||||||||||||
        932 CAGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGT 991

        180 lArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCy 200
            |   :::|||   |||||||||:::||||||:::|||   |||||||||         ||
        992 CACACTGGACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTG 1051

        200 sProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLy 220
            ||||   |||||||||:::||||||||||||:::   ::::::|||      :::   ||
       1052 CCCAACTGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAA 1111

        220 sTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLy 240
            ||||||||||||:::::|||||||||||||||||||||||||||||||||||||||||||
       1112 ATATGAGAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAA 1171

        240 sAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPr 260
            ||||||||||:::|||||||||||||||:::   |||||||||||||||||||||||||||
       1172 GAACTTGCAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCC 1228

        260 oAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGl 280
            ||||:::|||||||||||||||||||||||||||||   |||   |||::::::|||
       1229 TGACTCCTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCG 1288

        280 yLysAsnAsnArgGluLys----------------------LysAspArgLeuSerVa 292
```

```
                ||||      :::   |||                                |||             ||
Db       1289 CAAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGT 1348

Qy        292 lAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaAr 312
              |:::|||||||||   :::|||   |||   |||          :::   |||||||||::
Db       1349 AGAGAAGACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCA 1405

Qy        312 gAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
              :||||||||||||:::||||||   |||   ||||||   |||   |||
Db       1406 GGATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1454

RESULT 3
CD559605
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              8.37e-114      Length:        735
```

```
e:                  1111.50        Matches:       206
ent Similarity:     94.5%          Conservative:  18
 Local Similarity:  86.9%          Mismatches:    12
y Match:            63.3%          Indels:        1
                    5              Gaps:          1

0-821-670A-56 (1-328) x CD559605 (1-735)

        4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
          ||||||||||||||:::|||||||||||||||   ||||||   ||||||:::||||||
       26 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 85

       24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
          |||||||||:::|||:::|||||||||||||||||||||||||:::|||||||||||||||
       86 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 145

       44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
          ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
      146 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 205

       64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      206 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 265

       84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
          ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
      266 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 325

      104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
          :::||||||||||||||||||||||||||||||||||||||||||:::::|||||||||
      326 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 385

      124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
          |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||
      386 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 445

      144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
          |||||||||   ||||||||||||||||   |||:::|||||||||||||||||||||||
      446 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTCTTCT 505

      164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
          ||||||||||||||||||||||||||||||||||||||||||:::||||||   |||
      506 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 565

      184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
          |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
      566 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 622

      204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
          ||||||||||||||||||||:::|||||||||:::|||||||||||||||||||||||||
      623 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 682

      224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      683 TACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 733


LT 4
0264
S       CK130264                 756 bp    mRNA    linear   EST 02-DEC-2003
NITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
        IMAGE:6971871 5', mRNA sequence.
SSION   CK130264
ION     CK130264.1  GI:38622200
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 756)
THORS   NIH-MGC http://mgc.nci.nih.gov/.
TLE     National Institutes of Health, Mammalian Gene Collection (MGC)
URNAL   Unpublished (1999)

COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES              Location/Qualifiers
     source           1. .756
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971871"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              8.73e-114      Length:        756
Score:                  1111.50        Matches:       206
Percent Similarity:     94.1%          Conservative:  18
Best Local Similarity:  86.6%          Mismatches:    13
Query Match:            63.3%          Indels:        1
DB:                     5              Gaps:          1

US-10-821-670A-56 (1-328) x CK130264 (1-756)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              ||||||||||||||:::|||||||||||||||   ||||||   ||||||:::||||||
Db         43 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 102

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||||||:::|||||||||||||||
Db        103 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 162

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        163 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 222

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 282

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        283 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 342
```

```
       104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
           :::|||||||||||||||||||||||||||||||||||||||||:::::|||||||||
       343 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 402

       124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
           |||||||||   |||||||:::|||||||||||||||||||||||||||||||||||||||
       403 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 462

       144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
           |||||||||   |||||||||||||||   |||:::|||||||||||||||||||||||
       463 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 522

       164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
           ||||||||||||||||||||||||||||||||||||||||||:::||||||   |||
       523 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 582

       184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
           |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
       583 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 639

       204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
           ||||||||||||||||||||||:::|||||||||:::||||||||||||||||||||||
       640 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 699

       224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 241
           ||||||||||||||||||||||||||||||||   ||||||||||||||||||
       700 TACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAGAAC 753
```

```
ULT 5
59607
US        CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
INITION   AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
          IMAGE:6971868 5', mRNA sequence.
ESSION    CD559607
SION      CD559607.2  GI:38558941
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 747)
UTHORS    NIH-MGC http://mgc.nci.nih.gov/.
ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL    Unpublished (1999)
MENT      On Jun 10, 2003 this sequence version replaced gi:31585675.
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: g  column: 11
          High quality sequence start: 14
          High quality sequence stop: 671.
TURES               Location/Qualifiers
  source            1. .747
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971868"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
ORIGIN
```

```
Alignment Scores:
Pred. No.:              2.48e-112       Length:         747
Score:                  1098.50         Matches:        203
Percent Similarity:     93.7%           Conservative:   19
Best Local Similarity:  85.7%           Mismatches:     14
Query Match:            62.5%           Indels:         1
DB:                     5               Gaps:           1

US-10-821-670A-56 (1-328) x CD559607 (1-747)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              |||||||||||||||:::|||||||||||||||   ||||||   ||||||:::||||||
Db         38 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 97

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||||||:::||||||||||||||
Db         98 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 157

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              |||||||||||||||||||:::|||||||||||||||   ||||||||||   |||
Db        158 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 217

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 277

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        278 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 337

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
              :::|||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        338 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 397

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              |||||||||   |||||||:::|||||||||||||||||||||||||||||||||||||||
Db        398 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 457

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   |||||||||||||||   |||:::|||||||||||||||||||||||
Db        458 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 517

Qy        164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
              ||||||||||||||||||||||||||||||||||||||||||:::||||||   |||
Db        518 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 577

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db        578 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 634

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
              ||||||||||||||||||||||:::||||||   :::|||||||||:::|||||||||||
Db        635 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAAAAC 694

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              |||||||   ||||||||||||||||||||||||||||||||||||||||
Db        695 TACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAA 745
```

```
LT 6
9604
S       CD559604                 772 bp    mRNA    linear   EST 26-NOV-2003
NITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
        IMAGE:6971872 5', mRNA sequence.
SSION   CD559604
ION     CD559604.2  GI:38558934
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 772)
THORS   NIH-MGC http://mgc.nci.nih.gov/.
TLE     National Institutes of Health, Mammalian Gene Collection (MGC)
URNAL   Unpublished (1999)
ENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
        Contact: Daniela S. Gerhard, Ph.D.
        Office of Cancer Genomics
        National Cancer Institute / NIH
        Bldg. 31 Rm10A07 Bethesda, MD 20892
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: Narayan Bhat
         cDNA Library Preparation: Bhat Laboratory
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Agencourt Bioscience Corporation
         Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: IRBK2  row: h  column: 03
        High quality sequence start: 13
        High quality sequence stop: 750.
URES            Location/Qualifiers
 source         1. .772
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6971872"
                /tissue_type="mixed"
                /lab_host="DH5A (T1 phage-resistant)"
                /clone_lib="NIH_MGC_195"
                /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                loxP-HindIII; Clones from this library have been
                PCR-amplified using gene-specific primers to contain the
                complete open reading frame (based on known gene sequences
                available from NCBI's RefSeq). Template for PCR is cDNA
                derived from either pooled cytoplasmic polyA RNA from 30
                cells lines or pooled total RNA from 10 different tissues
                (from BD Biosciences/Clontech and Washington University).
                PCR products are directionally cloned into the loxP sites
                of the pDNR-Dual vector. Library constructed by Dr.
                Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                Expression Laboratory, Research Technology Program, SAIC
                Frederick, NCI-Frederick, Frederick, MD 21702). For
                information on which gene each clone represents, please
                visit our anonymous ftp site at
                ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                a Note: this is a NIH_MGC Library."
IN

nment Scores:
. No.:              1.11e-110       Length:         772
e:                  1084.00         Matches:        204
ent Similarity:     93.7%           Conservative:   18
 Local Similarity:  86.1%           Mismatches:     14
y Match:            61.7%           Indels:         2
                    5               Gaps:           1

0-821-670A-56 (1-328) x CD559604 (1-772)

        4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23

                  ||||||||||||||:::|||||||||||||||   ||||||   ||||||:::||||||
Db       47 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 106

Qy       24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
            |||||||||:::|||:::|||||||||||||||||||||||:::|||||||||||||||
Db      107 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 166

Qy       44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
            ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db      167 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 226

Qy       64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      227 CAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 286

Qy       84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
            |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db      287 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 346

Qy      104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
            :::|||||||||||||||||||||||||||||||||||||||||:::::|||||||||||
Db      347 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 406

Qy      124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
            ||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||||
Db      407 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 466

Qy      144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
            ||||||||   ||||||||||||||   |||:::|||||||||||||||||||||||||||
Db      467 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 526

Qy      164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
            |||||||||||||||||||||||||||||||||||||||||:::||||||   |||
Db      527 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 586

Qy      184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
            |||:::::|||   :::|||:::||||||||||||||   ||||||||||||||||||||
Db      587 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 643

Qy      204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
            ||||||||||||||||||||:::||||||||:::||||||||||||||||||||||||||
Db      644 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 703

Qy      224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||   ||||||   ||||||
Db      704 TACACCAGCAGCTTCTTCATCAGGGACATCATCAA-CCTGACCAACCCAAA 753

RESULT 7
CD559602
LOCUS       CD559602                 745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 05
High quality sequence start: 2
High quality sequence stop: 644.

TURES Location/Qualifiers
source 1. .745
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971874"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

3IN

gnment Scores:

d. No.:	3.47e-99	Length:	745
re:	981.50	Matches:	189
cent Similarity:	90.2%	Conservative:	23
t Local Similarity:	80.4%	Mismatches:	20
ry Match:	55.9%	Indels:	4
	5	Gaps:	3

10-821-670A-56 (1-328) x CD559602 (1-745)

```
  4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
    ||||||||||||||:::|||||||||||||||    ||||||   ||||||:::||||||
 15 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 74

 24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
    |||||||||:::|||:::|||||||||||||||||||||:::|||||||||||||||||
 75 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 134

 44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
    ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
135 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 194

 64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
195 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 254

 84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
    ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
255 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 314

104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
    :::||||||||||||||||||||||||||||||||||||||||:::::|||||||||
315 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 374

124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
    |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||
375 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 434
```

```
Qy      144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
            |||||||||   ||||||||||||||   |||:::||||||||||||||||||||||
Db      435 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 494

Qy      164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
            ||||||||||||||||||||||||||||||||||||||||:::||||||   |||
Db      495 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 554

Qy      184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
            |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db      555 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 611

Qy      204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
            ||||||||||||||||||||||||:::||||||||||   |||||||||      :::
Db      612 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGT-CACAAGCTCATGTTGAAAATA 670

Qy      224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspPro 238
            :::          ||||||:::   :::   ::::::   ||||||
Db      671 CAC---CACGGCTTCTTTCTCTGAAAT---CTTCAATCTGACCCA 709
```

RESULT 8
CD559448/c
LOCUS CD559448 785 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971874 5', mRNA sequence.
ACCESSION CD559448
VERSION CD559448.2 GI:38453466
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585516.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 05
High quality sequence stop: 696.

FEATURES Location/Qualifiers
source 1. .785
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971874"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC

Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

IN

nment Scores:

. No.:	7.54e-97	Length:	785
e:	961.00	Matches:	186
ent Similarity:	89.9%	Conservative:	18
Local Similarity:	81.9%	Mismatches:	22
y Match:	54.7%	Indels:	3
	5	Gaps:	1

0-821-670A-56 (1-328) x CD559448 (1-785)

```
      102 LeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLys 121
          |||         :::|||||||||||||   ||||||||||   |||::::::||||||
      771 CTCTGCTGCTCACAAAAGGAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAA 714

      122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141
          |||   |||||||||   ||||||:::||||||||||||||||||||||||||||||||
      713 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 654

      142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 161
          ||||||||||||||   ||||||||||||||   |||:::||||||||||||||||||
      653 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 594

      162 SerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 181
          |||||||||||||||||||||||||||||||||||||||||||||||:::||||||
      593 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 534

      182 ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysPro 201
          ||||||:::::|||   :::|||:::||||||||||||||   ||||||||||||
      533 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 477

      202 AlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 221
          |||||||||||||||||||||||||||||:::||||||||:::|||||||||||||||
      476 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 417

      222 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      416 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 357

      242 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
          ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
      356 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 297

      262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
          ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
      296 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 237

      282 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 301
          :::   ||||||||||||||||:::      ||||||||||||||   |||:::|||
      236 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 177

      302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 321
          |||:::|||   |||   |||:::|||:::||||||||||||||||||||||||||||
      176 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 117

      322 AsnTrpAlaSerValSerCys 328
          ||||||||||||   |||
      116 GAATGGGCATCTGTGCCCTGC 96
```

LT 9
9453/c
S CD559453 736 bp mRNA linear EST 19-NOV-2003
NITION AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
SSION CD559453
ION CD559453.2 GI:38453475
ORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 736)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585521.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 683.
FEATURES Location/Qualifiers
source 1. .736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:

Pred. No.:	1.01e-96	Length:	736
Score:	959.50	Matches:	181
Percent Similarity:	91.2%	Conservative:	17
Best Local Similarity:	83.4%	Mismatches:	18
Query Match:	54.6%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-56 (1-328) x CD559453 (1-736)

```
Qy      112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
            ||||||||||||   |||::::::|||||||||   |||||||||   ||||||:::|||
Db      727 TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGATGC 669

Qy      132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
            |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db      668 GAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACTGAT 609

Qy      152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
            |||   |||:::|||||||||||||||||||||||||||||||||||||||||||||||
Db      608 TTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGA 549
```

```
       172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
           ||||||||||||||||||||||:::||||||   ||||||:::::::|||   :::|||:::
       548 GCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTACTCA 492

       192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
           ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
       491 GTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTC 432

       212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
           :::||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
       431 ATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGG 372

       232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       371 GACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 312

       252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       311 CAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCC 252

       272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
           |||||||||   ||||||||||||||||:::   ||||||||||||||||||:::
       251 CTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTC 192

       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
           ||||||||||||||||   |||:::|||   |||:::|||   |||   |||:::|||
       191 ACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGCGGGCC 132

       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
           :::||||||||||||||||||||||||||||   ||||||||||||   |||
       131 CAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGC 81

JLT 10
59450/c
JS       CD559450                 772 bp    mRNA    linear   EST 19-NOV-2003
INITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
         IMAGE:6971872 5', mRNA sequence.
ESSION   CD559450
SION     CD559450.2  GI:38453469
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 772)
THORS    NIH-MGC http://mgc.nci.nih.gov/.
ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
URNAL    Unpublished (1999)
MENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
         Contact: Daniela S. Gerhard, Ph.D.
         Office of Cancer Genomics
         National Cancer Institute / NIH
         Bldg. 31 Rm10A07 Bethesda, MD 20892
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Narayan Bhat
          cDNA Library Preparation: Bhat Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: IRBK2  row: h  column: 03
         High quality sequence start: 2
         High quality sequence stop: 753.
TURES              Location/Qualifiers
  source           1. .772
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:6971872"
                   /tissue_type="mixed"
                   /lab_host="DH5A (T1 phage-resistant)"
                   /clone_lib="NIH_MGC_195"
                   /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                   loxP-HindIII; Clones from this library have been
                   PCR-amplified using gene-specific primers to contain the
                   complete open reading frame (based on known gene sequences
                   available from NCBI's RefSeq). Template for PCR is cDNA
                   derived from either pooled cytoplasmic polyA RNA from 30
                   cells lines or pooled total RNA from 10 different tissues
                   (from BD Biosciences/Clontech and Washington University).
                   PCR products are directionally cloned into the loxP sites
                   of the pDNR-Dual vector. Library constructed by Dr.
                   Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                   Expression Laboratory, Research Technology Program, SAIC
                   Frederick, NCI-Frederick, Frederick, MD 21702). For
                   information on which gene each clone represents, please
                   visit our anonymous ftp site at
                   ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                   a Note: this is a NIH_MGC Library."
ORIGIN
```

Alignment Scores:

Pred. No.:	2.35e-96	Length:	772
Score:	956.50	Matches:	184
Percent Similarity:	90.6%	Conservative:	18
Best Local Similarity:	82.5%	Mismatches:	20
Query Match:	54.4%	Indels:	3
DB:	5	Gaps:	1

US-10-821-670A-56 (1-328) x CD559450 (1-772)

```
Qy       106 LysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsn 125
             :::|||||||||   |||   |||||||||   |||::::::|||||||||    ||||||
Db       768 CAAAAGGAAGATGA-ATTNGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAAT 711

Qy       126 LysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeu 145
             |||   |||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       710 AAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTG 651

Qy       146 ThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspPro 165
             |||   ||||||||||||||||   |||:::||||||||||||||||||||||||||||||
Db       650 ACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCC 591

Qy       166 GlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArg 185
             ||||||||||||||||||||||||||||||||||:::||||||   ||||||:::
Db       590 CAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAG 531

Qy       186 AspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGlu 205
             :::|||   :::|||:::||||||||||||||   ||||||||||||||||||||||||
Db       530 GAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAG 474

Qy       206 SerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThr 225
             ||||||||||||||||||:::||||||||:::||||||||||||||||||||||||||||
Db       473 AGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACC 414

Qy       226 SerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLys 245
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       413 AGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAG 354

Qy       246 ProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThr 265
             ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db       353 CCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACT 294

Qy       266 ProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGlu 285
             ||||||||||||||||||||||||||   ||||||||||||||||||:::   ||||||
Db       293 CCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAA 234

Qy       286 LysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAla 305
             ||||||||||:::      ||||||||||||||   |||:::|||   |||:::|||
Db       233 AAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCC 174

Qy       306 LysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSer 325
                |||   |||:::|||:::||||||||||||||||||||||||||   |||||||||
```

```
      173 AGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCT 114

      326 ValSerCys 328
          |||   |||
      113 GTGCCCTGC 105

LT 11
9451/c
S       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
NITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
        IMAGE:6971871 5', mRNA sequence.
SSION   CD559451
ION     CD559451.2  GI:38453471
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1  (bases 1 to 762)
THORS   NIH-MGC http://mgc.nci.nih.gov/.
TLE     National Institutes of Health, Mammalian Gene Collection (MGC)
URNAL   Unpublished (1999)
ENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
        Contact: Daniela S. Gerhard, Ph.D.
        Office of Cancer Genomics
        National Cancer Institute / NIH
        Bldg. 31 Rm10A07 Bethesda, MD 20892
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: Narayan Bhat
         cDNA Library Preparation: Bhat Laboratory
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Agencourt Bioscience Corporation
         Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: IRBK2  row: h  column: 02
        High quality sequence start: 38
        High quality sequence stop: 761.
URES            Location/Qualifiers
 source         1. .762
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6971871"
                /tissue_type="mixed"
                /lab_host="DH5A (T1 phage-resistant)"
                /clone_lib="NIH_MGC_195"
                /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                loxP-HindIII; Clones from this library have been
                PCR-amplified using gene-specific primers to contain the
                complete open reading frame (based on known gene sequences
                available from NCBI's RefSeq). Template for PCR is cDNA
                derived from either pooled cytoplasmic polyA RNA from 30
                cells lines or pooled total RNA from 10 different tissues
                (from BD Biosciences/Clontech and Washington University).
                PCR products are directionally cloned into the loxP sites
                of the pDNR-Dual vector. Library constructed by Dr.
                Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                Expression Laboratory, Research Technology Program, SAIC
                Frederick, NCI-Frederick, Frederick, MD 21702). For
                information on which gene each clone represents, please
                visit our anonymous ftp site at
                ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                a Note: this is a NIH_MGC Library."
IN

nment Scores:
. No.:              8.42e-96        Length:         762
e:                  951.50          Matches:        183
ent Similarity:     90.5%           Conservative:   17
 Local Similarity:  82.8%           Mismatches:     20
y Match:            54.2%           Indels:         3

DB:                     5           Gaps:           1

US-10-821-670A-56 (1-328) x CD559451 (1-762)

Qy        108 GluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIle 127
              |||||||||   ||||||||||||   |||::::::||||||||||   |||||||||
Db        759 GAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACC 702

Qy        128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 TCTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACA 642

Qy        148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGly 167
              ||||||||||||||   |||:::|||||||||||||||||||||||||||||||||||||
Db        641 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 582

Qy        168 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 187
              |||||||||||||||||||||||||||||||:::||||||   ||||||::::::|||
Db        581 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 522

Qy        188 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 207
                :::|||:::||||||||||||||   ||||||||||||||||||||||||||||||
Db        521 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 465

Qy        208 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 227
              ||||||||||:::||||||||:::||||||||||||||||||||||||||||||||||||
Db        464 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 405

Qy        228 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 345

Qy        248 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 267
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        344 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 285

Qy        268 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 287
              ||||||||||||||||||||   ||||||||||||||||:::   ||||||||||||
Db        284 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 225

Qy        288 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 307
              ||||||:::      ||||||||||||||   |||:::|||   |||:::|||   |||
Db        224 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 165

Qy        308 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 327
              |||:::|||:::|||||||||||||||||||||||||||   ||||||||||||
Db        164 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 105

Qy        328 Cys 328
              |||
Db        104 TGC 102

RESULT 12
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
```

```
        Bldg. 31 Rm10A07 Bethesda, MD 20892
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: Narayan Bhat
         cDNA Library Preparation: Bhat Laboratory
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Agencourt Bioscience Corporation
         Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: IRBK2  row: h  column: 04
        High quality sequence stop: 641.
TURES           Location/Qualifiers
  source        1. .766
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6971873"
                /tissue_type="mixed"
                /lab_host="DH5A (T1 phage-resistant)"
                /clone_lib="NIH_MGC_195"
                /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                loxP-HindIII; Clones from this library have been
                PCR-amplified using gene-specific primers to contain the
                complete open reading frame (based on known gene sequences
                available from NCBI's RefSeq). Template for PCR is cDNA
                derived from either pooled cytoplasmic polyA RNA from 30
                cells lines or pooled total RNA from 10 different tissues
                (from BD Biosciences/Clontech and Washington University).
                PCR products are directionally cloned into the loxP sites
                of the pDNR-Dual vector. Library constructed by Dr.
                Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                Expression Laboratory, Research Technology Program, SAIC
                Frederick, NCI-Frederick, Frederick, MD 21702). For
                information on which gene each clone represents, please
                visit our anonymous ftp site at
                ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                a Note: this is a NIH_MGC Library."
GIN

gnment Scores:
d. No.:                 2.72e-90        Length:         766
re:                     902.50          Matches:        168
cent Similarity:        91.0%           Conservative:   15
: Local Similarity:     83.6%           Mismatches:     17
ry Match:               51.4%           Indels:         1
                        5               Gaps:           1

10-821-670A-56 (1-328) x CD559449 (1-766)

       128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
           ||||||:::|||||||||||||    ||||||||||||||||    ||||||||||||
       693 TTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTCACCTGGTGGTGGCTGACGACA 634

       148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGly 167
           ||||||||||||||    |||:::|||||||||||||||||||||||||||||||||||
       633 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 574

       168 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 187
           ||||||||||||||||||||||||||||||:::||||||    ||||||::::::|||
       573 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 514

       188 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 207
             :::|||:::|||||||||||||||    ||||||||||||||||||||||||||||||
       513 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 457

       208 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 227
           ||||||||||:::|||||||||:::||||||||||||||||||||||||||||||||||
       456 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 397

       228 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 247
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       396 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 337

Qy         248 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 267
               ||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db         336 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 277

Qy         268 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 287
               ||||||||||||||||||||    ||||||||||||||||||:::   ||||||||||||
Db         276 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 217

Qy         288 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 307
               ||||||:::      ||||||||||||||||   |||:::|||   |||:::|||   |||
Db         216 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 157

Qy         308 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 327
               |||:::|||:::|||||||||||||||||||||||||||||||   ||||||||||||
Db         156 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 97

Qy         328 Cys 328
               |||
Db          96 TGC 94

RESULT 13
CD559452/c
LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
FEATURES            Location/Qualifiers
     source         1. .754
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971870"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
```

Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

IN

nment Scores:

. No.:	2.11e-89	Length:	754
e:	894.50	Matches:	171
ent Similarity:	86.2%	Conservative:	17
Local Similarity:	78.4%	Mismatches:	29
y Match:	50.9%	Indels:	2
	5	Gaps:	1

0-821-670A-56 (1-328) x CD559452 (1-754)

```
      111 IleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLys 130
          |||||||||   |||   |||::::::|||||||||   |||||||||   ||||||:::
      750 ATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGA 692

      131 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThr 150
          ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
      691 TGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACT 632

      151 AspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCys 170
          ||||||   |||:::|||||||||||||||||||      ||||||||||||||||||||
      631 GATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTTTTTTGACCCCCAAGGGGTGACGTGC 572

      171 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 190
          ||||||||||||||   ||||||:::||||||   ||||||::::::|||   :::|||
      571 GGAGCTGCTACACTCTTTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTAC 515

      191 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 210
          :::|||||||||||||||   ||||||||||||||   ||||||||||||||||||||||
      514 TCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGGTGAGGAGAGTTTGCCCATTGAG 455

      211 ValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 230
          |||:::|||||||||:::|||||||||||||||||||||||||||||||   |||||||||
      454 GTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCATC 395

      231 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      394 AGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCT 335

      251 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 270
                |||||||||||||||||||||||||||||||||||||||||||||||||   |||
      334 TGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTAATTT 275

      271 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeu 290
          ||||||||||||   |||||||||||||||||:::   |||||||||||||||||||:::
      274 TCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTT 215

      291 SerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGln 310
          .  |||||||||   |||   |||:::|||   |||:::|||   |||   |||:::
      214 TTCACGGACAAGACCTTAGCCACGGTCATTTGCCGCAAAAATGCCAGCATTAGCGTGCGG 155

      311 AlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
          |||:::|||||||||||||||||||   ||||||   ||||||   |||   |||
      154 GCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGC 101
```

LT 14
9454/c

```
S       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
NITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
        IMAGE:6971868 5', mRNA sequence.
SSION   CD559454
ION     CD559454.2  GI:38453478
ORDS    EST.
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 13
            High quality sequence stop: 573.
FEATURES              Location/Qualifiers
     source           1. .725
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971868"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN
```

Alignment Scores:

Pred. No.:	4.68e-81	Length:	725
Score:	820.00	Matches:	164
Percent Similarity:	86.1%	Conservative:	15
Best Local Similarity:	78.8%	Mismatches:	27
Query Match:	46.7%	Indels:	3
DB:	5	Gaps:	2

US-10-821-670A-56 (1-328) x CD559454 (1-725)

```
Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||   |||   |||:::|||   |||       ||||||   |||   |||   |||
Db        722 AAAGAACCAAAAATAAAGCTTTTT---AAGATGGGGGCCAAGAAGTATTTGGGAAGTTTC 666

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
                      ||||||   ||||||||||||      |||:::|||||||||||||||||
Db        665 CCTCGCTGTCGGCTGACGACAATCAGTACTGATTG-AACTTCAGTGTCAAAAGCAGCAGA 607

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        606 GGTTCCTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 547

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
```

```
          |||   ||||||::::::|||   :::|||:::|||||||||||||||   |||||||||
      546 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 490

      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
          ||||||||||||||||||||||||||||||||:::|||||||||:::||||||||||||
      489 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 430

      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      429 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 370

      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
          |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
      369 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 310

      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
          |||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
      309 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 250

      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
          |||:::   |||||||||||||||||:::      |||||||||||||||   |||:::
      249 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 190

      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
          |||   |||:::|||  |||   |||:::|||:::|||||||||||||||||||||||
      189 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 130

      321 SerAsnTrpAlaSerValSerCys 328
          |||   ||||||||||||   |||
      129 AGCGAATGGGCATCTGTGCCCTGC 106
```

```
ULT 15
59603
US       CD559603                 724 bp    mRNA    linear   EST 26-NOV-2003
INITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
         IMAGE:6971873 5', mRNA sequence.
ESSION   CD559603
SION     CD559603.2  GI:38558932
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 724)
UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL   Unpublished (1999)
MENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
         Contact: Daniela S. Gerhard, Ph.D.
         Office of Cancer Genomics
         National Cancer Institute / NIH
         Bldg. 31 Rm10A07 Bethesda, MD 20892
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Narayan Bhat
          cDNA Library Preparation: Bhat Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: IRBK2  row: h  column: 04
         High quality sequence stop: 525.
TURES                Location/Qualifiers
  source             1. .724
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
```

```
Alignment Scores:
Pred. No.:              1.13e-76        Length:         724
Score:                  781.00          Matches:        143
Percent Similarity:     93.9%           Conservative:   11
Best Local Similarity:  87.2%           Mismatches:     10
Query Match:            44.5%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-56 (1-328) x CD559603 (1-724)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              |||||||||||||||:::|||||||||||||||   ||||||   ||||||:::||||||
Db         23 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 82

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||||:::|||||||||||||||
Db         83 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 142

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        143 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 202

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 262

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        263 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 322

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
              :::|||||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        323 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 382

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              |||||||||   |||||||:::|||||||||||||||||||||||||||||||||||||
Db        383 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 442

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   ||||||||||||||   |||:::|||||||||||||||||||||||||
Db        443 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 502

Qy        164 AspProGlnGly 167
              ||||||||||||
Db        503 GACCCCCAAGGG 514

Search completed: June 10, 2006, 10:30:55
Job time : 4026.2 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 01:33:29 ; Search time 4488.09 Seconds
(without alignments)
4210.361 Million cell updates/sec

tle: US-10-821-670A-36
ffect score: 197
quence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 6366136 seqs, 31973710525 residues

d size: 1

al number of hits satisfying chosen parameters: 12722138

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110449_27523/app_query.fasta_1
B=GenEmbl -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rge -MINMATCH=0.1
OOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
RANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
LIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
AXLEN=2000000000 -HOST=abss08
SER=US10821670_@CGN_1_1_6646_@runat_07062006_110449_27523 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	197	100.0	591	2	AR595954	AR595954 Sequence
2	197	100.0	591	2	AR595955	AR595955 Sequence
3	197	100.0	666	2	AR595952	AR595952 Sequence
c 4	197	100.0	666	2	AR595953	AR595953 Sequence
5	197	100.0	669	14	FCIL12P35	Y07761 Felis catus
6	197	100.0	1533	2	AR595959	AR595959 Sequence
c 7	197	100.0	1533	2	AR595960	AR595960 Sequence
8	197	100.0	1599	2	AR595956	AR595956 Sequence
c 9	197	100.0	1599	2	AR595957	AR595957 Sequence
10	195	99.0	591	2	AR242439	AR242439 Sequence
11	195	99.0	591	2	AR280207	AR280207 Sequence
12	195	99.0	591	2	AR322422	AR322422 Sequence
13	195	99.0	689	2	AR242451	AR242451 Sequence
14	195	99.0	689	2	AR280219	AR280219 Sequence
15	195	99.0	689	2	AR322434	AR322434 Sequence
16	195	99.0	1441	2	AR242438	AR242438 Sequence
17	195	99.0	1441	2	AR280206	AR280206 Sequence
18	195	99.0	1441	2	AR322421	AR322421 Sequence
19	187	94.9	561	2	AR596007	AR596007 Sequence
c 20	187	94.9	561	2	AR596008	AR596008 Sequence
21	154	78.2	669	14	FCU83185	U83185 Felis catus
22	84	42.6	285	14	AF054605	AF054605 Felis cat
23	59	29.9	660	2	AX154615	AX154615 Sequence
24	59	29.9	660	2	AX154619	AX154619 Sequence
25	59	29.9	660	2	AX154620	AX154620 Sequence
26	56	28.4	660	2	AX154616	AX154616 Sequence
27	54	27.4	669	2	AX076201	AX076201 Sequence
28	54	27.4	669	2	AX076483	AX076483 Sequence
29	54	27.4	4201	2	AX076477	AX076477 Sequence
30	52	26.4	591	2	BD171284	BD171284 Novel can
31	52	26.4	591	2	AR595963	AR595963 Sequence
c 32	52	26.4	591	2	AR595964	AR595964 Sequence
33	52	26.4	666	2	AR595961	AR595961 Sequence
c 34	52	26.4	666	2	AR595962	AR595962 Sequence
35	52	26.4	669	2	AR151062	AR151062 Sequence
36	52	26.4	669	2	AR151072	AR151072 Sequence
37	52	26.4	669	2	BD014654	BD014654 Process f
38	52	26.4	669	2	BD014664	BD014664 Process f
39	52	26.4	669	2	E15018	E15018 Canine mRNA
40	52	26.4	669	2	AR316461	AR316461 Sequence
41	52	26.4	669	2	AR316471	AR316471 Sequence
42	52	26.4	1282	2	BD171283	BD171283 Novel can
43	52	26.4	1455	2	AR596009	AR596009 Sequence
c 44	52	26.4	1455	2	AR596010	AR596010 Sequence
45	52	26.4	1533	2	AR595973	AR595973 Sequence
c 46	52	26.4	1533	2	AR595974	AR595974 Sequence
47	52	26.4	1599	2	AR595971	AR595971 Sequence
c 48	52	26.4	1599	2	AR595972	AR595972 Sequence
49	50	25.4	669	14	CFU49085	U49085 Canis famil
50	43	21.8	666	2	AX154613	AX154613 Sequence
51	42	21.3	618	14	AY603407	AY603407 Capra hir
52	42	21.3	666	14	AF173557	AF173557 Ovis arie
53	42	21.3	666	14	AY232819	AY232819 Bubalus b
54	42	21.3	690	14	AB246272	AB246272 Bubalus c
55	42	21.3	690	14	AB246352	AB246352 Bubalus b
56	42	21.3	690	14	AB246359	AB246359 Bubalus b
57	42	21.3	690	14	AF003542	AF003542 Capra hir
58	42	21.3	690	14	BTU14416	U14416 Bos taurus
59	40	20.3	666	14	CEU57751	U57751 Cervus elap
60	40	20.3	669	14	AB107653	AB107653 Lama glam
61	40	20.3	669	14	AB246672	AB246672 Camelus b
62	40	20.3	703	2	E35793	E35793 Process for
63	39	19.8	657	8	AY191828	AY191828 Synthetic
64	39	19.8	660	2	AX154614	AX154614 Sequence
65	39	19.8	660	2	AX154617	AX154617 Sequence
66	39	19.8	660	2	AX154621	AX154621 Sequence
67	37	18.8	660	2	AX154618	AX154618 Sequence
68	34	17.3	1426	14	PIGIL12PSU	L35765 Sus scrofa
69	31	15.7	666	2	AX154612	AX154612 Sequence
70	30	15.2	669	14	ECIL12P35	Y11130 Equus cabal
71	30	15.2	1626	8	AF401989	AF401989 Synthetic
72	29	14.7	660	2	AR008951	AR008951 Sequence
73	29	14.7	660	2	BD007071	BD007071 IL-12 gen
74	29	14.7	660	2	BD007079	BD007079 Gene expr
75	29	14.7	660	2	BD007080	BD007080 Gene expr

76	29	14.7	660	2	BD007081	BD007081 Gene expr
77	29	14.7	660	2	BD136037	BD136037 Interfero
78	29	14.7	660	2	BD136038	BD136038 Interfero
79	29	14.7	660	2	BD136039	BD136039 Interfero
80	29	14.7	660	2	I28592	I28592 Sequence 3
81	29	14.7	660	2	AX154634	AX154634 Sequence
82	29	14.7	702	2	CQ829447	CQ829447 Sequence
83	29	14.7	721	2	AR052862	AR052862 Sequence
84	29	14.7	721	2	AR288174	AR288174 Sequence
85	29	14.7	721	2	AR567161	AR567161 Sequence
86	29	14.7	762	2	BD105971	BD105971 Animal mo
87	29	14.7	762	2	CQ803343	CQ803343 Sequence
88	29	14.7	762	2	AR533401	AR533401 Sequence
89	29	14.7	762	5	AF101062	AF101062 Homo sapi
90	29	14.7	780	5	MMU19842	U19842 Macaca mula
91	29	14.7	823	5	AF180562	AF180562 Homo sapi
92	29	14.7	856	2	BD165801	BD165801 Antibody
93	29	14.7	1020	2	CQ716168	CQ716168 Sequence
94	29	14.7	1021	5	BC104982	BC104982 Homo sapi
95	29	14.7	1021	5	BC104984	BC104984 Homo sapi
96	29	14.7	1026	2	AR091390	AR091390 Sequence
97	29	14.7	1026	2	AR380496	AR380496 Sequence
98	29	14.7	1026	5	HUMCLMF35	M65271 Human cytot
99	29	14.7	1287	2	AR393790	AR393790 Sequence
100	29	14.7	1287	2	AX084108	AX084108 Sequence
101	29	14.7	1316	2	AR050785	AR050785 Sequence
102	29	14.7	1316	2	AR212036	AR212036 Sequence
103	29	14.7	1316	5	HUMNKSFP35	M65291 Human natur
104	29	14.7	1364	2	AR082685	AR082685 Sequence
105	29	14.7	1364	2	AR122961	AR122961 Sequence
106	29	14.7	1364	2	I28326	I28326 Sequence 3
107	29	14.7	1364	2	I89771	I89771 Sequence 3
108	29	14.7	1395	2	AR309637	AR309637 Sequence
109	29	14.7	1444	2	CS032085	CS032085 Sequence
110	29	14.7	1444	2	CS041037	CS041037 Sequence
111	29	14.7	1444	2	CS143811	CS143811 Sequence
112	29	14.7	1560	2	AR091395	AR091395 Sequence
113	29	14.7	1623	2	AR091394	AR091394 Sequence
114	29	14.7	1645	2	A92078	A92078 Sequence 2
115	29	14.7	1645	2	AR230689	AR230689 Sequence
116	29	14.7	3205	2	CS131489	CS131489 Sequence
117	29	14.7	5686	2	BD136048	BD136048 Interfero
118	29	14.7	6139	2	AR091393	AR091393 Sequence
119	29	14.7	11792	5	AF404773	AF404773 Homo sapi
120	29	14.7	157079	5	AC010370	AC010370 Homo sapi
121	29	14.7	176108	5	AC026118	AC026118 Homo sapi
122	29	14.7	300140	12	AC129109	AC129109 Homo sapi
123	27	13.7	785	5	AY234219	AY234219 Papio anu
124	27	13.7	786	5	CTU19835	U19835 Cercocebus
125	26	13.2	79	2	AR242449	AR242449 Sequence
126	26	13.2	79	2	AR280217	AR280217 Sequence
127	26	13.2	79	2	AR322432	AR322432 Sequence
128	26	13.2	817	14	AY686642	AY686642 Equus cab
129	23	11.7	71	2	AX076207	AX076207 Sequence
130	21	10.7	711	14	BTA271034	AJ271034 Bos tauru
131	21	10.7	714	14	OAR271035	AJ271035 Ovis arie
132	18	9.1	76	2	AX076205	AX076205 Sequence
133	18	9.1	76	2	AX076208	AX076208 Sequence
134	16	8.1	666	6	AB025723	AB025723 Cavia por
135	15	7.6	827	6	AF421396	AF421396 Sigmodon
136	14	7.1	559	7	BV429425	BV429425 S237P6482
137	14	7.1	1239	6	AB085791	AB085791 Mesocrice
138	13	6.6	60	2	CQ542775	CQ542775 Sequence
139	13	6.6	660	2	BD136054	BD136054 Interfero
140	12	6.1	36	2	AR242450	AR242450 Sequence
141	12	6.1	36	2	AR280218	AR280218 Sequence
142	12	6.1	36	2	AR322433	AR322433 Sequence
143	12	6.1	144	14	AY388980S3	AY388982 Sus scrof
144	12	6.1	1119	6	AF288849	AF288849 Meriones
145	11	5.6	39	2	AR595997	AR595997 Sequence
146	11	5.6	672	6	AF288520	AF288520 Marmota m
147	11	5.6	672	6	MMIL12P35	X97018 M.monax mRN
148	10	5.1	60	2	AR595989	AR595989 Sequence
c 149	10	5.1	60	2	AR595990	AR595990 Sequence
150	10	5.1	146	14	AY575615	AY575615 Ovis arie
151	10	5.1	146	14	AY575616	AY575616 Ovis arie
c 152	10	5.1	322	7	BV094414	BV094414 RPAMMSEQ0
c 153	10	5.1	483	7	BV300932	BV300932 S239P60FH
154	10	5.1	582	2	AR393785	AR393785 Sequence
155	10	5.1	582	2	AX084103	AX084103 Sequence
156	10	5.1	660	2	E26662	E26662 Improved me
157	10	5.1	700	6	S82412S4	S82418 interleukin
158	10	5.1	713	2	AR069652	AR069652 Sequence
159	10	5.1	713	6	AF128212	AF128212 Mus muscu
160	10	5.1	713	6	AF128213	AF128213 Mus muscu
161	10	5.1	786	6	AF128210	AF128210 Mus muscu
162	10	5.1	786	6	AF128211	AF128211 Mus muscu
163	10	5.1	793	6	AF177031	AF177031 Rattus no
164	10	5.1	1265	6	MUSIL35A	M86672 Mus musculu
165	10	5.1	1278	2	AR393789	AR393789 Sequence
166	10	5.1	1278	2	AX084107	AX084107 Sequence
167	10	5.1	1569	2	AR393796	AR393796 Sequence
168	10	5.1	1569	2	AX084114	AX084114 Sequence
169	10	5.1	1669	8	AF411293	AF411293 Synthetic
170	10	5.1	2013	2	AR393795	AR393795 Sequence
171	10	5.1	2013	2	AX084113	AX084113 Sequence
172	10	5.1	2438	2	CQ812173	CQ812173 Sequence
173	10	5.1	2709	2	AR393797	AR393797 Sequence
174	10	5.1	2709	2	AX084115	AX084115 Sequence
175	10	5.1	5252	2	CQ803341	CQ803341 Sequence
176	10	5.1	5966	2	BD136050	BD136050 Interfero
177	10	5.1	9049	2	CQ803350	CQ803350 Sequence
178	10	5.1	10633	2	CQ803349	CQ803349 Sequence
179	10	5.1	11746	2	CQ803348	CQ803348 Sequence
180	10	5.1	38246	2	CQ803351	CQ803351 Sequence
c 181	10	5.1	195059	6	AC121306	AC121306 Mus muscu
c 182	10	5.1	215198	6	AC113180	AC113180 Mus muscu
c 183	10	5.1	223879	12	AC111877	AC111877 Rattus no
c 184	10	5.1	256720	6	AC110241	AC110241 Mus muscu
c 185	9	4.6	51	2	AR596002	AR596002 Sequence
c 186	9	4.6	190	5	HUMEL10	M17273 Human elast
187	9	4.6	282	2	AX308844	AX308844 Sequence
188	9	4.6	572	7	BV408849	BV408849 S229P6135
189	9	4.6	1200	6	S82412S5	S82419 interleukin
c 190	9	4.6	1493	2	BD123597	BD123597 Secretory
c 191	9	4.6	1493	2	CS051325	CS051325 Sequence
c 192	9	4.6	1493	2	AX136289	AX136289 Sequence
c 193	9	4.6	1493	5	AK075494	AK075494 Homo sapi
c 194	9	4.6	1517	2	CQ716782	CQ716782 Sequence
c 195	9	4.6	1641	15	DQ302585	DQ302585 Listeria
c 196	9	4.6	1686	5	HUMELASTIN	M24782 Homo sapien
c 197	9	4.6	2210	2	AR152248	AR152248 Sequence
c 198	9	4.6	2241	5	HSELASRNA	X52896 H.sapiens R
c 199	9	4.6	2242	2	I91887	I91887 Sequence 37
c 200	9	4.6	2242	2	AX333060	AX333060 Sequence

ALIGNMENTS

```
RESULT 1
AR595954
LOCUS       AR595954                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 35 from patent US 6818444.
ACCESSION   AR595954
VERSION     AR595954.1  GI:56646935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 35 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
```

```
                /organism="unknown"
                /mol_type="genomic DNA"
:GIN

:gnment Scores:
ed. No.:              2e-198          Length:         591
ore:                  197.00          Matches:        197
:cent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            100.0%          Indels:         0
                      2               Gaps:           0

-10-821-670A-36 (1-197) x AR595954 (1-591)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

SULT 2
595955/c
CUS       AR595955                591 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 37 from patent US 6818444.
CESSION   AR595955
RSION     AR595955.1  GI:56646936
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 591)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 37 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES              Location/Qualifiers
   source           1. .591
                    /organism="unknown"
                    /mol_type="genomic DNA"
```

```
ORIGIN

Alignment Scores:
Pred. No.:              2e-198          Length:         591
Score:                  197.00          Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x AR595955 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 3
AR595952
LOCUS       AR595952                666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 32 from patent US 6818444.
ACCESSION   AR595952
VERSION     AR595952.1  GI:56646933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 32 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .666
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN
```

```
ignment Scores:
ed. No.:              2.21e-198      Length:        666
ore:                  197.00         Matches:       197
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            100.0%         Indels:        0
:                     2              Gaps:          0

-10-821-670A-36 (1-197) x AR595952 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

ULT 4
95953/c
US        AR595953                 666 bp    DNA     linear   PAT 15-DEC-2004
INITION   Sequence 34 from patent US 6818444.
CESSION   AR595953
RSION     AR595953.1  GI:56646934
WORDS     .
URCE      Unknown.
RGANISM   Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 666)
UTHORS    Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL    Patent: US 6818444-A 34 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
   source          1. .666
                   /organism="unknown"
                   /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:              2.21e-198      Length:        666

Score:                197.00         Matches:       197
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          100.0%         Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-36 (1-197) x AR595953 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 5
FCIL12P35
LOCUS       FCIL12P35                669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .669
```

```
                /organism="Felis catus"
                /mol_type="mRNA"
                /db_xref="taxon:9685"
                /cell_type="lymphocyte"
                /tissue_type="peripheral blood"
     gene       1. .669
                /gene="IL-12.p35"
     CDS        1. .669
                /gene="IL-12.p35"
                /function="heterodimer with IL-12 p40 chain"
                /codon_start=1
                /product="interleukin-12 p35 chain"
                /protein_id="CAA69067.1"
                /db_xref="GI:2102663"
                /db_xref="GOA:O02743"
                /db_xref="InterPro:IPR004281"
                /db_xref="InterPro:IPR009079"
                /db_xref="UniProtKB/Swiss-Prot:O02743"
                /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                LNAS"
:GIN

:gnment Scores:
ed. No.:                2.22e-198       Length:         669
ore:                    197.00          Matches:        197
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              100.0%          Indels:         0
                        14              Gaps:           0

-10-821-670A-36 (1-197) x FCIL12P35 (1-669)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 6
AR595959
LOCUS       AR595959               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.41e-198       Length:         1533
Score:                  197.00          Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x AR595959 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

```
SULT 7
595960/c
CUS       AR595960                1533 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 45 from patent US 6818444.
CESSION   AR595960
RSION     AR595960.1  GI:56646941
YWORDS    .
URCE      Unknown.
RGANISM   Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1533)
UTHORS    Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL    Patent: US 6818444-A 45 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES              Location/Qualifiers
   source           1. .1533
                    /organism="unknown"
                    /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:              4.41e-198      Length:         1533
ore:                  197.00         Matches:        197
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            100.0%         Indels:         0
:                     2              Gaps:           0

-10-821-670A-36 (1-197) x AR595960 (1-1533)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

SULT 8
595956
```

```
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.56e-198      Length:         1599
Score:                  197.00         Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR595956 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 9
AR595957/c
LOCUS       AR595957                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
```

```
CESSION   AR595957
RSION     AR595957.1  GI:56646938
WORDS     .
URCE      Unknown.
RGANISM   Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1599)
UTHORS    Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL    Patent: US 6818444-A 40 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
   source          1. .1599
                   /organism="unknown"
                   /mol_type="genomic DNA"
IGIN

lignment Scores:
ed. No.:              4.56e-198      Length:         1599
ore:                  197.00         Matches:        197
ercent Similarity:    100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            100.0%         Indels:         0
                      2              Gaps:           0

-10-821-670A-36 (1-197) x AR595957 (1-1599)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

SULT 10
242439
CUS       AR242439                591 bp    mRNA    linear   PAT 20-DEC-2002
FINITION  Sequence 9 from patent US 6472509.
CESSION   AR242439
RSION     AR242439.1  GI:27288856
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.61e-196      Length:         591
Score:                  195.00         Matches:        195
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.0%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR242439 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

RESULT 11
AR280207
LOCUS       AR280207                591 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6518045.
ACCESSION   AR280207
VERSION     AR280207.1  GI:29715597
```

```
WORDS    .
URCE     Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 591)
UTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE     Feline cytokine protein
OURNAL   Patent: US 6518045-A 9 11-FEB-2003;
         Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
         Kumamoto-ken;
         EPX;
TURES             Location/Qualifiers
   source         1. .591
                  /organism="unknown"
                  /mol_type="mRNA"
IGIN

gnment Scores:
d. No.:              2.61e-196      Length:         591
re:                  195.00         Matches:        195
cent Similarity:     100.0%         Conservative:   0
t Local Similarity:  100.0%         Mismatches:     0
ry Match:            99.0%          Indels:         0
                     2              Gaps:           0

10-821-670A-36 (1-197) x AR280207 (1-591)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

ULT 12
22422
US       AR322422                 591 bp    mRNA    linear   PAT 17-AUG-2003
INITION  Sequence 9 from patent US 6566097.
CESSION  AR322422
RSION    AR322422.1  GI:33708175
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.61e-196      Length:         591
Score:                  195.00         Matches:        195
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.0%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR322422 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

RESULT 13
AR242451
LOCUS       AR242451                 689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
```

```
WORDS    .
URCE     Unknown.
ORGANISM Unknown.
         Unclassified.
FERENCE  1  (bases 1 to 689)
AUTHORS  Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE     Feline cytokine protein
JOURNAL  Patent: US 6472509-A 26 29-OCT-2002;
         Juridical Foundation: The Chemo-Seso-Therapeutic Research
         Institute; Kumamoto;
         EPX;
ATURES             Location/Qualifiers
   source          1. .689
                   /organism="unknown"
                   /mol_type="mRNA"
IGIN

ignment Scores:
ed. No.:               2.96e-196      Length:         689
ore:                   195.00         Matches:        195
cent Similarity:       100.0%         Conservative:   0
st Local Similarity:   100.0%         Mismatches:     0
ery Match:             99.0%          Indels:         0
                       2              Gaps:           0

-10-821-670A-36 (1-197) x AR242451 (1-689)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

SULT 14
230219
CUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
FINITION  Sequence 26 from patent US 6518045.
CESSION   AR280219
RSION     AR280219.1  GI:29715609
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:             2.96e-196      Length:         689
Score:                 195.00         Matches:        195
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           99.0%          Indels:         0
DB:                    2              Gaps:           0

US-10-821-670A-36 (1-197) x AR280219 (1-689)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

RESULT 15
AR322434
LOCUS       AR322434                689 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 26 from patent US 6566097.
ACCESSION   AR322434
VERSION     AR322434.1  GI:33708187
```

```
;WORDS    .
IRCE      Unknown.
RGANISM   Unknown.
          Unclassified.
ERENCE    1  (bases 1 to 689)
UTHORS    Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE      Feline cytokine protein
OURNAL    Patent: US 6566097-A 26 20-MAY-2003;
          Juridical Foundation The Chemo-Sero-Therapeutic Research
          Institute;;
          EPX;
ATURES              Location/Qualifiers
   source           1. .689
                    /organism="unknown"
                    /mol_type="mRNA"
IGIN

gnment Scores:
ed. No.:              2.96e-196      Length:         689
re:                   195.00         Matches:        195
cent Similarity:      100.0%         Conservative:   0
t Local Similarity:   100.0%         Mismatches:     0
ry Match:             99.0%          Indels:         0
                      2              Gaps:           0

10-821-670A-36 (1-197) x AR322434 (1-689)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

SULT 16
242438
CUS       AR242438               1441 bp    mRNA    linear   PAT 20-DEC-2002
FINITION  Sequence 8 from patent US 6472509.
CESSION   AR242438
RSION     AR242438.1  GI:27288855
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES              Location/Qualifiers
     source           1. .1441
                      /organism="unknown"
                      /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.46e-196      Length:         1441
Score:                  195.00         Matches:        195
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.0%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR242438 (1-1441)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

RESULT 17
AR280206
LOCUS       AR280206               1441 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518045.
ACCESSION   AR280206
VERSION     AR280206.1  GI:29715596
```

```
:WORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1441)
UTHORS    Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE      Feline cytokine protein
OURNAL    Patent: US 6518045-A 8 11-FEB-2003;
          Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
          Kumamoto-ken;
          EPX;
ATURES             Location/Qualifiers
   source          1. .1441
                   /organism="unknown"
                   /mol_type="mRNA"
IGIN

lignment Scores:
ed. No.:              5.46e-196      Length:          1441
ore:                  195.00         Matches:         195
cent Similarity:      100.0%         Conservative:    0
st Local Similarity:  100.0%         Mismatches:      0
ery Match:            99.0%          Indels:          0
                      2              Gaps:            0

-10-821-670A-36 (1-197) x AR280206 (1-1441)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

SULT 18
322421
CUS       AR322421              1441 bp    mRNA    linear   PAT 17-AUG-2003
FINITION  Sequence 8 from patent US 6566097.
CESSION   AR322421
RSION     AR322421.1  GI:33708174
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 8 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.46e-196      Length:          1441
Score:                  195.00         Matches:         195
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            99.0%          Indels:          0
DB:                     2              Gaps:            0

US-10-821-670A-36 (1-197) x AR322421 (1-1441)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

RESULT 19
AR596007
LOCUS       AR596007               561 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 101 from patent US 6818444.
ACCESSION   AR596007
VERSION     AR596007.1  GI:56646988
```

```
WORDS    .
URCE     Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 561)
UTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
OURNAL   Patent: US 6818444-A 101 16-NOV-2004;
         Heska Corporation; Fort Collins, CO
TURES             Location/Qualifiers
   source         1. .561
                  /organism="unknown"
                  /mol_type="genomic DNA"
IGIN

gnment Scores:
d. No.:              7.22e-188      Length:        561
re:                  187.00         Matches:       187
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            94.9%          Indels:        0
                     2              Gaps:          0

10-821-670A-36 (1-197) x AR596007 (1-561)

        11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

        31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

        51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

        71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

        91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

       111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

       131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

       151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

       171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

       191 MetSerTyrLeuAsnAlaSer 197
           |||||||||||||||||||||
       541 ATGAGCTATCTGAATGCTTCC 561

ULT 20
96008/c
US       AR596008                561 bp    DNA     linear   PAT 15-DEC-2004
INITION  Sequence 103 from patent US 6818444.
CESSION  AR596008
SION     AR596008.1  GI:56646989
WORDS    .
URCE     Unknown.
```

```
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 103 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.22e-188      Length:        561
Score:                  187.00         Matches:       187
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            94.9%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x AR596008 (1-561)

Qy         11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        191 MetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 21
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
          Felinae; Felis.
FERENCE   1  (bases 1 to 669)
AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
          Pedersen,N.C. and Lutz,H.
ITLE      Nucleotide and predicted peptide sequence of feline interleukin-12
          (IL-12)
JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
 PUBMED   9522125
FERENCE   2  (bases 1 to 669)
AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
          Pedersen,N.C. and Lutz,H.
ITLE      Direct Submission
JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
          Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
          Zurich, ZH 8057, Switzerland
ATURES             Location/Qualifiers
   source          1. .669
                   /organism="Felis catus"
                   /mol_type="mRNA"
                   /db_xref="taxon:9685"
   CDS             1. .669
                   /note="cytokine"
                   /codon_start=1
                   /product="interleukin-12 p35 subunit"
                   /protein_id="AAB93836.1"
                   /db_xref="GI:2735053"
                   /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                   QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                   REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                   NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                   LNSS"
IGIN

ignment Scores:
ed. No.:              6.63e-153      Length:        669
ore:                  154.00         Matches:       154
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            78.2%          Indels:        0
:                     14             Gaps:          0

-10-821-670A-36 (1-197) x FCU83185 (1-669)

        42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 258

        62 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 81
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

        82 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCys 101
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       319 CTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGC 378

       102 LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAla 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       379 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 438

       122 LysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       439 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 498

       142 AspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeu 161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       499 GATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTG 558

       162 GluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArg 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618

       182 IleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
```

```
           ||||||||||||||||||||||||||||||||||||||||||
Db     619 ATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

RESULT 22
AF054605
LOCUS       AF054605                285 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION   AF054605
VERSION     AF054605.1  GI:3126818
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
REFERENCE   2  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>285
                     /codon_start=3
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAC15978.1"
                     /db_xref="GI:3126819"
                     /translation="LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLP
                     LELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE"
ORIGIN

Alignment Scores:
Pred. No.:              3.5e-79      Length:        285
Score:                  84.00        Matches:       84
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            42.6%        Indels:        0
DB:                     14           Gaps:          0

US-10-821-670A-36 (1-197) x AF054605 (1-285)

Qy         32 LysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAsp 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 92

Qy         52 IleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsn 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 152

Qy         72 GluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 212

Qy         92 ArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMet 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 272

Qy        112 TyrGlnValGlu 115
              ||||||||||||
```

```
        273 TACCAGGTGGAG 284

SULT 23
.54615
:US       AX154615                660 bp    DNA     linear   PAT 22-JUN-2001
'INITION  Sequence 19 from Patent WO0140257.
'ESSION   AX154615
'SION     AX154615.1  GI:14536190
'WORDS    .
'RCE      synthetic construct
'RGANISM  synthetic construct
          other sequences; artificial sequences.
'ERENCE   1
'UTHORS   Leong,S.R. and Punnonen,J.
'ITLE     Cytokine polypeptides and nucleic acids
'OURNAL   Patent: WO 0140257-A 19 07-JUN-2001;
          Maxygen, Inc. (US)
'TURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
IGIN

lgnment Scores:
ed. No.:              1.93e-52       Length:         660
ore:                  59.00          Matches:        59
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            29.9%          Indels:         0
:                     2              Gaps:           0

-10-821-670A-36 (1-197) x AX154615 (1-660)

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 99
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

        100 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        364 CTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

        120 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 138
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

SULT 24
.54619
'US       AX154619                660 bp    DNA     linear   PAT 22-JUN-2001
'INITION  Sequence 23 from Patent WO0140257.
'ESSION   AX154619
'SION     AX154619.1  GI:14536194
'WORDS    .
'RCE      synthetic construct
'RGANISM  synthetic construct
          other sequences; artificial sequences.
'ERENCE   1
'UTHORS   Leong,S.R. and Punnonen,J.
'ITLE     Cytokine polypeptides and nucleic acids
'OURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
          Maxygen, Inc. (US)
'TURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
IGIN

lgnment Scores:
ed. No.:              1.93e-52       Length:         660
ore:                  59.00          Matches:        59
```

```
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            29.9%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AX154619 (1-660)

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 99
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACAACC 363

Qy         100 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 119
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy         120 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 138
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 25
AX154620
LOCUS       AX154620                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 24 from Patent WO0140257.
ACCESSION   AX154620
VERSION     AX154620.1  GI:14536195
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 24 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              1.93e-52       Length:         660
Score:                  59.00          Matches:        59
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            29.9%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AX154620 (1-660)

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 99
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

Qy         100 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 119
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy         120 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 138
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 AATGCAAAGCTGTTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 26
AX154616
LOCUS       AX154616                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 20 from Patent WO0140257.
ACCESSION   AX154616
VERSION     AX154616.1  GI:14536191
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
```

```
          other sequences; artificial sequences.
FERENCE   1
AUTHORS   Leong,S.R. and Punnonen,J.
ITLE      Cytokine polypeptides and nucleic acids
JOURNAL   Patent: WO 0140257-A 20 07-JUN-2001;
          Maxygen, Inc. (US)
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
IGIN

lignment Scores:
ed. No.:              2.87e-49       Length:         660
ore:                  56.00          Matches:        56
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            28.4%          Indels:         0
:                     2              Gaps:           0

-10-821-670A-36 (1-197) x AX154616 (1-660)

        83 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       313 ATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTT 372

       103 SerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLys 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       373 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 432

       123 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||
       433 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

SULT 27
076201
CUS       AX076201                 669 bp    DNA     linear   PAT 06-FEB-2001
FINITION  Sequence 2 from Patent WO0104155.
CESSION   AX076201
RSION     AX076201.1  GI:12710826
YWORDS    .
URCE      synthetic construct
ORGANISM  synthetic construct
          other sequences; artificial sequences.
FERENCE   1
AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
ITLE      Feline interleukin-12 as an immune stimulant
JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
          Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
          Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
          CALIFORNIA (US)
ATURES              Location/Qualifiers
   source           1. .669
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="feline IL-12 p35"
IGIN

lignment Scores:
ed. No.:              3.78e-47       Length:         669
ore:                  54.00          Matches:        54
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            27.4%          Indels:         0
:                     2              Gaps:           0

-10-821-670A-36 (1-197) x AX076201 (1-669)

        91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
              ||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507

RESULT 28
AX076483
LOCUS       AX076483                 669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
ORIGIN

Alignment Scores:
Pred. No.:              3.78e-47       Length:         669
Score:                  54.00          Matches:        54
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            27.4%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AX076483 (1-669)

Qy         91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
              ||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507

RESULT 29
AX076477
LOCUS       AX076477                 4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
```

```
          Universitaet Zuerich (CH)
ATURES              Location/Qualifiers
   source           1. .4201
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
IGIN

gnment Scores:
d. No.:                 1.73e-46        Length:         4201
re:                     54.00           Matches:        54
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               27.4%           Indels:         0
                        2               Gaps:           0

10-821-670A-36 (1-197) x AX076477 (1-4201)

        91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3392 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 3451

       111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3452 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 3511

       131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
           ||||||||||||||||||||||||||||||||||||||||||
      3512 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 3553

ULT 30
.71284
US        BD171284                  591 bp    DNA     linear   PAT 18-FEB-2003
INITION   Novel canine cytokine protein.
ESSION    BD171284
SION      BD171284.1  GI:28412574
WORDS     JP 2002241398-A/4.
RCE       unidentified
RGANISM   unidentified
          unclassified sequences.
ERENCE    1  (bases 1 to 591)
UTHORS    Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
ITLE      Novel canine cytokine protein
OURNAL    Patent: JP 2002241398-A 4 28-AUG-2002;
          CHEMO SERO THERAPEUT RES INST
MENT      OS   Canine splenocyte
          PN   JP 2002241398-A/4
          PD   28-AUG-2002
          PF   03-JUN-1997 JP 1997161936
          PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
            C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
          C12P21/02//
          PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
            Strandedness: Double;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers.
ATURES              Location/Qualifiers
   source           1. .591
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
IGIN

gnment Scores:
d. No.:                 4.45e-45        Length:         591
re:                     52.00           Matches:        52
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               26.4%           Indels:         0
                        2               Gaps:           0

10-821-670A-36 (1-197) x BD171284 (1-591)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               ||||||||||||||||||||||||||||||||||
Db         238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 31
AR595963
LOCUS       AR595963                  591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 49 from patent US 6818444.
ACCESSION   AR595963
VERSION     AR595963.1  GI:56646944
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 49 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .591
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.45e-45        Length:         591
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x AR595963 (1-591)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               ||||||||||||||||||||||||||||||||||
Db         238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 32
AR595964/c
LOCUS       AR595964                  591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 51 from patent US 6818444.
ACCESSION   AR595964
VERSION     AR595964.1  GI:56646945
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 51 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .591
```

```
                /organism="unknown"
                /mol_type="genomic DNA"
:GIN

:gnment Scores:
ed. No.:              4.45e-45        Length:         591
ore:                  52.00           Matches:        52
:cent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            26.4%           Indels:         0
:                     2               Gaps:           0

-10-821-670A-36 (1-197) x AR595964 (1-591)

         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

:ULT 33
:95961
:US       AR595961                 666 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 46 from patent US 6818444.
:CESSION  AR595961
RSION     AR595961.1  GI:56646942
:WORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 666)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
:ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 46 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES              Location/Qualifiers
   source           1. .666
                    /organism="unknown"
                    /mol_type="genomic DNA"
:GIN

:gnment Scores:
ed. No.:              4.91e-45        Length:         666
ore:                  52.00           Matches:        52
:cent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            26.4%           Indels:         0
:                     2               Gaps:           0

-10-821-670A-36 (1-197) x AR595961 (1-666)

         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

:ULT 34
595962/c
:US       AR595962                 666 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 48 from patent US 6818444.
ACCESSION   AR595962
VERSION     AR595962.1  GI:56646943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 48 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .666
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.91e-45        Length:         666
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x AR595962 (1-666)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 35
AR151062
LOCUS       AR151062                 669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.93e-45        Length:         669
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x AR151062 (1-669)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252
```

```
        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

ULT 36
51072
US       AR151072                669 bp    DNA     linear   PAT 08-AUG-2001
INITION  Sequence 12 from patent US 6231850.
CESSION  AR151072
SION     AR151072.1  GI:15117122
WORDS    .
URCE     Unknown.
RGANISM  Unknown.
         Unclassified.
FERENCE  1  (bases 1 to 669)
UTHORS   Okano,F., Satoh,M. and Yamada,K.
ITLE     Canine interleukin 12
OURNAL   Patent: US 6231850-A 12 15-MAY-2001;
ATURES             Location/Qualifiers
   source          1. .669
                   /organism="unknown"
                   /mol_type="unassigned DNA"
IGIN

gnment Scores:
d. No.:              4.93e-45       Length:        669
re:                  52.00          Matches:       52
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            26.4%          Indels:        0
                     2              Gaps:          0

-10-821-670A-36 (1-197) x AR151072 (1-669)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

ULT 37
014654
US       BD014654                669 bp    DNA     linear   PAT 27-AUG-2002
INITION  Process for producing highly pure protein, interleukin 12, protein
         inhibiting interleukin-12 activity, remedies for mammalian
         immunopathy and method of treating immunopathy.
CESSION  BD014654
SION     BD014654.1  GI:22555437
WORDS    JP 2001161378-A/2.
URCE     Canis sp.
RGANISM  Canis sp.
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
         Canis.
FERENCE  1  (bases 1 to 669)
UTHORS   Okano,F.
ITLE     Process for producing highly pure protein, interleukin 12, protein
         inhibiting interleukin-12 activity, remedies for mammalian
         immunopathy and method of treating immunopathy
OURNAL   Patent: JP 2001161378-A 2 19-JUN-2001;
         TORAY INDUSTRIES INC
MMENT    OS   Canis sp. (dog)
         PN   JP 2001161378-A/2
         PD   19-JUN-2001
         PF   26-SEP-2000 JP 2000292946
         PI   FUMIYOSHI OKANO
         PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
         PC   A61P35/00,
         PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
         PC   C12R1:91),
         PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
         CC   Process for producing highly pure protein, interleukin 12,  CC
              protein
         CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
              immunopathy and
         CC   method of treating immunopathy
         FH   Key             Location/Qualifiers
         FT   CDS             (1). .(666)
         FT   mat_peptide     (76). .(666).
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:              4.93e-45       Length:        669
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x BD014654 (1-669)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 38
BD014664
LOCUS       BD014664                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014664
VERSION     BD014664.1  GI:22555447
KEYWORDS    JP 2001161378-A/12.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 12 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/12
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
```

```
          PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
          PC   C12R1:91),
          PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
          CC   Process for producing highly pure protein, interleukin 12,  CC
                    protein
          CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                    immunopathy and
          CC   method of treating immunopathy
          FH   Key             Location/Qualifiers
          FT   CDS             (1). .(666)
          FT   mat_peptide     (76). .(666).
ATURES                Location/Qualifiers
   source             1. .669
                      /organism="Canis sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9616"
IGIN

ignment Scores:
ed. No.:                  4.93e-45        Length:         669
ore:                      52.00           Matches:        52
rcent Similarity:         100.0%          Conservative:   0
st Local Similarity:      100.0%          Mismatches:     0
ery Match:                26.4%           Indels:         0
:                         2               Gaps:           0

-10-821-670A-36 (1-197) x BD014664 (1-669)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

ULT 39
5018
US       E15018                  669 bp    DNA     linear   PAT 28-JUL-1999
FINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
CESSION   E15018
RSION     E15018.1  GI:5709701
YWORDS    JP 1998036397-A/2.
URCE      Canis sp.
ORGANISM  Canis sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
          Canis.
FERENCE   1  (bases 1 to 669)
AUTHORS   Okano,F.
ITLE      CANINE INTERLEUKIN 12 AND ITS PRODUCTION
JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
          TORAY IND INC
MMENT     OS   Canis sp. (dog)
          PN   JP 1998036397-A/2
          PD   10-FEB-1998
          PF   08-NOV-1996 JP 1996296789
          PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
          OKANO FUMIYOSHI
          PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
            C12R1:91),
          PC   (C12P21/02,C12R1:91);
          CC   strandedness: Double;
          CC   topology: Linear;
          FH   Key             Location/Qualifiers
          FH
          FT   source          1. .669
          FT                   /organism='Canis sp.'
          FT                   /tissue_type='liver'
          FT   CDS             1. .669
          FT                   /product='interleukin12 35kDa subunit'.
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="Canis sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:                4.93e-45        Length:         669
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.4%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-36 (1-197) x E15018 (1-669)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 40
AR316461
LOCUS       AR316461                669 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 2 from patent US 6562334.
ACCESSION   AR316461
VERSION     AR316461.1  GI:33695289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 2 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="unknown"
                      /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                4.93e-45        Length:         669
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.4%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-36 (1-197) x AR316461 (1-669)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
```

```
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 41
816471
CUS       AR316471                669 bp    mRNA    linear   PAT 17-AUG-2003
FINITION  Sequence 12 from patent US 6562334.
CESSION   AR316471
RSION     AR316471.1  GI:33695299
YWORDS    .
URCE      Unknown.
RGANISM   Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 669)
UTHORS    Okano,F., Satoh,M. and Yamada,K.
ITLE      Canine interleukin 12 administration as an immune disease treatment
OURNAL    Patent: US 6562334-A 12 13-MAY-2003;
          Toray Industries, Inc.;;
          JPX;
ATURES              Location/Qualifiers
   source           1. .669
                    /organism="unknown"
                    /mol_type="mRNA"
IGIN

lgnment Scores:
ed. No.:              4.93e-45       Length:        669
ore:                  52.00          Matches:       52
cent Similarity:      100.0%         Conservative:  0
t Local Similarity:   100.0%         Mismatches:    0
ry Match:             26.4%          Indels:        0
                      2              Gaps:          0

10-821-670A-36 (1-197) x AR316471 (1-669)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 42
.71283
CUS       BD171283                1282 bp    DNA     linear   PAT 18-FEB-2003
FINITION  Novel canine cytokine protein.
CESSION   BD171283
RSION     BD171283.1  GI:28412573
YWORDS    JP 2002241398-A/3.
URCE      unidentified
RGANISM   unidentified
          unclassified sequences.
FERENCE   1  (bases 1 to 1282)
UTHORS    Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
ITLE      Novel canine cytokine protein
OURNAL    Patent: JP 2002241398-A 3 28-AUG-2002;
          CHEMO SERO THERAPEUT RES INST
MENT      OS   Canine splenocyte
          PN   JP 2002241398-A/3
          PD   28-AUG-2002
          PF   03-JUN-1997 JP 1997161936
          PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
            C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
          C12P21/02//
          PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
            Strandedness: Double;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers.
ATURES              Location/Qualifiers
   source           1. .1282
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              8.44e-45       Length:        1282
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x BD171283 (1-1282)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 317

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 377

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        378 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 413

RESULT 43
AR596009
LOCUS       AR596009                1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 104 from patent US 6818444.
ACCESSION   AR596009
VERSION     AR596009.1  GI:56646990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 104 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .1455
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              9.37e-45       Length:        1455
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x AR596009 (1-1455)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

RESULT 44
AR596010/c
```

```
CUS       AR596010                1455 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 106 from patent US 6818444.
CESSION   AR596010
RSION     AR596010.1  GI:56646991
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1455)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 106 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
   source          1. .1455
                   /organism="unknown"
                   /mol_type="genomic DNA"
IGIN

lignment Scores:
ed. No.:              9.37e-45       Length:         1455
ore:                  52.00          Matches:        52
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            26.4%          Indels:         0
                      2              Gaps:           0

-10-821-670A-36 (1-197) x AR596010 (1-1455)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

SULT 45
595973
CUS       AR595973                1533 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 66 from patent US 6818444.
CESSION   AR595973
RSION     AR595973.1  GI:56646954
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1533)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
ITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
   source          1. .1533
                   /organism="unknown"
                   /mol_type="genomic DNA"
IGIN

lignment Scores:
ed. No.:              9.79e-45       Length:         1533
ore:                  52.00          Matches:        52
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            26.4%          Indels:         0
                      2              Gaps:           0

-10-821-670A-36 (1-197) x AR595973 (1-1533)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy      60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy      80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
Db    1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 46
AR595974/c
LOCUS       AR595974                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              9.79e-45       Length:         1533
Score:                  52.00          Matches:        52
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            26.4%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR595974 (1-1533)

Qy      40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy      60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy      80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
Db     354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 47
AR595971
LOCUS       AR595971                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
```

```
:GIN

.gnment Scores:
:d. No.:              1.01e-44       Length:         1599
:re:                  52.00          Matches:        52
:cent Similarity:     100.0%         Conservative:   0
:t Local Similarity:  100.0%         Mismatches:     0
:ry Match:            26.4%          Indels:         0
                      2              Gaps:           0

10-821-670A-36 (1-197) x AR595971 (1-1599)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
      1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

SULT 48
595972/c
:US       AR595972              1599 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 63 from patent US 6818444.
:CESSION  AR595972
RSION     AR595972.1  GI:56646953
YWORDS    .
JRCE      Unknown.
:RGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1599)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
:ITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
:OURNAL   Patent: US 6818444-A 63 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
   source          1. .1599
                   /organism="unknown"
                   /mol_type="genomic DNA"
:GIN

.gnment Scores:
:d. No.:              1.01e-44       Length:         1599
:re:                  52.00          Matches:        52
:cent Similarity:     100.0%         Conservative:   0
:t Local Similarity:  100.0%         Mismatches:     0
:ry Match:            26.4%          Indels:         0
                      2              Gaps:           0

-10-821-670A-36 (1-197) x AR595972 (1-1599)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 49
J49085
:US       CFU49085              669 bp    mRNA    linear   MAM 13-MAR-1996
FINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
:CESSION  U49085
RSION     U49085.1  GI:1223905
KEYWORDS  .
SOURCE    Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE 1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE 2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LNSS"
ORIGIN

Alignment Scores:
Pred. No.:            6.43e-43       Length:         669
Score:                50.00          Matches:        50
Percent Similarity:   100.0%         Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:          25.4%          Indels:         0
DB:                   14             Gaps:           0

US-10-821-670A-36 (1-197) x CFU49085 (1-669)

Qy          42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAG 258

Qy          62 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 81
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

Qy          82 LeuIleThrAsnGlySerCysLeuAlaSer 91
               ||||||||||||||||||||||||||||||
Db         319 TTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 50
AX154613
LOCUS       AX154613               666 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 17 from Patent WO0140257.
ACCESSION   AX154613
VERSION     AX154613.1  GI:14536188
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 17 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="synthetic construct"
```

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

:GIN

:gnment Scores:
ed. No.: 1.62e-35 Length: 666
ore: 43.00 Matches: 43
:cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 21.8% Indels: 0
2 Gaps: 0

-10-821-670A-36 (1-197) x AX154613 (1-666)

```
 71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

 91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAG 402

111 MetTyrGln 113
    |||||||||
403 ATGTACCAG 411
```

SULT 51
603407
CUS AY603407 618 bp mRNA linear MAM 18-JUL-2004
FINITION Capra hircus interleukin 12 p35 subunit precursor, mRNA, partial cds.
CESSION AY603407
RSION AY603407.1 GI:50261481
YWORDS .
URCE Capra hircus (goat)
RGANISM Capra hircus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Capra.
FERENCE 1 (bases 1 to 618)
AUTHORS Rasool,T.J., Shebannavar,S., Hosamani,M., Sreekumar,E., George,A.A. and Premraj,A.
ITLE cloning and sequencing of goat cytokines
JOURNAL Unpublished
FERENCE 2 (bases 1 to 618)
AUTHORS Rasool,T.J., Shebannavar,S., Hosamani,M., Sreekumar,E., George,A.A. and Premraj,A.
ITLE Direct Submission
JOURNAL Submitted (20-APR-2004) Division of Virology, Indian Veterinary Research Institute, Mukteswar, Nainital, Uttaranchal 263138, India
ATURES Location/Qualifiers
source 1. .618
/organism="Capra hircus"
/mol_type="mRNA"
/isolation_source="peripheral blood mononuclear cells stimulated with Concanavalin A"
/db_xref="taxon:9925"
/note="breed: Pashmina"
CDS <1. .618
/codon_start=1
/product="interleukin 12 p35 subunit precursor"
/protein_id="AAT72317.1"
/db_xref="GI:50261482"
/translation="HHLPHLSLGRSLPTTTAGPGRSCLDYSQNLLRAVSNTLQKARQT
LEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRETSLITNGHCLASGKT
SFMTTLCLRSIYKDLKMYHMEFQAMNAKLLMDPKRQVSLDQNMLAAIAELMQALNFDS
ETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYLSSS"

:GIN

:gnment Scores:
ed. No.: 1.74e-34 Length: 618
ore: 42.00 Matches: 42
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 21.3% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-36 (1-197) x AY603407 (1-618)

```
Qy   27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  103 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 162

Qy   47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  163 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 222

Qy   67 GluLeu 68
        ||||||
Db  223 GAATTA 228
```

RESULT 52
AF173557
LOCUS AF173557 666 bp mRNA linear MAM 13-NOV-2000
DEFINITION Ovis aries interleukin-12 p35 subunit precursor, mRNA, complete cds.
ACCESSION AF173557
VERSION AF173557.1 GI:5805389
KEYWORDS .
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 666)
AUTHORS Swinburne,S.J., Russ,G.R. and Krishnan,R.
TITLE Ovine interleukin 12 has biological activity on ovine and human activated peripheral blood mononuclear cells
JOURNAL Cytokine 12 (10), 1546-1552 (2000)
PUBMED 11023671
REFERENCE 2 (bases 1 to 666)
AUTHORS Swinburne,S.J., Russ,G.R. and Krishnan,R.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1999) Transplantation Immunology Laboratory, The Queen Elizabeth Hospital, Woodville Road, Adelaide, South Australia 5011, Australia
FEATURES Location/Qualifiers
source 1. .666
/organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
/tissue_type="inflammed renal tissue"
CDS 1. .666
/note="Il-12; cytokine"
/codon_start=1
/product="interleukin-12 p35 subunit precursor"
/protein_id="AAD51976.1"
/db_xref="GI:5805390"
/translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTAGPGTSCLDYSQ
NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
ETSLITNGHCLSSGKTSFMTTLCLRSIYKDLKMYHMEFQAMNAKLLMDPKRQVFLDQN
MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
SSS"
sig_peptide 1. .75
mat_peptide 76. .663
/product="interleukin-12 p35 subunit"
ORIGIN

Alignment Scores:
Pred. No.: 1.85e-34 Length: 666
Score: 42.00 Matches: 42
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 21.3% Indels: 0
DB: 14 Gaps: 0

```
-10-821-670A-36 (1-197) x AF173557 (1-666)

         27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

         47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        211 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

         67 GluLeu 68
            ||||||
        271 GAATTA 276

SULT 53
232819
CUS       AY232819                 666 bp    mRNA    linear   MAM 09-JUN-2005
FINITION  Bubalus bubalis interleukin-12 p35 subunit precursor, mRNA,
          complete cds.
ESSION    AY232819
SION      AY232819.1  GI:31322541
WORDS     .
RCE       Bubalus bubalis (water buffalo)
RGANISM   Bubalus bubalis
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bubalus.
ERENCE    1  (bases 1 to 666)
UTHORS    Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
ITLE      Interleukin-12 subunits p35 and p40 of Indian water buffalo
          (Bubalus bubalis) maintain high sequence homology with those of
          other ruminants
OURNAL    Eur. J. Immunogenet. 32 (3), 179-186 (2005)
ERENCE    2  (bases 1 to 666)
UTHORS    Premraj,A., Sreekumar,E. and Rasool,T.J.
ITLE      Direct Submission
OURNAL    Submitted (07-FEB-2003) Animal Biotechnology, Rajiv Gandhi Centre
          for Biotechnology, Jagathy, Trivandrum, Kerala 695014, India
TURES             Location/Qualifiers
   source         1. .666
                  /organism="Bubalus bubalis"
                  /mol_type="mRNA"
                  /db_xref="taxon:89462"
                  /cell_type="concanavalin A stimulated splenocytes"
   CDS            1. .666
                  /note="cytokine"
                  /codon_start=1
                  /product="interleukin-12 p35 subunit precursor"
                  /protein_id="AAO61417.1"
                  /db_xref="GI:31322542"
                  /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                  NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                  ETSFITNGRCLASGKTSFMTTLCLKSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                  MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                  SSS"
GIN

gnment Scores:
d. No.:              1.85e-34       Length:        666
re:                  42.00          Matches:       42
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            21.3%          Indels:        0
                     14             Gaps:          0

-10-821-670A-36 (1-197) x AY232819 (1-666)

         27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

         47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy       67 GluLeu 68
            ||||||
Db      271 GAATTA 276

RESULT 54
AB246272
LOCUS       AB246272                 690 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus carabanensis IL-12p35 mRNA for interleukin-12p35, complete
            cds.
ACCESSION   AB246272
VERSION     AB246272.1  GI:84871693
KEYWORDS    .
SOURCE      Bubalus carabanensis
  ORGANISM  Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:346063"
                     /sex="female"
                     /cell_type="PBMC"
     gene            1. .690
                     /gene="IL-12p35"
     CDS             1. .666
                     /gene="IL-12p35"
                     /codon_start=1
                     /product="interleukin-12p35"
                     /protein_id="BAE75849.1"
                     /db_xref="GI:84871694"
                     /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                     NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                     ETSFITNGRCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                     MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
ORIGIN

Alignment Scores:
Pred. No.:              1.9e-34       Length:        690
Score:                  42.00         Matches:       42
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            21.3%         Indels:        0
DB:                     14            Gaps:          0

US-10-821-670A-36 (1-197) x AB246272 (1-690)

Qy       27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy       47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270
```

```
        67 GluLeu 68
           ||||||
       271 GAACTA 276

SULT 55
246352
CUS       AB246352                 690 bp    mRNA    linear   MAM 13-JAN-2006
FINITION  Bubalus bubalis IL-12p35 mRNA for interleukin-12p35, complete cds.
CESSION   AB246352
RSION     AB246352.1  GI:84871715
YWORDS    .
URCE      Bubalus bubalis (water buffalo)
RGANISM   Bubalus bubalis
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bubalus.
FERENCE   1
UTHORS    Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
ITLE      Comparative assessment of Th1 and Th2 cytokines of swamp type
          buffalo and other bubaline breeds by molecular cloning, sequencing
          and phylogenetics
OURNAL    Unpublished
FERENCE   2  (bases 1 to 690)
UTHORS    Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
ITLE      Direct Submission
OURNAL    Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
          Veterinary Medicine, Hokkaido University, Department of Disease
          Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
          9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
          Tel:81-11-706-5216, Fax:81-11-706-5217)
ATURES             Location/Qualifiers
   source          1. .690
                   /organism="Bubalus bubalis"
                   /mol_type="mRNA"
                   /db_xref="taxon:89462"
                   /sex="female"
                   /cell_type="PBMC"
                   /note="Bulgarian Murrah buffalo - crossbreed between
                   Mediterranean and Indian buffalo both are Riverine type
                   water buffalo"
   gene            1. .690
                   /gene="IL-12p35"
   CDS             1. .666
                   /gene="IL-12p35"
                   /codon_start=1
                   /product="interleukin-12p35"
                   /protein_id="BAE75857.1"
                   /db_xref="GI:84871716"
                   /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                   NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                   ETSFITNGRCLASGKTSYMTTLCLKSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                   MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                   SSS"
IGIN

ignment Scores:
ed. No.:              1.9e-34        Length:         690
ore:                  42.00          Matches:        42
cent Similarity:      100.0%         Conservative:   0
t Local Similarity:   100.0%         Mismatches:     0
ry Match:             21.3%          Indels:         0
                      14             Gaps:           0

-10-821-670A-36 (1-197) x AB246352 (1-690)

         27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

         47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270
```

```
Qy         67 GluLeu 68
              ||||||
Db        271 GAATTA 276

RESULT 56
AB246359
LOCUS       AB246359                 690 bp    mRNA    linear   MAM 14-JAN-2006
DEFINITION  Bubalus bubalis x Bubalus carabanensis IL-12p35 mRNA for
            interleukin-12p35, complete cds.
ACCESSION   AB246359
VERSION     AB246359.1  GI:84875358
KEYWORDS    .
SOURCE      Bubalus bubalis x Bubalus carabanensis
  ORGANISM  Bubalus bubalis x Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Bubalus bubalis x Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:365610"
                     /sex="female"
                     /cell_type="PBMC"
                     /note="Philippine carabao crossbreed (CB) - crossbreed
                     between Philippine carabao (Swamp type water buffalo) and
                     Indian Murrah buffalo (Riverine type water buffalo)"
     gene            1. .690
                     /gene="IL-12p35"
     CDS             1. .666
                     /gene="IL-12p35"
                     /codon_start=1
                     /product="interleukin-12p35"
                     /protein_id="BAE75893.1"
                     /db_xref="GI:84875359"
                     /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                     NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                     ETSFITNGHCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                     MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
ORIGIN

Alignment Scores:
Pred. No.:              1.9e-34        Length:         690
Score:                  42.00          Matches:        42
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            21.3%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-36 (1-197) x AB246359 (1-690)

Qy         27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy         47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

        67 GluLeu 68
           ||||||
       271 GAATTA 276

SULT 57
C03542
CUS       AF003542                 690 bp    mRNA    linear   MAM 17-JUN-1997
FINITION  Capra hircus interleukin 12 35kD subunit mRNA, complete cds.
CESSION   AF003542
SION      AF003542.1  GI:2197070
WORDS     .
URCE      Capra hircus (goat)
RGANISM   Capra hircus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Caprinae; Capra.
FERENCE   1  (bases 1 to 690)
AUTHORS   Beyer,J.C., Kumpula-McWhirter,N.M. and Cheevers,W.P.
CITLE     Caprine Interleukin 12 35kD subunit
COURNAL   Unpublished
FERENCE   2  (bases 1 to 690)
AUTHORS   Beyer,J.C., Kumpula-McWhirter,N.M. and Cheevers,W.P.
CITLE     Direct Submission
COURNAL   Submitted (09-MAY-1997) Veterinary Microbiology and Pathology,
          Washington State University, P.O Box 647040, Pullman, WA
          99164-7040, USA
ATURES              Location/Qualifiers
   source           1. .690
                    /organism="Capra hircus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9925"
                    /cell_type="LPS stimulated caprine microglial cells"
   CDS              1. .666
                    /codon_start=1
                    /product="interleukin 12 35kD subunit"
                    /protein_id="AAB61287.1"
                    /db_xref="GI:2197071"
                    /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPITTAGPGRSCLDYSQ
                    NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                    ETSLITNGHCLASGKTSFMTTLCLRSIYKDLKMYHMEFQAINAKLLMDPKRQVSLDQN
                    MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                    SSS"
GIN

gnment Scores:
ed. No.:              1.9e-34        Length:        690
ore:                  42.00          Matches:       42
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            21.3%          Indels:        0
:                     14             Gaps:          0

-10-821-670A-36 (1-197) x AF003542 (1-690)

        27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

        47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       211 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

        67 GluLeu 68
           ||||||
       271 GAATTA 276

SULT 58
U14416
CUS       BTU14416                 690 bp    mRNA    linear   MAM 27-JAN-1996
FINITION  Bos taurus interleukin 12 35 kDa subunit mRNA, complete cds.
CESSION   U14416
VERSION     U14416.1  GI:555917
KEYWORDS    .
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Zarlenga,D.S., Canals,A., Aschenbrenner,R.A. and Gasbarre,L.C.
  TITLE     Enzymatic amplification and molecular cloning of cDNA encoding the
            small and large subunits of bovine interleukin 12
  JOURNAL   Biochim. Biophys. Acta 1270 (2-3), 215-217 (1995)
   PUBMED   7727547
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Zarlenga,D.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-SEP-1994) Dante S. Zarlenga, U.S. Department of
            Agriculture, ARS, LPSI, PIL, Beltsville, MD 20705, USA
FEATURES              Location/Qualifiers
     source           1. .690
                      /organism="Bos taurus"
                      /mol_type="mRNA"
                      /strain="Holstein"
                      /db_xref="taxon:9913"
                      /clone="BIL12 35"
                      /sex="male"
                      /cell_type="lymphocytes and macrophages"
                      /tissue_type="lymphoid"
     CDS              1. .666
                      /codon_start=1
                      /product="interleukin 12 35 kDa subunit"
                      /protein_id="AAA85810.1"
                      /db_xref="GI:555918"
                      /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                      NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                      ETSFITNGHCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQN
                      MLAAIAELMQALNFDSETVPQKPSLKELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                      SSS"
ORIGIN

Alignment Scores:
Pred. No.:              1.9e-34        Length:        690
Score:                  42.00          Matches:       42
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            21.3%          Indels:        0
DB:                     14             Gaps:          0

US-10-821-670A-36 (1-197) x BTU14416 (1-690)

Qy         27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy         47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy         67 GluLeu 68
              ||||||
Db        271 GAATTA 276

RESULT 59
CEU57751
LOCUS       CEU57751                 666 bp    mRNA    linear   MAM 28-OCT-1999
DEFINITION  Cervus elaphus interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U57751
VERSION     U57751.1  GI:1373385
KEYWORDS    .
SOURCE      Cervus elaphus (red deer)
  ORGANISM  Cervus elaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
```

```
          Pecora; Cervidae; Cervinae; Cervus.
ERENCE    1  (bases 1 to 666)
UTHORS    Lockhart,E., Slobbe,L. and Buchan,G.
ITLE      The characterisation of a cervine immunoregulatory cytokine,
          interleukin 12
OURNAL    DNA Seq. 10 (2), 139-148 (1999)
 PUBMED   10376218
ERENCE    2  (bases 1 to 666)
UTHORS    Lockhart,E.A.
ITLE      Direct Submission
OURNAL    Submitted (08-MAY-1996) Euan A. Lockhart, Microbiology, University
          of Otago, Cumberland St, Dunedin, New Zealand
ATURES               Location/Qualifiers
   source            1. .666
                     /organism="Cervus elaphus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9860"
                     /cell_type="peripheral blood mononuclear cells"
   CDS               1. .666
                     /note="IL-12 p35 subunit"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB02257.1"
                     /db_xref="GI:1373386"
                     /translation="MCPLRSLLLLSTLVLLHHLPHLSLGRSLPPTTAGPGRSCLNYSQ
                     NLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLVSR
                     ETSLITHGSCLASGKTSFMTTLCLKSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQN
                     MLAAIAELMQALNFNSETVPQKPSLEEMDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                     SSS"
   primer_bind       1. .17
   primer_bind       complement(658. .666)
IGIN

gnment Scores:
ed. No.:              2.41e-32        Length:         666
ore:                  40.00           Matches:        40
cent Similarity:      100.0%          Conservative:   0
t Local Similarity:   100.0%          Mismatches:     0
ery Match:            20.3%           Indels:         0
                      14              Gaps:           0

10-821-670A-36 (1-197) x CEU57751 (1-666)

         29 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 48
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        157 ACACTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 216

         49 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        217 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 276

SULT 60
107653
CUS       AB107653                669 bp    mRNA    linear   MAM 29-APR-2004
FINITION  Lama glama IL-12 p35 mRNA for interleukin 12 p35 subunit, complete
          cds.
CESSION   AB107653
RSION     AB107653.1  GI:29603616
YWORDS    .
URCE      Lama glama (llama)
ORGANISM  Lama glama
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
          Camelidae; Lama.
FERENCE   1
UTHORS    Odbileg,R., Lee,S.I., Yoshida,R., Chang,K.S., Ohashi,K.,
          Sugimoto,C. and Onuma,M.
ITLE      Cloning and sequence analysis of llama cytokines related to
          cell-mediated immunity
OURNAL    Vet. Immunol. Immunopathol. 99 (1-2), 1-10 (2004)
 PUBMED   15113649
FERENCE   2  (bases 1 to 669)
UTHORS    Ohashi,K., Raadan,O. and Lee,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2003) Kazuhiko Ohashi, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control; Kita-ku Kita 18 Nishi 9, Sapporo, Hokkaido 060-0818, Japan
            (E-mail:okazu@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
            Fax:81-11-706-5217)
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="Lama glama"
                      /mol_type="mRNA"
                      /db_xref="taxon:9844"
                      /sex="Female"
                      /cell_type="PBMC"
                      /country="Japan"
     gene             1. .669
                      /gene="IL-12 p35"
     CDS              1. .669
                      /gene="IL-12 p35"
                      /codon_start=1
                      /product="interleukin 12 p35 subunit"
                      /protein_id="BAC75390.1"
                      /db_xref="GI:29603617"
                      /translation="MCPLRSLFLMATLVFLNHLDHLSLARSLPTTTAGPGMFQCLSHS
                      QNLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLAS
                      RETSLITHGSCLASGKTSFMTTLCLSSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQ
                      NMLVAIAELMQALNVSGETVPQKPSLEEPDFYKTKVKLCILLHAFRIRAVTIDRMMSY
                      LSSS"
ORIGIN

Alignment Scores:
Pred. No.:              2.42e-32        Length:         669
Score:                  40.00           Matches:        40
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            20.3%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x AB107653 (1-669)

Qy         29 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ACACTTCAGAAGGCCAGACAAACCCTAGAATTTTACTCTTGCACTTCTGAAGAGATTGAC 219

Qy         49 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

RESULT 61
AB246672
LOCUS       AB246672                669 bp    mRNA    linear   MAM 12-JAN-2006
DEFINITION  Camelus bactrianus IL-12p35 mRNA for interleukin-12p35, complete
            cds.
ACCESSION   AB246672
VERSION     AB246672.1  GI:84794455
KEYWORDS    .
SOURCE      Camelus bactrianus (Bactrian camel)
  ORGANISM  Camelus bactrianus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
            Camelidae; Camelus.
REFERENCE   1
  AUTHORS   Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Molecular cloning and sequence analysis of Th1 and Th2 cytokine
            cDNAs from the bactrian camel (Camelus bactrianus)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-2006) Odbileg Raadan, Graduate School of
            Veterinary Medicine, Hokkaido University, Disease Control,
            Laboratory of Infectious Disease; Kita ku, Kita-18, Nishi-9,
            Sapporo, Hokkaido 060-0818, Japan
            (E-mail:odbileg@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
```

```
          Fax:81-11-706-5217)
ATURES             Location/Qualifiers
   source          1. .669
                   /organism="Camelus bactrianus"
                   /mol_type="mRNA"
                   /db_xref="taxon:9837"
                   /sex="female"
                   /cell_type="PBMC"
                   /country="Japan"
   gene            1. .669
                   /gene="IL-12p35"
   CDS             1. .669
                   /gene="IL-12p35"
                   /codon_start=1
                   /product="interleukin-12p35"
                   /protein_id="BAE75803.1"
                   /db_xref="GI:84794456"
                   /translation="MCPLRSLFLMATLVFLIHLDHLSLARSLPTTTAGPGMFQCLSHS
                   QNLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLAS
                   RETSLITHGSCLASGKTPFMTTLCLSSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQ
                   NMLVAIAELMQALNVSSETVPQKPSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                   LSSS"
IGIN

gnment Scores:
d. No.:              2.42e-32       Length:        669
re:                  40.00          Matches:       40
cent Similarity:     100.0%         Conservative:  0
st Local Similarity: 100.0%         Mismatches:    0
ery Match:           20.3%          Indels:        0
:                    14             Gaps:          0

-10-821-670A-36 (1-197) x AB246672 (1-669)

        29 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 48
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       160 ACGCTTCAGAAGGCCAGACAAACCCTAGAATTTTACTCTTGCACTTCTGAAGAGATTGAC 219

        49 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       220 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

ULT 62
793
US       E35793                 703 bp    DNA     linear   PAT 31-JAN-2002
INITION  Process for producing interleukin 12.
CESSION  E35793
RSION    E35793.1  GI:18624617
YWORDS   JP 2000157274-A/5.
URCE     Bos sp.
RGANISM  Bos sp.
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
         Pecora; Bovidae; Bovinae; Bos.
ERENCE   1  (bases 1 to 703)
UTHORS   Nakamura,M., Takehara,K. and Ohara,E.
ITLE     Process for producing interleukin 12
URNAL    Patent: JP 2000157274-A 5 13-JUN-2000;
         DAI ICHI SEIYAKU CO LTD
MENT     OS   Bos sp. (bovine)
         PN   JP 2000157274-A/5
         PD   13-JUN-2000
         PF   20-NOV-1998 JP 1998331052
         PR
         PI   MASAYUKI NAKAMURA,KAZUAKI TAKEHARA,EIJI OHARA PC
         C12N15/09,C07K14/54,C12N5/10,C12P21/02//(C12N15/09,C12R1:91), PC
         (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC
         (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
         CC
         FH   Key             Location/Qualifiers
         FT   source          1. .703
         FT                   /organism='Bos sp. (bovine)'.
ATURES             Location/Qualifiers
```

```
   source          1. .703
                   /organism="Bos sp."
                   /mol_type="genomic DNA"
                   /db_xref="taxon:29061"
ORIGIN

Alignment Scores:
Pred. No.:              2.52e-32       Length:        703
Score:                  40.00          Matches:       40
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            20.3%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x E35793 (1-703)

Qy         29 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 ACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 227

Qy         49 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 287

RESULT 63
AY191828
LOCUS       AY191828                657 bp    mRNA    linear   SYN 04-FEB-2003
DEFINITION  Synthetic construct evolved IL-12 p35 precursor, mRNA, partial cds.
ACCESSION   AY191828
VERSION     AY191828.1  GI:27729523
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Optimized expression and specific activity of IL-12 by directed
            molecular evolution
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
   PUBMED   12529500
REFERENCE   2  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
            Drive, Redwood City, CA 94063, USA
FEATURES             Location/Qualifiers
     source          1. .657
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .>657
                     /codon_start=1
                     /transl_table=11
                     /product="evolved IL-12 p35 precursor"
                     /protein_id="AAO19111.1"
                     /db_xref="GI:27729524"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRGI
                     SLITNGSCLASRKTSFMTTLCLGSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNML
                     TAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS
                     S"
     sig_peptide     1. .66
     mat_peptide     67. .657
                     /product="evolved IL-12 p35"
ORIGIN

Alignment Scores:
Pred. No.:              2.72e-31       Length:        657
Score:                  39.00          Matches:       39
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
```

```
ery Match:            19.8%          Indels:        0
:                     8              Gaps:          0

-10-821-670A-36 (1-197) x AY191828 (1-657)

         30 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 49
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

         50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 270

SULT 64
:54614
:US        AX154614                 660 bp    DNA     linear   PAT 22-JUN-2001
FINITION   Sequence 18 from Patent WO0140257.
:ESSION    AX154614
RSION      AX154614.1  GI:14536189
'WORDS     .
'RCE       synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
FERENCE    1
AUTHORS    Leong,S.R. and Punnonen,J.
'ITLE      Cytokine polypeptides and nucleic acids
JOURNAL    Patent: WO 0140257-A 18 07-JUN-2001;
           Maxygen, Inc. (US)
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
:GIN

:gnment Scores:
ed. No.:              2.73e-31       Length:        660
ore:                  39.00          Matches:       39
:cent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            19.8%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-36 (1-197) x AX154614 (1-660)

         30 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 49
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

         50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

SULT 65
:54617
:US        AX154617                 660 bp    DNA     linear   PAT 22-JUN-2001
FINITION   Sequence 21 from Patent WO0140257.
:ESSION    AX154617
RSION      AX154617.1  GI:14536192
'WORDS     .
'RCE       synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
FERENCE    1
AUTHORS    Leong,S.R. and Punnonen,J.
'ITLE      Cytokine polypeptides and nucleic acids
JOURNAL    Patent: WO 0140257-A 21 07-JUN-2001;
           Maxygen, Inc. (US)
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:            2.73e-31       Length:        660
Score:                39.00          Matches:       39
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          19.8%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-36 (1-197) x AX154617 (1-660)

Qy         30 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 270

RESULT 66
AX154621
LOCUS       AX154621                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:            2.73e-31       Length:        660
Score:                39.00          Matches:       39
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          19.8%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-36 (1-197) x AX154621 (1-660)

Qy         30 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

RESULT 67
AX154618
LOCUS       AX154618                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
```

```
ERENCE   1
UTHORS   Leong,S.R. and Punnonen,J.
ITLE     Cytokine polypeptides and nucleic acids
OURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
         Maxygen, Inc. (US)
TURES             Location/Qualifiers
   source         1. .660
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="Synthetic Sequence"
IGIN

gnment Scores:
ed. No.:              3.56e-29       Length:        660
re:                   37.00          Matches:       37
cent Similarity:      100.0%         Conservative:  0
t Local Similarity:   100.0%         Mismatches:    0
ry Match:             18.8%          Indels:        0
                      2              Gaps:          0

10-821-670A-36 (1-197) x AX154618 (1-660)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

       179 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       601 GCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

ULT 68
IL12PSU
US       PIGIL12PSU              1426 bp    mRNA    linear   MAM 09-JUL-2001
INITION  Sus scrofa interleukin-12 p35 subunit mRNA, complete cds.
CESSION  L35765
SION     L35765.1  GI:927204
WORDS    .
RCE      Sus scrofa (pig)
RGANISM  Sus scrofa
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
         Sus.
ERENCE   1  (bases 1 to 1426)
UTHORS   Foss,D.L. and Murtaugh,M.P.
ITLE     Molecular cloning and mRNA expression of porcine interleukin-12
OURNAL   Vet. Immunol. Immunopathol. 57 (1-2), 121-134 (1997)
 PUBMED  9239844
MMENT    On Aug 2, 1995 this sequence version replaced gi:755667.
ATURES            Location/Qualifiers
   source         1. .1426
                  /organism="Sus scrofa"
                  /mol_type="mRNA"
                  /db_xref="taxon:9823"
                  /cell_type="mononuclear"
                  /tissue_type="peripheral blood"
   CDS            108. .878
                  /codon_start=1
                  /product="interleukin 12 p35 subunit"
                  /protein_id="AAA73897.1"
                  /db_xref="GI:927205"
                  /translation="MCSPGFGLQTSDLTCDVHPSASSRRLAVTAAPLSMCPLRNLLLV
                  ATLVLLNHLDHLSLGRSLPATTAGPGMFKCLNHSQNLLKAVSNTLQKAKQTLEFYSCT
                  SEEIDHEDITKDKTSTVEACLPLELATNESCLAARETSLITNGNCLTSGKTSFMTTLC
                  LSSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQNMLTAITELMQALNFNSETVPQKP
                  SLEELDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS"
   primer_bind    196. .216
   primer_bind    complement(859. .878)
   polyA_site     1426
IGIN

gnment Scores:
ed. No.:              1e-25          Length:        1426
```

```
Score:                34.00          Matches:       34
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          17.3%          Indels:        0
DB:                   14             Gaps:          0

US-10-821-670A-36 (1-197) x PIGIL12PSU (1-1426)

Qy         35 GlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLys 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CAAACCCTAGAATTTTACTCCTGCACTTCAGAAGAGATCGATCATGAAGATATCACCAAA 446

Qy         55 AspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
              |||||||||||||||||||||||||||||||||||||||||||
Db        447 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTTGAACTA 488

RESULT 69
AX154612
LOCUS       AX154612                 666 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 16 from Patent WO0140257.
ACCESSION   AX154612
VERSION     AX154612.1  GI:14536187
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 16 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:            7.95e-23       Length:        666
Score:                31.00          Matches:       31
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          15.7%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-36 (1-197) x AX154612 (1-666)

Qy         71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

Qy         91 SerArgLysThrSerPheMetThrThrLeuCys 101
              |||||||||||||||||||||||||||||||
Db        343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGC 375

RESULT 70
ECIL12P35
LOCUS       ECIL12P35                669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Equus caballus mRNA for interleukin 12 p35 subunit.
ACCESSION   Y11130
VERSION     Y11130.1  GI:5441624
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1
  AUTHORS   Nicolson,L., Penha-Goncalves,M.N., Keanie,J.L., Logan,N.A.,
            Argyle,D.J. and Onions,D.E.
  TITLE     Cloning and sequencing of horse interleukin-12 and interleukin-18
            cDNAs
```

```
JOURNAL   Immunogenetics 50 (1-2), 94-97 (1999)
 PUBMED   10541814
ERENCE    2  (bases 1 to 669)
AUTHORS   Nicolson,L.
ITLE      Direct Submission
JOURNAL   Submitted (04-FEB-1997) L. Nicolson, Dept. of Vet. Pathology,
          University of Glasgow Vet. School, Bearsden Rd., Glasgow G61 1QH,
          UK
ATURES             Location/Qualifiers
   source          1. .669
                   /organism="Equus caballus"
                   /mol_type="mRNA"
                   /db_xref="taxon:9796"
                   /cell_line="LPS-stimulated alveolar macrophages"
                   /cell_type="alveolar macrophages"
   gene            1. .669
                   /gene="IL-12 p35"
   CDS             1. .669
                   /gene="IL-12 p35"
                   /codon_start=1
                   /product="interleukin 12 p35 subunit"
                   /protein_id="CAA72012.1"
                   /db_xref="GI:5441625"
                   /db_xref="GOA:Q9XSQ6"
                   /db_xref="InterPro:IPR004281"
                   /db_xref="InterPro:IPR009079"
                   /db_xref="UniProtKB/Swiss-Prot:Q9XSQ6"
                   /translation="MCPPRGLLLVAILVLLNHLDHLSLARNLPTATPGPGMFQCLNHS
                   QNLLRTVSNTLQKARQTLEFYSCTSEEIDHEDITKDKSSTVAACLPLELAPNESCLAS
                   REISFITNGSCLTPGKASSMMTLCLSSIYEDLKMYQVEFKAMNAKLLIDPQRQIFLDE
                   NMLTAIDKLMQALNFNSETVPQKPSLEGLDFYKTKVKLCILLHAFRIRAVTINRMMGY
                   LNAS"
   sig_peptide     1. .69
                   /gene="IL-12 p35"
   misc_feature    1. .16
                   /gene="IL-12 p35"
                   /note="primer-derived sequence"
   misc_feature    651. .669
                   /gene="IL-12 p35"
                   /note="primer-derived sequence"
IGIN

gnment Scores:
d. No.:              9.11e-22       Length:         669
ore:                 30.00          Matches:        30
cent Similarity:     100.0%         Conservative:   0
t Local Similarity:  100.0%         Mismatches:     0
ry Match:            15.2%          Indels:         0
                     14             Gaps:           0

10-821-670A-36 (1-197) x ECIL12P35 (1-669)

         27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        154 AGCAACACGCTTCAGAAGGCCAGGCAAACCCTAGAATTCTACTCCTGCACTTCTGAAGAG 213

         47 IleAspHisGluAspIleThrLysAspLys 56
            |||||||||||||||||||||||||||||
        214 ATCGATCATGAGGATATCACAAAAGACAAG 243

SULT 71
401989
CUS       AF401989                1626 bp    mRNA    linear   SYN 14-FEB-2002
FINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
CESSION   AF401989
RSION     AF401989.1  GI:18656516
YWORDS    .
URCE      synthetic construct
ORGANISM  synthetic construct
          other sequences; artificial sequences.
FERENCE   1  (bases 1 to 1626)
AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
          Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
          Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
     source          1. .1626
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .1626
                     /note="derived from Equus caballus; N-terminal p40 subunit
                     linked by (Gly4Ser)3 linker to signal-peptide deleted p35
                     subunit"
                     /codon_start=1
                     /transl_table=11
                     /product="single chain interleukin-12"
                     /protein_id="AAL77817.1"
                     /db_xref="GI:18656517"
                     /translation="MGHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
                     MVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHL
                     LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                     LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
                     QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCSGGGGS
                     GGGGSGGGGSRNLPTATPGPGMFQCLNHSQNLLRTVSNTLQKARQTLEFYSCTSEEID
                     HEDITKDKSSTVAACLPLELAPNESCLASREISFITNGSCLTPGKASSMMTLCLSSIY
                     EDLKMYQVEFKAMNAKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETVPQKPSLEGL
                     DFYKTKVKLCILLHAFRIRAVTINRMMGYLNAS"
     primer_bind     1. .14
     misc_feature    15. .987
                     /note="interleukin-12 p40 sequence"
     misc_feature    988. .1032
                     /note="linker"
     misc_feature    1033. .1611
                     /note="interleukin-12 p35 sequence"
     primer_bind     complement(1612. .1626)
ORIGIN

Alignment Scores:
Pred. No.:              1.9e-21        Length:         1626
Score:                  30.00          Matches:        30
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            15.2%          Indels:         0
DB:                     8              Gaps:           0

US-10-821-670A-36 (1-197) x AF401989 (1-1626)

Qy          27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1111 AGCAACACGCTTCAGAAGGCCAGGCAAACCCTAGAATTCTACTCCTGCACTTCTGAAGAG 1170

Qy          47 IleAspHisGluAspIleThrLysAspLys 56
               |||||||||||||||||||||||||||||
Db        1171 ATCGATCATGAGGATATCACAAAAGACAAG 1200

RESULT 72
AR008951
LOCUS       AR008951                660 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5756085.
ACCESSION   AR008951
VERSION     AR008951.1  GI:3967756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

```
        Unclassified.
FERENCE   1  (bases 1 to 660)
AUTHORS   Sykes,M. and Wolf,S.F.
ITLE      Use of interleukin-12 to prevent graft versus host disease
OURNAL    Patent: US 5756085-A 3 26-MAY-1998;
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="unknown"
                    /mol_type="unassigned DNA"
IGIN

gnment Scores:
d. No.:              1.03e-20       Length:        660
re:                  29.00          Matches:       29
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            14.7%          Indels:        0
:                    2              Gaps:          0

10-821-670A-36 (1-197) x AR008951 (1-660)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 73
007071
CUS       BD007071                  660 bp    DNA     linear   PAT 31-JAN-2002
FINITION  IL-12 gene expression and delivery systems and uses.
CESSION   BD007071
RSION     BD007071.1  GI:18635442
/WORDS    JP 2001503257-A/2.
URCE      unidentified
RGANISM   unidentified
          unclassified sequences.
FERENCE   1  (bases 1 to 660)
AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
ITLE      IL-12 gene expression and delivery systems and uses
OURNAL    Patent: JP 2001503257-A 2 13-MAR-2001;
          BARENTISU INC,SYNTEX INC
MMENT     OS   Unidentified
          PN   JP 2001503257-A/2
          PD   13-MAR-2001
          PF   10-OCT-1997 JP 1998519514
          PR   18-OCT-1996 US    60/028676
          PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
          C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
          A61P11/06,
          PC   C12N15/00,A61K37/02
          CC   Strandedness: Single;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers
          FT   source          1. .660
          FT                   /organism='Unidentified'.
TURES               Location/Qualifiers
   source           1. .660
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
GIN

gnment Scores:
d. No.:              1.03e-20       Length:        660
re:                  29.00          Matches:       29
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            14.7%          Indels:        0
:                    2              Gaps:          0
```

```
US-10-821-670A-36 (1-197) x BD007071 (1-660)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 74
BD007079
LOCUS       BD007079                  660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007079
VERSION     BD007079.1  GI:18635450
KEYWORDS    JP 2001503258-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 4 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/4
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-20       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            14.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x BD007079 (1-660)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 75
BD007080
LOCUS       BD007080                  660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007080
VERSION     BD007080.1  GI:18635451
KEYWORDS    JP 2001503258-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
```

```
FERENCE   1  (bases 1 to 660)
AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
ITLE      Gene expression and delivery systems and uses
JOURNAL   Patent: JP 2001503258-A 5 13-MAR-2001;
          BARENTISU INC
MMENT     OS   Unidentified
          PN   JP 2001503258-A/5
          PD   13-MAR-2001
          PF   10-OCT-1997 JP 1998519520
          PR   18-OCT-1996 US    60/028687
          PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
          C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
          C12N15/00
          CC   Strandedness: Single;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers
          FT   source          1. .660
          FT                   /organism='Unidentified'.
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
IGIN

gnment Scores:
ed. No.:              1.03e-20       Length:        660
ore:                  29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            14.7%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-36 (1-197) x BD007080 (1-660)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       601 GCCTTCCGCATCCGCGCCGTGACCATC 627

SULT 76
007081
CUS       BD007081                660 bp    DNA     linear   PAT 31-JAN-2002
FINITION  Gene expression and delivery systems and uses.
CESSION   BD007081
RSION     BD007081.1  GI:18635452
YWORDS    JP 2001503258-A/6.
URCE      unidentified
ORGANISM  unidentified
          unclassified sequences.
FERENCE   1  (bases 1 to 660)
AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
ITLE      Gene expression and delivery systems and uses
JOURNAL   Patent: JP 2001503258-A 6 13-MAR-2001;
          BARENTISU INC
MMENT     OS   Unidentified
          PN   JP 2001503258-A/6
          PD   13-MAR-2001
          PF   10-OCT-1997 JP 1998519520
          PR   18-OCT-1996 US    60/028687
          PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
          C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
          C12N15/00
          CC   Strandedness: Single;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers
          FT   source          1. .660
          FT                   /organism='Unidentified'.
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-20       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            14.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x BD007081 (1-660)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         601 GCCTTCCGCATCCGGGCCGTGACCATC 627

RESULT 77
BD136037
LOCUS       BD136037                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136037
VERSION     BD136037.1  GI:23230982
KEYWORDS    JP 2002506647-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 4 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506647-A/4
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                 preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-20       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            14.7%          Indels:        0
DB:                     2              Gaps:          0
```

```
10-821-670A-36 (1-197) x BD136037 (1-660)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 78
.36038
:US       BD136038                 660 bp    DNA     linear   PAT 18-SEP-2002
FINITION  Interferon alpha plasmid and delivery system and method of
          preparing and using the same.
CESSION   BD136038
RSION     BD136038.1  GI:23230983
WORDS     JP 2002506647-A/5.
URCE      synthetic construct
RGANISM   synthetic construct
          other sequences; artificial sequences.
FERENCE   1  (bases 1 to 660)
UTHORS    Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
ITLE      Interferon alpha plasmid and delivery system and method of
          preparing and using the same
OURNAL    Patent: JP 2002506647-A 5 05-MAR-2002;
          VALENTIS INC
MMENT     OS   Artificial Sequence
          PN   JP 2002506647-A/5
          PD   05-MAR-2002
          PF   12-MAR-1999 JP 2000536861
          PR   19-MAR-1998 US    60/078654
          PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
          PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
          PC   C12N1/15,
          PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
           C12N5/00
          CC   Sequence source: all optimized codons
          FH   Key             Location/Qualifiers
          FT   source          1. .660
          FT                   /organism='Artificial Sequence'.
TURES               Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
IGIN

lgnment Scores:
ed. No.:              1.03e-20       Length:         660
ore:                  29.00          Matches:        29
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            14.7%          Indels:         0
:                     2              Gaps:           0

10-821-670A-36 (1-197) x BD136038 (1-660)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       601 GCCTTCCGCATCCGCGCCGTGACCATC 627

SULT 79
.36039
:US       BD136039                 660 bp    DNA     linear   PAT 18-SEP-2002
FINITION  Interferon alpha plasmid and delivery system and method of
          preparing and using the same.
CESSION   BD136039
RSION     BD136039.1  GI:23230984
```

```
KEYWORDS    JP 2002506647-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 6 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/6
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: most codons optimized
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-20       Length:         660
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            14.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x BD136039 (1-660)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         601 GCCTTCCGCATCCGGGCCGTGACCATC 627

RESULT 80
I28592
LOCUS       I28592                   660 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5573764.
ACCESSION   I28592
VERSION     I28592.1  GI:1819368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 3 12-NOV-1996;
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-20       Length:         660
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
```

```
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            14.7%           Indels:        0
                      2               Gaps:          0

-10-821-670A-36 (1-197) x I28592 (1-660)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 81
I54634
CUS       AX154634                660 bp    DNA     linear   PAT 22-JUN-2001
FINITION  Sequence 38 from Patent WO0140257.
CESSION   AX154634
RSION     AX154634.1  GI:14536198
YWORDS    .
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1
AUTHORS   Leong,S.R. and Punnonen,J.
ITLE      Cytokine polypeptides and nucleic acids
JOURNAL   Patent: WO 0140257-A 38 07-JUN-2001;
          Maxygen, Inc. (US)
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
IGIN

lgnment Scores:
ed. No.:              1.03e-20        Length:        660
ore:                  29.00           Matches:       29
cent Similarity:      100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            14.7%           Indels:        0
                      2               Gaps:          0

-10-821-670A-36 (1-197) x AX154634 (1-660)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 82
829447
CUS       CQ829447                702 bp    DNA     linear   PAT 05-JUL-2004
FINITION  Sequence 6 from Patent WO2004052929.
CESSION   CQ829447
RSION     CQ829447.1  GI:49732783
YWORDS    .
URCE      synthetic construct
ORGANISM  synthetic construct
          other sequences; artificial sequences.
FERENCE   1
AUTHORS   Vandenbroeck,K. and Alloza,I.
ITLE      Recombinant cell line
JOURNAL   Patent: WO 2004052929-A 6 24-JUN-2004;
          The Queen's University of Belfast (GB)
ATURES              Location/Qualifiers
   source           1. .702
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="cDNA for alpha chain of IL-12"
ORIGIN

Alignment Scores:
Pred. No.:            1.08e-20        Length:        702
Score:                29.00           Matches:       29
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          14.7%           Indels:        0
DB:                   2               Gaps:          0

US-10-821-670A-36 (1-197) x CQ829447 (1-702)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 615

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||
Db        616 GCTTTCAGAATTCGGGCAGTGACTATT 642

RESULT 83
AR052862
LOCUS       AR052862                721 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 199 from patent US 5833975.
ACCESSION   AR052862
VERSION     AR052862.1  GI:5977724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 199 10-NOV-1998;
FEATURES              Location/Qualifiers
     source           1. .721
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:            1.11e-20        Length:        721
Score:                29.00           Matches:       29
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          14.7%           Indels:        0
DB:                   2               Gaps:          0

US-10-821-670A-36 (1-197) x AR052862 (1-721)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 84
AR288174
LOCUS       AR288174                721 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 199 from patent US 6537594.
ACCESSION   AR288174
VERSION     AR288174.1  GI:31675453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
FERENCE   1  (bases 1 to 721)
AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
ITLE      Vaccina virus comprising cytokine and/or tumor associated antigen
          genes
OURNAL    Patent: US 6537594-A 199 25-MAR-2003;
          Virogenetics Corporation; Troy, NY
ATURES             Location/Qualifiers
   source          1. .721
                   /organism="unknown"
                   /mol_type="mRNA"
IGIN

gnment Scores:
ed. No.:              1.11e-20       Length:        721
re:                   29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
t Local Similarity:   100.0%         Mismatches:    0
ry Match:             14.7%          Indels:        0
                      2              Gaps:          0

 10-821-670A-36 (1-197) x AR288174 (1-721)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

ULT 85
67161
US       AR567161                721 bp    mRNA    linear   PAT 08-OCT-2004
INITION  Sequence 199 from patent US 6780407.
ESSION   AR567161
SION     AR567161.1  GI:53984803
WORDS    .
URCE     Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 721)
AUTHORS  Paoletti,E., Tartaglia,J. and Cox,W.I.
ITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
OURNAL   Patent: US 6780407-A 199 24-AUG-2004;
         Aventis Pasteur; Swiftwater, PA
ATURES             Location/Qualifiers
   source          1. .721
                   /organism="unknown"
                   /mol_type="mRNA"
IGIN

gnment Scores:
ed. No.:              1.11e-20       Length:        721
re:                   29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
t Local Similarity:   100.0%         Mismatches:    0
ry Match:             14.7%          Indels:        0
                      2              Gaps:          0

 10-821-670A-36 (1-197) x AR567161 (1-721)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

ULT 86
05971
US       BD105971                762 bp    DNA     linear   PAT 18-SEP-2002
INITION  Animal model for evaluation of vaccines.
```

```
ACCESSION   BD105971
VERSION     BD105971.1  GI:23200789
KEYWORDS    JP 2002501375-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 21 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/21
            PD   15-JAN-2002
            PF   09-APR-1998 JP 1998543062
            PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
            09-DEC-1997 US    60/069163
            PI   LUNG JI CHANG
            PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
              C12N7/04,
            PC   A61K39/21
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              1.16e-20       Length:        762
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            14.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x BD105971 (1-762)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 87
CQ803343
LOCUS       CQ803343                762 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 3 from Patent WO2004035799.
ACCESSION   CQ803343
VERSION     CQ803343.1  GI:47110209
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 3 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
```

```
:gnment Scores:
ed. No.:                1.16e-20        Length:         762
ore:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-36 (1-197) x CQ803343 (1-762)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 88
533401
:US       AR533401                762 bp    DNA     linear   PAT 08-OCT-2004
FINITION  Sequence 21 from patent US 6730512.
:ESSION   AR533401
:SION     AR533401.1  GI:53923067
:WORDS    .
:RCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 762)
AUTHORS   Chang,L.-J.
:ITLE     Combination immunogene therapy
JOURNAL   Patent: US 6730512-A 21 04-MAY-2004;
          Amdl, Inc.; Tustin, CA
ATURES              Location/Qualifiers
   source           1. .762
                    /organism="unknown"
                    /mol_type="unassigned DNA"
:GIN

:gnment Scores:
ed. No.:                1.16e-20        Length:         762
ore:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-36 (1-197) x AR533401 (1-762)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 89
.01062
:US       AF101062                762 bp    mRNA    linear   PRI 03-MAR-1999
FINITION  Homo sapiens interleukin 12 mRNA, complete cds.
:ESSION   AF101062
:SION     AF101062.1  GI:4323578
:WORDS    .
:RCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 762)
AUTHORS   Liu,y., Guo,Y. and Wu,M.
:ITLE     Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
          Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Liu,Y., Guo,Y. and Wu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1998) Molecular Biology Department, Cancer
            Institute of Second Military Medical University, 800 XianYin Road,
            Shanghai 200433, P.R. China
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /map="3p12-q13.2"
                     /cell_line="lymphoblastoid B-cell line NC37"
                     /note="cells induced by phorbol 12-myristate 13 acetate
                     (PMA) and ionophore A23187"
     CDS             1. .762
                     /note="natural killer cell stimulatory factor; cytotoxic
                     lymphocyte maturation factor 35kDa subunit; p35"
                     /codon_start=1
                     /product="interleukin 12"
                     /protein_id="AAD16432.1"
                     /db_xref="GI:4323579"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
     variation       132
                     /replace="c"
     variation       732
                     /replace="c"
     variation       740
                     /replace="c"
ORIGIN

Alignment Scores:
Pred. No.:              1.16e-20        Length:         762
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-36 (1-197) x AF101062 (1-762)

Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy      179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
Db      703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 90
MMU19842
LOCUS       MMU19842                780 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Macaca mulatta interleukin-12 beta p35 subunit (IL-12b) mRNA,
            complete cds.
ACCESSION   U19842
VERSION     U19842.1  GI:644801
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
```

```
PUBMED   7561102
ERENCE   2  (bases 1 to 780)
UTHORS   Villinger,F.J.
ITLE     Direct Submission
OURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
         Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
TURES             Location/Qualifiers
  source          1. .780
                  /organism="Macaca mulatta"
                  /mol_type="mRNA"
                  /db_xref="taxon:9544"
                  /clone="RNc IL-12b"
                  /cell_type="peripheral blood mononuclear cells"
                  /tissue_type="blood"
  gene            1. .780
                  /gene="IL-12b"
  CDS             10. .771
                  /gene="IL-12b"
                  /function="NK cell stimulatory factor"
                  /codon_start=1
                  /product="interleukin-12 beta p35 subunit"
                  /protein_id="AAA86707.1"
                  /db_xref="GI:644802"
                  /translation="MWPPGSASQPPPSPATATGLHPAARPEPPQCRLSMCPARSLLLV
                  ATLVLLDYLSLARNLSVATPGPEMFPCLHHSQNLLKAASNTLQKARQILEFYPCTSEE
                  IDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTSFMMALCLRS
                  IYEDLKMYQVEFKTMNAKLLRDPKRQIFLDQNILGVIDELMQALNFNSETVPQKSSLE
                  EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
IGIN

gnment Scores:
d. No.:              1.18e-20       Length:        780
re:                  29.00          Matches:       29
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            14.7%          Indels:        0
                     5              Gaps:          0

10-821-670A-36 (1-197) x MMU19842 (1-780)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       652 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 711

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||
       712 GCTTTCAGAATTCGGGCAGTGACTATT 738

SULT 91
80562
US       AF180562                 823 bp    mRNA    linear   PRI 26-SEP-1999
FINITION Homo sapiens interleukin 12, P35 mRNA, complete cds.
CESSION  AF180562
SION     AF180562.1  GI:5923852
WORDS    .
URCE     Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 823)
UTHORS   Hongyuan,J. and Meiyun,Z.
ITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
OURNAL   Unpublished
ERENCE   2  (bases 1 to 823)
UTHORS   Hongyuan,J. and Meiyun,Z.
ITLE     Direct Submission
OURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
         Yingxinjie, Xuanwuqu, Beijing 100052, China
TURES             Location/Qualifiers
   source         1. .823
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /chromosome="3"
                  /map="3p12-q13.2"
                  /cell_type="peripheral mononuclear"
      CDS         60. .821
                  /note="NKSF/CLMF; IL12p35; 35kD"
                  /codon_start=1
                  /product="interleukin 12, P35"
                  /protein_id="AAD56385.1"
                  /db_xref="GI:5923853"
                  /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                  ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                  IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                  IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                  EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

Alignment Scores:
Pred. No.:              1.23e-20       Length:        823
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            14.7%          Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-36 (1-197) x AF180562 (1-823)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 761

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||
Db        762 GCTTTCAGAATTCGGGCAGTGACTATT 788

RESULT 92
BD165801
LOCUS       BD165801                 856 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165801
VERSION     BD165801.1  GI:27871613
KEYWORDS    JP 2002167400-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
  TITLE     Antibody against cytotoxic lymphocyte maturing factors
  JOURNAL   Patent: JP 2002167400-A 2 11-JUN-2002;
            PROTEIN DESIGN LABS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002167400-A/2
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
            PI   GUBLER,
            PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
            PI   ALVIN SETH STERN
            PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
              Antibody against cytotoxic lymphocyte maturing factors FH   Key
                    Location/Qualifiers
            FT   CDS             (170). .(826).
FEATURES              Location/Qualifiers
     source           1. .856
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
```

```
d. No.:                 1.27e-20        Length:         856
re:                     29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               14.7%           Indels:         0
                        2               Gaps:           0

-10-821-670A-36 (1-197) x BD165801 (1-856)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       770 GCTTTCAGAATTCGGGCAGTGACTATT 796

SULT 93
716168
US       CQ716168                1020 bp    DNA     linear   PAT 03-FEB-2004
FINITION  Sequence 2102 from Patent WO02068579.
CESSION  CQ716168
RSION    CQ716168.1  GI:42277025
YWORDS   .
URCE     Homo sapiens (human)
ORGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
FERENCE  1
AUTHORS  Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
ITLE     Kits, such as nucleic acid arrays, comprising a majority of
         humanexons or transcripts, for detecting expression and other uses
         thereof
JOURNAL  Patent: WO 02068579-A 2102 06-SEP-2002;
         PE Corporation (NY) (US)
ATURES             Location/Qualifiers
   source          1. .1020
                   /organism="Homo sapiens"
                   /mol_type="unassigned DNA"
                   /db_xref="taxon:9606"
GIN

gnment Scores:
d. No.:                 1.47e-20        Length:         1020
re:                     29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               14.7%           Indels:         0
                        2               Gaps:           0

-10-821-670A-36 (1-197) x CQ716168 (1-1020)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       703 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 762

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       763 GCTTTCAGAATTCGGGCAGTGACTATT 789

SULT 94
.04982
US       BC104982                1021 bp    mRNA    linear   PRI 19-JAN-2006
FINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
         factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
         (cDNA clone MGC:132642 IMAGE:8143985), complete cds.
CESSION  BC104982
RSION    BC104982.1  GI:85397857
YWORDS   MGC.
URCE     Homo sapiens (human)
ORGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
REFERENCE  1  (bases 1 to 1021)
  AUTHORS  Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
           Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
           Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
           Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
           Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
           Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
           Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
           Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
           Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
           McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
           Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
           Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
           Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
           Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
           Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
           Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
           Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
           Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM  Mammalian Gene Collection Program Team
  TITLE    Generation and initial analysis of more than 15,000 full-length
           human and mouse cDNA sequences
  JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED  12477932
REFERENCE  2  (bases 1 to 1021)
  AUTHORS  .
  CONSRTM  NIH MGC Project
  TITLE    Direct Submission
  JOURNAL  Submitted (13-SEP-2005) National Institutes of Health, Mammalian
           Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT    Contact: MGC help desk
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Mike Brownstein, NIMH
           cDNA Library Preparation: British Columbia Cancer Research Center
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Genome Sequence Centre,
           BC Cancer Agency, Vancouver, BC, Canada
           info@bcgsc.bc.ca
           Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
           Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
           Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
           Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
           Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
           Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
           Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
           Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
           Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

           Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Series: IRCB Plate: 3 Row: j Column: 15.
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:132642 IMAGE:8143985"
                     /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                     /clone_lib="NIH_MGC_287"
                     /note="Vector: pCR4-TOPO with reversed insert; Clone
                     identification sequence tag: TCGTTGCT"
     gene            1. .1021
                     /gene="IL12A"
                     /note="synonyms: IL-12A, NFSK, CLMF"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
     CDS             154. .915
                     /gene="IL12A"
```

/codon_start=1
/product="interleukin 12A, precursor"
/protein_id="AAI04983.1"
/db_xref="GI:85397858"
/db_xref="GeneID:3592"
/db_xref="HGNC:5969"
/db_xref="IMGT/GENE-DB:5969"
/db_xref="MIM:161560"
/translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"

GIN

gnment Scores:

d. No.:	1.47e-20	Length:	1021
re:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	14.7%	Indels:	0
	5	Gaps:	0

10-821-670A-36 (1-197) x BC104982 (1-1021)

```
159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
796 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 855

179 AlaPheArgIleArgAlaValThrIle 187
    |||||||||||||||||||||||||
856 GCTTTCAGAATTCGGGCAGTGACTATT 882
```

ULT 95
04984

US	BC104984 1021 bp mRNA linear PRI 19-JAN-2006
INITION	Homo sapiens interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA (cDNA clone MGC:132644 IMAGE:8143987), complete cds.
ESSION	BC104984
SION	BC104984.1 GI:85397860
WORDS	MGC.
RCE	Homo sapiens (human)
RGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
ERENCE	1 (bases 1 to 1021)
UTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
ONSRTM	Mammalian Gene Collection Program Team
ITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
OURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
ERENCE	2 (bases 1 to 1021)
UTHORS	.

CONSRTM	NIH MGC Project
TITLE	Direct Submission
JOURNAL	Submitted (13-SEP-2005) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Mike Brownstein, NIMH cDNA Library Preparation: British Columbia Cancer Research Center cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRCB Plate: 3 Row: j Column: 17.

FEATURES	Location/Qualifiers
source	1. .1021 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:132644 IMAGE:8143987" /tissue_type="Brain, cerebral cortex, PCR rescued clones" /clone_lib="NIH_MGC_287" /note="Vector: pCR4-TOPO with reversed insert; Clone identification sequence tag: AAATAGCC"
gene	1. .1021 /gene="IL12A" /note="synonyms: IL-12A, NFSK, CLMF" /db_xref="GeneID:3592" /db_xref="HGNC:5969" /db_xref="IMGT/GENE-DB:5969" /db_xref="MIM:161560"
CDS	154. .915 /gene="IL12A" /codon_start=1 /product="interleukin 12A, precursor" /protein_id="AAI04985.1" /db_xref="GI:85397861" /db_xref="GeneID:3592" /db_xref="HGNC:5969" /db_xref="IMGT/GENE-DB:5969" /db_xref="MIM:161560" /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"

ORIGIN

Alignment Scores:

Pred. No.:	1.47e-20	Length:	1021
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-36 (1-197) x BC104984 (1-1021)

```
Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      796 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 855
```

```
       179 AlaPheArgIleArgAlaValThrIle 187
           ||||||||||||||||||||||||||
       856 GCTTTCAGAATTCGGGCAGTGACTATT 882

SULT 96
091390
CUS       AR091390               1026 bp    DNA     linear   PAT 07-SEP-2000
FINITION  Sequence 1 from patent US 5994104.
CESSION   AR091390
RSION     AR091390.1  GI:10018145
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1026)
AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
ITLE      Interleukin-12 fusion protein
JOURNAL   Patent: US 5994104-A 1 30-NOV-1999;
ATURES             Location/Qualifiers
   source          1. .1026
                   /organism="unknown"
                   /mol_type="unassigned DNA"
IGIN

lignment Scores:
ed. No.:              1.48e-20       Length:         1026
ore:                  29.00          Matches:        29
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            14.7%          Indels:         0
                      2              Gaps:           0

-10-821-670A-36 (1-197) x AR091390 (1-1026)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

       179 AlaPheArgIleArgAlaValThrIle 187
           ||||||||||||||||||||||||||
       770 GCTTTCAGAATTCGGGCAGTGACTATT 796

SULT 97
380496
CUS       AR380496               1026 bp    DNA     linear   PAT 18-DEC-2003
FINITION  Sequence 1041 from patent US 6607879.
CESSION   AR380496
RSION     AR380496.1  GI:40088130
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1026)
AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
ITLE      Compositions for the detection of blood cell and immunological
          response gene expression
JOURNAL   Patent: US 6607879-A 1041 19-AUG-2003;
          Incyte Corporation; Palo Alto, CA
ATURES             Location/Qualifiers
   source          1. .1026
                   /organism="unknown"
                   /mol_type="genomic DNA"
IGIN

lignment Scores:
ed. No.:              1.48e-20       Length:         1026
ore:                  29.00          Matches:        29
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            14.7%          Indels:         0
                      2              Gaps:           0

US-10-821-670A-36 (1-197) x AR380496 (1-1026)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              ||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 98
HUMCLMF35
LOCUS       HUMCLMF35              1026 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human cytotoxic lymphocyte maturation factor 35 kDa subunit mRNA,
            complete cds.
ACCESSION   M65271 M38443
VERSION     M65271.1  GI:180623
KEYWORDS    cytotoxic lymphocyte maturation factor 35 kDa subunit; interleukin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
            Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
            and Gately,M.K.
  TITLE     Coexpression of two distinct genes is required to generate secreted
            bioactive cytotoxic lymphocyte maturation factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
   PUBMED   1674604
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             170. .829
                     /codon_start=1
                     /product="cytotoxic lymphocyte maturation factor 35 kDa
                     subunit"
                     /protein_id="AAA35694.1"
                     /db_xref="GI:180624"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
                     SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNML
                     AVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNA
                     S"
ORIGIN

Alignment Scores:
Pred. No.:              1.48e-20       Length:         1026
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            14.7%          Indels:         0
DB:                     5              Gaps:           0

US-10-821-670A-36 (1-197) x HUMCLMF35 (1-1026)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              ||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 99
AR393790
LOCUS       AR393790               1287 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6617135.
ACCESSION   AR393790
```

```
SION     AR393790.1  GI:40120794
WORDS    .
RCE      Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 1287)
UTHORS   Gillies,S.D. and Lo,K.-M.
ITLE     Multiple cytokine protein complexes
OURNAL   Patent: US 6617135-A 6 09-SEP-2003;
         EMD Lexigen Research Center Corp.; Billerica, MA
TURES             Location/Qualifiers
  source          1. .1287
                  /organism="unknown"
                  /mol_type="genomic DNA"
GIN

gnment Scores:
d. No.:              1.79e-20       Length:        1287
re:                  29.00          Matches:       29
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            14.7%          Indels:        0
                     2              Gaps:          0

10-821-670A-36 (1-197) x AR393790 (1-1287)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||
      1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254

ULT 100
84108
US       AX084108               1287 bp    DNA     linear   PAT 28-FEB-2001
INITION  Sequence 6 from Patent WO0110912.
ESSION   AX084108
SION     AX084108.1  GI:13185658
WORDS    .
RCE      synthetic construct
RGANISM  synthetic construct
         other sequences; artificial sequences.
ERENCE   1
UTHORS   Gillies,S.D. and Lo,K.M.
ITLE     Multiple cytokine-antibody complexes
OURNAL   Patent: WO 0110912-A 6 15-FEB-2001;
         Lexigen Pharmaceuticals Corp. (US)
TURES             Location/Qualifiers
  source          1. .1287
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="human Fc-p35 fusion protein coding sequence"
GIN

gnment Scores:
d. No.:              1.79e-20       Length:        1287
re:                  29.00          Matches:       29
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            14.7%          Indels:        0
                     2              Gaps:          0

10-821-670A-36 (1-197) x AX084108 (1-1287)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||
      1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254

Search completed: June 10, 2006, 12:08:00
Job time : 4495.09 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 01:23:11 ; Search time 477.317 Seconds
(without alignments)
4316.416 Million cell updates/sec

le: US-10-821-670A-36
fect score: 197
quence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 5244920 seqs, 3486124231 residues

rd size: 1

al number of hits satisfying chosen parameters: 10484871

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110446_27507/app_query.fasta_1
B=N_Geneseq -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rng -MINMATCH=0.1
OOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
RANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
LIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
AXLEN=2000000000 -HOST=abss05h
SER=US10821670_@CGN_1_1_1666_@runat_07062006_110446_27507 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
AIN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	197	100.0	591	6	ABK98948	Abk98948 Feline in
2	197	100.0	591	6	ABK98949	Abk98949 Feline in
3	197	100.0	591	14	ADV34688	Adv34688 Feline si
c 4	197	100.0	591	14	ADV34690	Adv34690 Feline si
c 5	197	100.0	666	6	ABK98947	Abk98947 Feline in
6	197	100.0	666	6	ABK98946	Abk98946 Feline in
7	197	100.0	666	14	ADV34685	Adv34685 Feline si
c 8	197	100.0	666	14	ADV34687	Adv34687 Feline si
c 9	197	100.0	1533	6	ABK98954	Abk98954 Feline in
10	197	100.0	1533	6	ABK98953	Abk98953 Feline in
c 11	197	100.0	1533	14	ADV34697	Adv34697 Feline si
12	197	100.0	1533	14	ADV34695	Adv34695 Feline si
13	197	100.0	1599	6	ABK98950	Abk98950 Feline in
c 14	197	100.0	1599	6	ABK98951	Abk98951 Feline in
15	197	100.0	1599	14	ADV34691	Adv34691 Feline si
c 16	197	100.0	1599	14	ADV34693	Adv34693 Feline si
17	195	99.0	591	2	AAV56629	Aav56629 Feline FL
18	195	99.0	689	2	AAV56641	Aav56641 Feline FL
19	195	99.0	1441	2	AAV56628	Aav56628 Feline FL
20	187	94.9	561	6	ABK99001	Abk99001 Feline in
c 21	187	94.9	561	6	ABK99002	Abk99002 Feline in
22	187	94.9	561	14	ADV34751	Adv34751 Feline N-
c 23	187	94.9	561	14	ADV34753	Adv34753 Feline N-
24	69	35.0	679	4	AAF26097	Aaf26097 Feline fi
25	59	29.9	660	5	AAD15219	Aad15219 Modified
26	59	29.9	660	5	AAD15214	Aad15214 Modified
27	59	29.9	660	5	AAD15218	Aad15218 Modified
28	56	28.4	660	5	AAD15215	Aad15215 Modified
29	54	27.4	639	4	AAF26098	Aaf26098 Plasmid p
30	54	27.4	669	4	AAF26083	Aaf26083 Feline IL
31	54	27.4	669	4	AAF26086	Aaf26086 Feline IL
32	54	27.4	4201	4	AAF26077	Aaf26077 Feline IL
33	52	26.4	591	2	AAX18179	Aax18179 Canine ma
c 34	52	26.4	591	6	ABK98958	Abk98958 Canine in
35	52	26.4	591	6	ABK98957	Abk98957 Canine in
36	52	26.4	591	14	ADV34701	Adv34701 Canine si
c 37	52	26.4	591	14	ADV34703	Adv34703 Canine si
38	52	26.4	666	6	ABK98955	Abk98955 Canine in
c 39	52	26.4	666	6	ABK98956	Abk98956 Canine in
c 40	52	26.4	666	14	ADV34700	Adv34700 Canine si
41	52	26.4	666	14	ADV34698	Adv34698 Canine si
42	52	26.4	669	2	AAV13818	Aav13818 Canine IL
43	52	26.4	669	2	AAV13819	Aav13819 Canine IL
44	52	26.4	669	2	AAX03163	Aax03163 Nucleic a
45	52	26.4	669	2	AAX03153	Aax03153 Nucleic a
46	52	26.4	669	2	AAX35616	Aax35616 Nucleic a
47	52	26.4	669	2	AAX35626	Aax35626 Nucleic a
48	52	26.4	669	4	AAI64389	Aai64389 Canine co
49	52	26.4	669	4	AAI64379	Aai64379 Canine co
50	52	26.4	669	11	ADZ25701	Adz25701 Canine in
51	52	26.4	1282	2	AAX18178	Aax18178 Canine fu
52	52	26.4	1455	6	ABK99003	Abk99003 Canine in
c 53	52	26.4	1455	6	ABK99004	Abk99004 Canine in
c 54	52	26.4	1455	14	ADV34756	Adv34756 Canine si
55	52	26.4	1455	14	ADV34754	Adv34754 Canine si
56	52	26.4	1533	6	ABK98967	Abk98967 Canine in
c 57	52	26.4	1533	6	ABK98968	Abk98968 Canine in
c 58	52	26.4	1533	14	ADV34718	Adv34718 Canine si
59	52	26.4	1533	14	ADV34716	Adv34716 Canine si
60	52	26.4	1599	6	ABK98965	Abk98965 Canine in
c 61	52	26.4	1599	6	ABK98966	Abk98966 Canine in
c 62	52	26.4	1599	14	ADV34715	Adv34715 Canine si
63	52	26.4	1599	14	ADV34713	Adv34713 Canine si
64	50	25.4	669	13	ADT04852	Adt04852 Canine in
65	43	21.8	666	5	AAD15212	Aad15212 Modified
66	42	21.3	554	2	AAT50757	Aat50757 Partial s
67	40	20.3	703	3	AAA70708	Aaa70708 Bovine in
68	39	19.8	660	5	AAD15213	Aad15213 Modified
69	39	19.8	660	5	AAD15216	Aad15216 Modified
70	39	19.8	660	5	AAD15220	Aad15220 Modified
71	37	18.8	660	5	AAD15217	Aad15217 Modified
72	31	15.7	666	5	AAD15211	Aad15211 Modified
73	29	14.7	201	13	ADQ41825	Adq41825 Myocardia
74	29	14.7	201	13	ADQ41824	Adq41824 Myocardia
75	29	14.7	201	13	ADQ41835	Adq41835 Myocardia

76	29	14.7	201	13	ADQ41829	Adq41829 Myocardia
77	29	14.7	201	13	ADQ41838	Adq41838 Myocardia
78	29	14.7	201	13	ADQ41833	Adq41833 Myocardia
79	29	14.7	630	12	ADF77258	Adf77258 Human IL-
80	29	14.7	657	12	ADG39431	Adg39431 Human CLM
81	29	14.7	660	2	AAQ97485	Aaq97485 Human int
82	29	14.7	660	2	AAV07274	Aav07274 Human Int
83	29	14.7	660	2	AAV07218	Aav07218 DNA encod
84	29	14.7	660	2	AAZ40408	Aaz40408 Human int
85	29	14.7	660	2	AAZ40407	Aaz40407 Human int
86	29	14.7	660	2	AAZ40409	Aaz40409 Human int
87	29	14.7	660	5	AAD15221	Aad15221 Human cyt
88	29	14.7	660	6	AAL44226	Aal44226 Human int
89	29	14.7	660	6	ACC47589	Acc47589 Human int
90	29	14.7	660	12	ADF77245	Adf77245 Human IL-
91	29	14.7	660	12	ADF77257	Adf77257 Human IL-
92	29	14.7	660	12	ADF77246	Adf77246 Human IL-
93	29	14.7	660	12	ADF77244	Adf77244 Human IL-
94	29	14.7	683	4	AAF26096	Aaf26096 Human pG-
95	29	14.7	702	12	ADP88401	Adp88401 Human int
96	29	14.7	721	2	AAQ67880	Aaq67880 EPV 42 kD
97	29	14.7	721	2	AAZ08515	Aaz08515 Vaccinia
98	29	14.7	721	13	ADR21891	Adr21891 Vaccinia
99	29	14.7	761	10	ADK98708	Adk98708 Human int
100	29	14.7	761	10	ADK98706	Adk98706 Human int
101	29	14.7	762	2	AAV83207	Aav83207 Interleuk
102	29	14.7	762	3	AAA35201	Aaa35201 Human ade
103	29	14.7	762	3	AAF21323	Aaf21323 Human low
104	29	14.7	762	10	ABZ97017	Abz97017 Human nuc
105	29	14.7	762	11	ABD20866	Abd20866 Human pul
106	29	14.7	762	12	ADO07654	Ado07654 Human int
107	29	14.7	762	13	ADS88021	Ads88021 Tumour tr
108	29	14.7	762	14	ADV42511	Adv42511 Human psy
109	29	14.7	823	10	ACD26420	Acd26420 cDNA enco
110	29	14.7	856	2	AAQ12150	Aaq12150 Cytotoxic
111	29	14.7	856	2	AAT77850	Aat77850 35 kDa su
112	29	14.7	856	2	AAT97970	Aat97970 35 kDa su
113	29	14.7	856	2	AAV00402	Aav00402 35 kDa su
114	29	14.7	856	2	AAV37772	Aav37772 Cytotoxic
115	29	14.7	856	12	ADG39389	Adg39389 Human cyt
116	29	14.7	856	12	ADO03760	Ado03760 Human CLM
117	29	14.7	889	13	ADU04652	Adu04652 Human ext
118	29	14.7	1026	3	AAZ40020	Aaz40020 Human p35
119	29	14.7	1026	8	ACA61266	Aca61266 DNA encod
120	29	14.7	1026	11	ADI31715	Adi31715 Human cDN
121	29	14.7	1026	13	ADS83782	Ads83782 Human lym
122	29	14.7	1172	8	ACC42373	Acc42373 Human ext
123	29	14.7	1200	8	ACF64408	Acf64408 Human IL1
124	29	14.7	1287	4	AAF76882	Aaf76882 DNA encod
125	29	14.7	1289	8	ACC42375	Acc42375 Human ext
126	29	14.7	1316	2	AAT63621	Aat63621 Interleuk
127	29	14.7	1316	6	AAD41639	Aad41639 Human int
128	29	14.7	1364	2	AAT48099	Aat48099 Human int
129	29	14.7	1364	2	AAV42536	Aav42536 Human int
130	29	14.7	1364	2	AAV15228	Aav15228 Heterodim
131	29	14.7	1364	3	AAZ28863	Aaz28863 Human int
132	29	14.7	1364	4	AAF56281	Aaf56281 IL-12 vac
133	29	14.7	1384	15	AEF92723	Aef92723 Human int
134	29	14.7	1396	2	AAQ24371	Aaq24371 Natural k
135	29	14.7	1444	12	ACF57533	Acf57533 Human IL1
136	29	14.7	1444	12	ADJ62891	Adj62891 Human int
137	29	14.7	1444	12	ADN12152	Adn12152 Interleuk
138	29	14.7	1444	14	ADY15785	Ady15785 DNA encod
139	29	14.7	1444	14	ADZ26544	Adz26544 Human IL1
140	29	14.7	1444	14	AEB56478	Aeb56478 Radiochem
141	29	14.7	1494	12	ADQ59495	Adq59495 Human can
142	29	14.7	1526	12	ADQ59549	Adq59549 Human can
143	29	14.7	1532	13	ADQ38388	Adq38388 Human SNP
144	29	14.7	1532	14	ADZ13866	Adz13866 Human can
145	29	14.7	1607	13	ADQ38387	Adq38387 Human SNP
146	29	14.7	1607	14	ADZ13864	Adz13864 Human can
147	29	14.7	2300	3	AAA92406	Aaa92406 Human int
148	29	14.7	2336	14	AEE03207	Aee03207 Human int
149	29	14.7	2390	12	ADM29103	Adm29103 Human int
150	29	14.7	3205	14	AEB48820	Aeb48820 Monoclona
151	29	14.7	4521	3	AAA35204	Aaa35204 Human ade
152	29	14.7	4521	3	AAF21326	Aaf21326 Human low
153	29	14.7	4521	10	ABZ97020	Abz97020 Human nuc
154	29	14.7	4521	11	ABD20869	Abd20869 Human pul
155	29	14.7	5013	14	AEA40941	Aea40941 T-DNA reg
156	29	14.7	5686	2	AAZ40415	Aaz40415 Plasmid p
157	29	14.7	5686	12	ADF77239	Adf77239 Human IL-
158	29	14.7	6139	3	AAZ40023	Aaz40023 Interleuk
159	29	14.7	8578	6	AAD31546	Aad31546 pIRES-hB7
160	29	14.7	8578	6	AAD31545	Aad31545 pIRES-hB7
161	29	14.7	8608	6	AAD31548	Aad31548 pIRES-hB7
162	29	14.7	8623	6	AAD31547	Aad31547 pIRES-hB7
163	29	14.7	8629	6	AAD31552	Aad31552 pIRES-IL1
164	29	14.7	8638	6	AAD31549	Aad31549 pIRES-hB7
165	29	14.7	8644	6	AAD31551	Aad31551 pIRES-IL1
166	29	14.7	8659	6	AAD31550	Aad31550 pIRES-IL1
167	29	14.7	11441	6	AAL44225	Aal44225 Human int
168	29	14.7	11453	10	ADG25152	Adg25152 Vector pS
169	29	14.7	11569	10	ADG25150	Adg25150 Vector pA
170	29	14.7	27277	12	ADQ59494	Adq59494 Human can
171	29	14.7	27277	14	ADZ13863	Adz13863 Human can
172	28	14.2	700	8	ACF64405	Acf64405 Human IL1
173	26	13.2	79	2	AAV56639	Aav56639 Feline FL
174	26	13.2	79	2	AAX18181	Aax18181 Primer fo
175	25	12.7	666	2	AAT50758	Aat50758 Sequence
176	23	11.7	71	4	AAF26092	Aaf26092 Feline IL
177	23	11.7	71	4	AAF26099	Aaf26099 Feline Il
178	20	10.2	201	13	ADQ41830	Adq41830 Myocardia
179	20	10.2	201	13	ADQ41821	Adq41821 Myocardia
180	20	10.2	700	8	ACF64406	Acf64406 Human IL1
181	20	10.2	700	8	ACF64407	Acf64407 Human IL1
182	18	9.1	76	4	AAF26100	Aaf26100 Feline Il
c 183	18	9.1	76	4	AAF26093	Aaf26093 Feline IL
c 184	18	9.1	76	4	AAF26090	Aaf26090 Feline IL
185	13	6.6	60	6	ABN39662	Abn39662 Human spl
186	13	6.6	660	2	AAV31481	Aav31481 Human int
187	13	6.6	660	2	AAZ40421	Aaz40421 Human int
188	13	6.6	660	12	ADF77255	Adf77255 Human IL-
c 189	12	6.1	36	2	AAV56640	Aav56640 Feline FL
c 190	12	6.1	36	2	AAX18182	Aax18182 Primer fo
191	11	5.6	39	6	ABK98991	Abk98991 Synthetic
192	11	5.6	39	14	ADV34741	Adv34741 Feline IL
193	10	5.1	60	6	ABK98983	Abk98983 Feline se
c 194	10	5.1	60	6	ABK98984	Abk98984 Feline an
c 195	10	5.1	60	14	ADV34734	Adv34734 Feline IL
196	10	5.1	60	14	ADV34733	Adv34733 Feline IL
197	10	5.1	582	4	AAF76877	Aaf76877 Mature mu
198	10	5.1	660	2	AAX78396	Aax78396 IL-12p35
199	10	5.1	660	2	AAX25946	Aax25946 Interleuk
200	10	5.1	713	2	AAT35199	Aat35199 Mouse int

ALIGNMENTS

RESULT 1
ABK98948
ID ABK98948 standard; cDNA; 591 BP.
XX
AC ABK98948;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69305.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 1; Page 56-57; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.86e-192	Length:	591
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98948 (1-591)

```
          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy      141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy      161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy      181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

RESULT 2
ABK98949/c
ID ABK98949 standard; cDNA; 591 BP.
XX
AC ABK98949;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 58; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.86e-192	Length:	591
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

```
                    6             Gaps:          0

US-10-821-670A-36 (1-197) x ABK98949 (1-591)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

SULT 3
/34688
   ADV34688 standard; cDNA; 591 BP.

   ADV34688;

   24-FEB-2005  (first entry)

   Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; gene; ss.

   Felis catus.

   Key             Location/Qualifiers
   CDS             1. .591
                   /*tag=  a
                   /product= "PFeIL-12p35 197 protein"
                   /partial
                   /note= "No start and stop codon"

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.

PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34689.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 35; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.86e-192      Length:          591
Score:                  197.00         Matches:         197
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     14             Gaps:            0

US-10-821-670A-36 (1-197) x ADV34688 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
```

```
       181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

SULT 4
V34690/c
ADV34690 standard; DNA; 591 BP.

ADV34690;

24-FEB-2005 (first entry)

Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Felis catus.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 3; SEQ ID NO 37; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain mature IL-12p35 subunit complementary DNA.

Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

gnment Scores:			
ed. No.:	6.86e-192	Length:	591
ore:	197.00	Matches:	197
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	100.0%	Indels:	0
:	14	Gaps:	0

-10-821-670A-36 (1-197) x ADV34690 (1-591)

```
         1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

        21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

        41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412
```

```
Qy      61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy      81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy     101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy     121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy     141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy     161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy     181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 5
ABK98947/c
ID ABK98947 standard; cDNA; 666 BP.
XX
AC ABK98947;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 56; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,

or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

```
.gnment Scores:
ed. No.:              7.7e-192      Length:         666
ore:                  197.00        Matches:        197
cent Similarity:      100.0%        Conservative:   0
t Local Similarity:   100.0%        Mismatches:     0
ry Match:             100.0%        Indels:         0
                      6             Gaps:           0

-10-821-670A-36 (1-197) x ABK98947 (1-666)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

SULT 6
:98946
   ABK98946 standard; cDNA; 666 BP.

   ABK98946;

   21-OCT-2002  (first entry)

   Feline interleukin-12 nFeIL-12p35-666 coding strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; gene; ss.
```

```
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.7e-192      Length:         666
Score:                  197.00        Matches:        197
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            100.0%        Indels:         0
DB:                     6             Gaps:           0

US-10-821-670A-36 (1-197) x ABK98946 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
```

```
      121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

      141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

      161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

      181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
```

SULT 7
V34685
ADV34685 standard; cDNA; 666 BP.

ADV34685;

24-FEB-2005 (first entry)

Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; gene; ss.

Felis catus.

Key	Location/Qualifiers
CDS	1. .666
	/*tag= a
	/product= "PFeIL-12p35 222 protein "
	/partial
	/note= "No stop codon"

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.
P-PSDB; ADV34686.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Claim 23; SEQ ID NO 32; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12p35 subunit protein encoding full-length cDNA.

Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.7e-192	Length:	666
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-36 (1-197) x ADV34685 (1-666)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
```

RESULT 8
ADV34687/c
ID ADV34687 standard; DNA; 666 BP.
XX
AC ADV34687;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 3; SEQ ID NO 34; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12p35 subunit full-length complementary DNA.

Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

gnment Scores:			
ed. No.:	7.7e-192	Length:	666
ore:	197.00	Matches:	197
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	100.0%	Indels:	0
	14	Gaps:	0

10-821-670A-36 (1-197) x ADV34687 (1-666)

```
  1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

 21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

 61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

 81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
    |||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db 51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
ABK98954/c
ID ABK98954 standard; cDNA; 1533 BP.
XX
AC ABK98954;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 66-67; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1.73e-191	Length:	1533
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98954 (1-1533)

```
Qy   1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy  21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472
```

```
 41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

 61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

 81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
    |||||||||||||||||||||||||||||||||||||||||||||||||||
 51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

SULT 10
K98953
ABK98953 standard; cDNA; 1533 BP.

ABK98953;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12-1533 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69307.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 63-64; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.73e-191	Length:	1533
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98953 (1-1533)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

RESULT 11
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Felis catus.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 3; SEQ ID NO 45; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12 complementary DNA.

Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:

ed. No.:	1.73e-191	Length:	1533
ore:	197.00	Matches:	197
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	100.0%	Indels:	0
	14	Gaps:	0

10-821-670A-36 (1-197) x ADV34697 (1-1533)

```
          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy      141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy      161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy      181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 12
ADV34695
ID ADV34695 standard; cDNA; 1533 BP.
XX
AC ADV34695;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .1533
FT		/*tag= a
FT		/product= "PFeIL-12 511 protein"
FT		/partial
FT		/note= "No start and stop codon"

XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34696.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.73e-191	Length:	1533
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0

```
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            100.0%        Indels:        0
:                     14            Gaps:          0

-10-821-670A-36 (1-197) x ADV34695 (1-1533)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

SULT 13
K98950
   ABK98950 standard; cDNA; 1599 BP.

   ABK98950;

   21-OCT-2002  (first entry)

   Feline interleukin-12 nFeIL-12-1599 coding strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; gene; ss.

   Felis catus.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.8e-191      Length:          1599
Score:                  197.00        Matches:         197
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            100.0%        Indels:          0
DB:                     6             Gaps:            0

US-10-821-670A-36 (1-197) x ABK98950 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548
```

```
       181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

ULT 14
98951/c
   ABK98951 standard; cDNA; 1599 BP.

   ABK98951;

   21-OCT-2002  (first entry)

   Feline interleukin-12 nFeIL-12-1599 complementary strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; ss.

   Felis catus.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Claim 6; Page 61-62; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a feline interleukin 12 DNA sequence, as described in
   the invention

   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

gnment Scores:
d. No.:              1.8e-191      Length:        1599
re:                  197.00        Matches:       197
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            100.0%        Indels:        0
                     6             Gaps:          0

10-821-670A-36 (1-197) x ABK98951 (1-1599)

         1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

        21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy       101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy       121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy       141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy       161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy       181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 15
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
```

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Claim 24; SEQ ID NO 38; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12 protein encoding cDNA.

Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

```
ignment Scores:
ed. No.:                1.8e-191        Length:         1599
ore:                    197.00          Matches:        197
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              100.0%          Indels:         0
:                       14              Gaps:           0

-10-821-670A-36 (1-197) x ADV34691 (1-1599)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

SULT 16
V34693/c
   ADV34693 standard; DNA; 1599 BP.

   ADV34693;

   24-FEB-2005  (first entry)
```

```
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.8e-191        Length:         1599
Score:                  197.00          Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x ADV34693 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232
```

```
       121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

       141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

       161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

       181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
        51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

```
;ULT 17
/56629
   AAV56629 standard; cDNA; 591 BP.

   AAV56629;

   23-NOV-1998  (first entry)

   Feline FLAFp35 cDNA mature transcript.

   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
   T lymphocyte cell; autoimmune disease; ds.

   Felis catus.

   WO9746583-A1.

   11-DEC-1997.

   29-MAY-1997;   97WO-JP001824.

   04-JUN-1996;   96JP-00165249.

   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.

   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;

   WPI; 1998-042118/04.
   P-PSDB; AAW76176.

   Novel feline cytokine protein - useful for treating feline auto:immune
   diseases, e.g. those caused by feline herpes virus or feline calcivirus.

   Claim 23; Page 59; 94pp; Japanese.

   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
   This protein can be used in the production of a FLAFp35/FLAFp40
   heterodimer which can potentiate the cytotoxic activity of feline
   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
   feline autoimmune diseases e.g. as caused by feline herpes virus or
   feline calcivirus

   Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 U; 0 Other;

.gnment Scores:
:d. No.:              7.66e-190      Length:        591
)re:                  195.00         Matches:       195
:cent Similarity:     100.0%         Conservative:  0
:t Local Similarity:  100.0%         Mismatches:    0
:ry Match:            99.0%          Indels:        0
                      2              Gaps:          0

-10-821-670A-36 (1-197) x AAV56629 (1-591)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585
```

```
RESULT 18
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
```

FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40 heterodimer which can potentiate the cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins are used for treatment of feline autoimmune diseases e.g. as caused by feline herpes virus or feline calcivirus

Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

Alignment Scores:

ed. No.:	8.89e-190	Length:	689
ore:	195.00	Matches:	195
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	99.0%	Indels:	0
:	2	Gaps:	0

-10-821-670A-36 (1-197) x AAV56641 (1-689)

```
          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666
```

SULT 19
V56628
AAV56628 standard; cDNA; 1441 BP.

AAV56628;

23-NOV-1998 (first entry)

Feline FLAFp35 cDNA.

Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment; T lymphocyte cell; autoimmune disease; ds.

Felis catus.

FH Key Location/Qualifiers
FT CDS 133. .811
FT /*tag= a
FT sig_peptide 133. .217
FT /*tag= b
FT mat_peptide 218. .808
FT /*tag= c
FT /product= "FLAFp35"
FT /note= "feline cytokine"
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76175.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 22; Page 57-58; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC which can potentiate the cytotoxic activity of feline cytotoxic T
CC lymphocyte cells. Such proteins are used for treatment of feline
CC autoimmune diseases e.g. as caused by feline herpes virus or feline
CC calcivirus
XX
SQ Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.81e-189	Length:	1441
Score:	195.00	Matches:	195
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.0%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-36 (1-197) x AAV56628 (1-1441)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577
```

```
       121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

       141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

       161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

       181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
           |||||||||||||||||||||||||||||||||||||||||||||
       758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

SULT 20
C99001
   ABK99001 standard; cDNA; 561 BP.

   ABK99001;

   21-OCT-2002  (first entry)

   Feline interleukin-12 nFeIL-12p35-N561 coding strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; gene; ss.

   Felis catus.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.
   P-PSDB; ABG69315.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Disclosure; Page 92-93; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a feline interleukin 12 DNA sequence, as described in
   the invention

   Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

gnment Scores:
d. No.:              1.13e-181      Length:        561
re:                  187.00         Matches:       187
```

```
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            94.9%           Indels:        0
DB:                     6               Gaps:          0

US-10-821-670A-36 (1-197) x ABK99001 (1-561)

Qy          11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy          31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy          51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy          71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy          91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy         111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy         131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy         151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy         171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy         191 MetSerTyrLeuAsnAlaSer 197
               |||||||||||||||||||||
Db         541 ATGAGCTATCTGAATGCTTCC 561

RESULT 21
ABK99002/c
ID   ABK99002 standard; cDNA; 561 BP.
XX
AC   ABK99002;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12nFeIL-12p35-N561 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
```

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Disclosure; Page 94; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Alignment Scores:

ed. No.:	1.13e-181	Length:	561
ore:	187.00	Matches:	187
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	94.9%	Indels:	0
:	6	Gaps:	0

-10-821-670A-36 (1-197) x ABK99002 (1-561)

```
        11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

        31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

        51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

        71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

        91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

       111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

       131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

       151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

       171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22
```

```
Qy         191 MetSerTyrLeuAsnAlaSer 197
               |||||||||||||||||||||
Db          21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 22
ADV34751
ID ADV34751 standard; cDNA; 561 BP.
XX
AC ADV34751;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal single chain IL-12p35 cDNA, nFeIL-12p35-N561.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .561
FT		/*tag= a
FT		/product= "PFeIL-12p35-N187 protein"
FT		/partial
FT		/note= "No start and stop codon"

XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34752.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 101; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline N-terminal single chain IL-12p35 subunit
CC protein encoding cDNA.
XX
SQ Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.13e-181	Length:	561
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	94.9%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-36 (1-197) x ADV34751 (1-561)

```
Qy          11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
```

```
        31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

        51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

        71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

        91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

       111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

       131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

       151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

       171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

       191 MetSerTyrLeuAsnAlaSer 197
           |||||||||||||||||||||
       541 ATGAGCTATCTGAATGCTTCC 561
```

```
SULT 23
J34753/c
   ADV34753 standard; cDNA; 561 BP.

   ADV34753;

   24-FEB-2005  (first entry)

   Feline N-terminal IL-12p35 complementary DNA, nFeIL-12p35-N561.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; gene; ss.

   Felis catus.

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Disclosure; SEQ ID NO 103; 103pp; English.
```

```
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein complementary DNA.
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.13e-181      Length:          561
Score:                  187.00         Matches:         187
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            94.9%          Indels:          0
DB:                     14             Gaps:            0

US-10-821-670A-36 (1-197) x ADV34753 (1-561)

Qy          11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy          31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy          51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy          71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy          91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy         111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy         131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy         151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy         171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy         191 MetSerTyrLeuAsnAlaSer 197
               |||||||||||||||||||||
Db          21 ATGAGCTATCTGAATGCTTCC 1
```

```
RESULT 24
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
```

immunostimulant; tumor; antiviral; antitumor; interferon-gamma; Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.

Felis sp.

WO200104155-A2.

18-JAN-2001.

08-JUL-2000; 2000WO-DE002263.

08-JUL-1999; 99CH-00001259.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.
(REGC) UNIV CALIFORNIA.

Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;

WPI; 2001-147178/15.

Recombinant feline interleukin-12, useful as immunostimulant and for treating e.g. viral infections in cats, and related nucleic acid constructs.

Disclosure; Fig 2; 35pp; German.

This invention describes a novel feline interleukin-12 (fIL-12) polypeptide (I) that is expressed, by recombinant gene expression in eukaryotic or prokaryotic cells, in the form of both polypeptide chains of subunits p35 and p40. These proteins are formed so that, in equimolar concentrations and in presence of an immunizing antigen, they can be administered to carnivores, particularly domestic cats. The invention also describes a nucleic acid construct (II) encoding fIL-12 containing sequences at least 95% identical with the p40- and p35-encoding sequences (A, 990 bp and B, 669 bp respectively), reproduced in the specification, as immunostimulants for immunization against infectious diseases and/or for treating infections or tumors in felines, especially domestic cats. The products of the invention have immunostimulatory, antiviral and antitumor activity. Nucleic acid constructs that encode (II) are useful as adjuvants for prophylactic immunization against viral diseases and for treating diseases associated with a Th1 defect. IL-12 induces synthesis of interferon gamma (Th1 response). The feline interleukin-12 polypeptide is useful for carnivores, and particularly domestic cats in the following: (i) as immunostimulant, for preventative or therapeutic use; and (ii) treating tumors and autoimmune diseases, or diseases associated with a Th1 defect, especially pre-existing infections by feline immune deficiency virus (FIV), feline leukemia virus and corona virus

Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.92e-61	Length:	679
Score:	69.00	Matches:	69
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	35.0%	Indels:	0
DB:	4	Gaps:	0

-10-821-670A-36 (1-197) x AAF26097 (1-679)

```
         89 LeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAsp 108
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        340 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 399

        109 LeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLys 128
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        400 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 459

        129 ArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeu 148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        460 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 519
```

```
Qy      149 AsnValAsnSerValThrValProGln 157
            |||||||||||||||||||||||||||
Db      520 AATGTCAACAGTGTGACTGTGCCACAG 546
```

RESULT 25
AAD15219
ID AAD15219 standard; DNA; 660 BP.
XX
AC AAD15219;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-157.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a
FT		/product= "Modified p35 protein precursor"
FT	sig_peptide	1. .66
FT		/*tag= b
FT	mat_peptide	67. .657
FT		/*tag= c
FT		/product= "Mature modified p35 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08612.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 140; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 660 BP; 181 A; 178 C; 144 G; 157 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.5e-50	Length:	660
Score:	59.00	Matches:	59
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	29.9%	Indels:	0
DB:	5	Gaps:	0

```
10-821-670A-36 (1-197) x AAD15219 (1-660)

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 99
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

       100 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

       120 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       424 AATGCAAAGCTGTTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

SULT 26
)15214
   AAD15214 standard; DNA; 660 BP.

   AAD15214;

   01-NOV-2001  (first entry)

   Modified human cytokine p35 encoding DNA from clone R2-631.

   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
   p35; mutant; ds.

   Homo sapiens.
   Synthetic.

   Key             Location/Qualifiers
   CDS             1. .660
                   /*tag=  a
                   /product= "Modified p35 protein precursor"
   sig_peptide     1. .66
                   /*tag=  b
   mat_peptide     67. .657
                   /*tag=  c
                   /product= "Mature modified p35 protein"

   WO200140257-A2.

   07-JUN-2001.

   30-NOV-2000; 2000WO-US032664.

   02-DEC-1999;   99US-0169035P.
   28-NOV-2000; 2000US-00725324.

   (MAXY-) MAXYGEN INC.

   Leong SR,  Punnonen J;

   WPI; 2001-502381/55.
   P-PSDB; AAE08607.

   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
   and p35 polypeptides), useful for treating various diseases e.g. diabetic
   retinopathy and cancer.

   Claim 87; Page 139; 223pp; English.

   The invention relates to nucleic acids encoding modified cytokine
   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
   gamma induction activities. The polypeptides and polynucleotides of the
   invention are useful for treating various diseases e.g. bacterial
   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
   vaccinated host's cell-mediated immunity for protective response to a
   pathogen. The present sequence is a modified human p35 protein encoding

CC   DNA
XX
SQ   Sequence 660 BP; 182 A; 178 C; 142 G; 158 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.5e-50       Length:          660
Score:                  59.00         Matches:         59
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            29.9%         Indels:          0
DB:                     5             Gaps:            0

US-10-821-670A-36 (1-197) x AAD15214 (1-660)

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

Qy        100 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy        120 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 27
AAD15218
ID   AAD15218 standard; DNA; 660 BP.
XX
AC   AAD15218;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-162.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08611.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
```

Claim 87; Page 140; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is a modified human p35 protein encoding DNA

Sequence 660 BP; 182 A; 180 C; 144 G; 154 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	1.5e-50	Length:	660
ore:	59.00	Matches:	59
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	29.9%	Indels:	0
:	5	Gaps:	0

-10-821-670A-36 (1-197) x AAD15218 (1-660)

```
         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 99
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACAACC 363

        100 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 119
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

        120 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 138
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
        424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480
```

SULT 28
D15215
AAD15215 standard; DNA; 660 BP.

AAD15215;

01-NOV-2001 (first entry)

Modified human cytokine p35 encoding DNA from clone R2-613.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p35; mutant; ds.

Homo sapiens.
Synthetic.

Key	Location/Qualifiers
CDS	1. .660
	/*tag= a
	/product= "Modified p35 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .657
	/*tag= c
	/product= "Mature modified p35 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.
28-NOV-2000; 2000US-00725324.

PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08608.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 139-140; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 660 BP; 190 A; 171 C; 137 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.77e-47	Length:	660
Score:	56.00	Matches:	56
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	28.4%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-36 (1-197) x AAD15215 (1-660)

```
Qy          83 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu 102
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         313 ATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTT 372

Qy         103 SerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLys 122
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         373 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 432

Qy         123 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 138
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         433 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480
```

RESULT 29
AAF26098
ID AAF26098 standard; DNA; 639 BP.
XX
AC AAF26098;
XX
DT 24-APR-2001 (first entry)
XX
DE Plasmid pMOL-fIL12 p35 DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.

(UYZU-) UNIV ZUERICH.
(REGC) UNIV CALIFORNIA.

Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;

WPI; 2001-147178/15.

Recombinant feline interleukin-12, useful as immunostimulant and for treating e.g. viral infections in cats, and related nucleic acid constructs.

Disclosure; Fig 2; 35pp; German.

This invention describes a novel feline interleukin-12 (fIL-12) polypeptide (I) that is expressed, by recombinant gene expression in eukaryotic or prokaryotic cells, in the form of both polypeptide chains of subunits p35 and p40. These proteins are formed so that, in equimolar concentrations and in presence of an immunizing antigen, they can be administered to carnivores, particularly domestic cats. The invention also describes a nucleic acid construct (II) encoding fIL-12 containing sequences at least 95% identical with the p40- and p35-encoding sequences (A, 990 bp and B, 669 bp respectively), reproduced in the specification, as immunostimulants for immunization against infectious diseases and/or for treating infections or tumors in felines, especially domestic cats. The products of the invention have immunostimulatory, antiviral and antitumor activity. Nucleic acid constructs that encode (II) are useful as adjuvants for prophylactic immunization against viral diseases and for treating diseases associated with a Th1 defect. IL-12 induces synthesis of interferon gamma (Th1 response). The feline interleukin-12 polypeptide is useful for carnivores, and particularly domestic cats in the following: (i) as immunostimulant, for preventative or therapeutic use; and (ii) treating tumors and autoimmune diseases, or diseases associated with a Th1 defect, especially pre-existing infections by feline immune deficiency virus (FIV), feline leukemia virus and corona virus

Sequence 639 BP; 189 A; 166 C; 133 G; 151 T; 0 U; 0 Other;

.gnment Scores:
ed. No.: 1.92e-45 Length: 639
ore: 54.00 Matches: 54
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ery Match: 27.4% Indels: 0
4 Gaps: 0

10-821-670A-36 (1-197) x AAF26098 (1-639)

```
 91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
293 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 352

111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
353 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 412

131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
    ||||||||||||||||||||||||||||||||||||||||
413 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 454
```

SULT 30
26083
AAF26083 standard; DNA; 669 BP.

AAF26083;

24-APR-2001 (first entry)

Feline IL-12p35 encoding DNA SEQ ID 4.

Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection; interleukin; antiviral; cytotoxic immune response; Th1 response; ds.

Felis sp.

XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Claim 14; Page 37; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2e-45 Length: 669
Score: 54.00 Matches: 54
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 27.4% Indels: 0
DB: 4 Gaps: 0

US-10-821-670A-36 (1-197) x AAF26083 (1-669)

```
Qy          91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy         111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy         131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
               ||||||||||||||||||||||||||||||||||||||||
Db         466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507
```

RESULT 31
AAF26086
ID AAF26086 standard; DNA; 669 BP.
XX
AC AAF26086;
XX
DT 24-APR-2001 (first entry)
XX

Feline IL-12p35 encoding DNA.

Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection; immunostimulant; tumor; antiviral; antitumor; interferon-gamma; Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.

Felis sp.

WO200104155-A2.

18-JAN-2001.

08-JUL-2000; 2000WO-DE002263.

08-JUL-1999; 99CH-00001259.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.
(REGC) UNIV CALIFORNIA.

Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;

WPI; 2001-147178/15.

Recombinant feline interleukin-12, useful as immunostimulant and for treating e.g. viral infections in cats, and related nucleic acid constructs.

Claim 3; Page 31; 35pp; German.

This invention describes a novel feline interleukin-12 (fIL-12) polypeptide (I) that is expressed, by recombinant gene expression in eukaryotic or prokaryotic cells, in the form of both polypeptide chains of subunits p35 and p40. These proteins are formed so that, in equimolar concentrations and in presence of an immunizing antigen, they can be administered to carnivores, particularly domestic cats. The invention also describes a nucleic acid construct (II) encoding fIL-12 containing sequences at least 95% identical with the p40- and p35-encoding sequences (A, 990 bp and B, 669 bp respectively), reproduced in the specification, as immunostimulants for immunization against infectious diseases and/or for treating infections or tumors in felines, especially domestic cats. The products of the invention have immunostimulatory, antiviral and antitumor activity. Nucleic acid constructs that encode (II) are useful as adjuvants for prophylactic immunization against viral diseases and for treating diseases associated with a Th1 defect. IL-12 induces synthesis of interferon gamma (Th1 response). The feline interleukin-12 polypeptide is useful for carnivores, and particularly domestic cats in the following: (i) as immunostimulant, for preventative or therapeutic use; and (ii) treating tumors and autoimmune diseases, or diseases associated with a Th1 defect, especially pre-existing infections by feline immune deficiency virus (FIV), feline leukemia virus and corona virus

Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2e-45	Length:	669
Score:	54.00	Matches:	54
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	27.4%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-36 (1-197) x AAF26086 (1-669)

```
Qy         91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
              ||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507
```

RESULT 32
AAF26077
ID AAF26077 standard; DNA; 4201 BP.
XX
AC AAF26077;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Disclosure; Page 31-33; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.19e-44	Length:	4201
Score:	54.00	Matches:	54
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	27.4%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-36 (1-197) x AAF26077 (1-4201)

```
Qy         91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3392 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 3451
```

```
       111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3452 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 3511

       131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
           |||||||||||||||||||||||||||||||||||||||||||
      3512 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 3553
```

SULT 33
(18179
AAX18179 standard; cDNA; 591 BP.

AAX18179;

07-MAY-1999 (first entry)

Canine mature CLAF p35 subunit coding sequence.

CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog; viral disease; canine distemper; canine parvovirus; autoimmune disease; canine infectious hepatitis; ds.

Canis sp.

WO9855511-A1.

10-DEC-1998.

26-MAY-1998; 98WO-JP002295.

03-JUN-1997; 97JP-00161936.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Imamura T, Maeda H, Tokiyoshi S, Eda Y;

WPI; 1999-070260/06.
P-PSDB; AAW74325.

Canine cytokine protein which activates canine cytotoxic T lymphocytes - is useful for treatment of viral and autoimmune diseases in dogs.

Claim 8; Page 34-35; 51pp; Japanese.

This sequence encodes the canine lymphocyte activation factor (CLAF) of the invention. CLAF activates lymphocytes, especially canine cytotoxic T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies recognising it may be used in the treatment of viral diseases in dogs (such as canine distemper, canine parvovirus and canine infectious hepatitis). The antibodies may also be used in isolation of CLAF from culture of the transformant host cells by affinity chromatography. The p40 homodimer can be used for the treatment of autoimmune diseases in dogs

Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

gnment Scores:

ed. No.:	1.98e-43	Length:	591
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	26.4%	Indels:	0
	2	Gaps:	0

10-821-670A-36 (1-197) x AAX18179 (1-591)

```
        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy       80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||||
Db      238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273
```

RESULT 34
ABK98958/c
ID ABK98958 standard; cDNA; 591 BP.
XX
AC ABK98958;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p35-591 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 70; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.98e-43	Length:	591
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.4%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98958 (1-591)

```
Qy       40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415
```

```
        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 35
K98957
   ABK98957 standard; cDNA; 591 BP.

   ABK98957;

   21-OCT-2002  (first entry)

   Canine interleukin-12 nCaIL-12p35-591 coding strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; gene; ss.

   Canis familiaris.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.
   P-PSDB; ABG69309.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Claim 1; Page 69; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a canine interleukin 12 DNA sequence, as described in
   the invention

   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              1.98e-43        Length:         591
ore:                  52.00           Matches:        52
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            26.4%           Indels:         0
:                     6               Gaps:           0

-10-821-670A-36 (1-197) x ABK98957 (1-591)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy      60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy      80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||||
Db     238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 36
ADV34701
ID   ADV34701 standard; cDNA; 591 BP.
XX
AC   ADV34701;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag= a
FT                   /product= "PCaIL-12P35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34702.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 49; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.98e-43        Length:         591
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.4%           Indels:         0
```

```
                    14              Gaps:          0

-10-821-670A-36 (1-197) x ADV34701 (1-591)

         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

;ULT 37
'34703/c
   ADV34703 standard; DNA; 591 BP.

   ADV34703;

   24-FEB-2005  (first entry)

   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 591.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; ds.

   Canis familiaris.

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Example 4; SEQ ID NO 51; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the canine single chain IL-12p35 subunit
   complementary DNA.

   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

.gnment Scores:
:d. No.:              1.98e-43        Length:         591
)re:                  52.00           Matches:        52
:cent Similarity:     100.0%          Conservative:   0
:t Local Similarity:  100.0%          Mismatches:     0
:ry Match:            26.4%           Indels:         0
                      14              Gaps:           0

-10-821-670A-36 (1-197) x ADV34703 (1-591)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 38
ABK98955
ID   ABK98955 standard; cDNA; 666 BP.
XX
AC   ABK98955;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69308.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 67-68; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:            2.23e-43        Length:         666
Score:                52.00           Matches:        52
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          26.4%           Indels:         0
```

```
:                    6              Gaps:          0

-10-821-670A-36 (1-197) x ABK98955 (1-666)

         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 39
K98956/c
   ABK98956 standard; cDNA; 666 BP.

   ABK98956;

   21-OCT-2002  (first entry)

   Canine interleukin-12 nCaIL-12p35-66 complementary strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; ss.

   Canis familiaris.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Disclosure; Page 68-69; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a canine interleukin 12 DNA sequence, as described in
   the invention

   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              2.23e-43       Length:          666
ore:                  52.00          Matches:         52
rcent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%       Mismatches:      0
Query Match:            26.4%        Indels:          0
DB:                     6            Gaps:            0

US-10-821-670A-36 (1-197) x ABK98956 (1-666)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 40
ADV34700/c
ID   ADV34700 standard; DNA; 666 BP.
XX
AC   ADV34700;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 48; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.23e-43       Length:          666
Score:                  52.00          Matches:         52
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            26.4%          Indels:          0
DB:                     14             Gaps:            0
```

```
-10-821-670A-36 (1-197) x ADV34700 (1-666)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 41
/34698
   ADV34698 standard; cDNA; 666 BP.

   ADV34698;

   24-FEB-2005  (first entry)

   Canine single chain IL-12p35 full-length cDNA, nCaIL-12p35 666.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; gene; ss.

   Canis familiaris.

   Key             Location/Qualifiers
   CDS             1. .666
                   /*tag=  a
                   /product= "PCaIL-12p222 protein"
                   /partial
                   /note= "No stop codon"

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.
   P-PSDB; ADV34699.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Example 4; SEQ ID NO 46; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the canine single chain IL-12p35 subunit protein
   encoding full-length cDNA.

   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

.gnment Scores:
:d. No.:              2.23e-43       Length:        666
Score:                52.00          Matches:       52
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          26.4%          Indels:        0
DB:                   14             Gaps:          0

US-10-821-670A-36 (1-197) x ADV34698 (1-666)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 42
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:            2.24e-43       Length:        669
Score:                52.00          Matches:       52
```

```
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            26.4%           Indels:        0
:                     2               Gaps:          0

-10-821-670A-36 (1-197) x AAV13818 (1-669)

         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 43
V13819
   AAV13819 standard; cDNA to mRNA; 669 BP.

   AAV13819;

   14-MAY-1998  (first entry)

   Canine IL-12 P35 subunit cDNA.

   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
   antiviral; vaccine adjuvant; ds.

   Canis sp.

   Key             Location/Qualifiers
   CDS             1. .669
                   /*tag=  a
                   /product= "interleukin-12_P35_subunit"

   JP10036397-A.

   10-FEB-1998.

   08-NOV-1996;   96JP-00296789.

   08-NOV-1995;   95JP-00289729.
   23-MAY-1996;   96JP-00128104.

   (TORA ) TORAY IND INC.

   WPI; 1998-174914/16.
   P-PSDB; AAW41793.

   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
   activities are expected.

   Claim 11; Page 11-12; 12pp; Japanese.

   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
   antiviral activating factor and the expression of class II MHC molecules
   in canine tumour cells, stimulating proliferation of canine blastogenic
   lymphocytes and activating canine leukocytes to inhibit canine tumour
   cells. The canine IL-12 can be used in veterinary medicines, e.g.
   antitumour, antivirus and vaccine adjuvant activities are expected

   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 U; 0 Other;

:gnment Scores:
ed. No.:              2.24e-43        Length:        669
ore:                  52.00           Matches:       52
rcent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.4%         Indels:        0
DB:                     2             Gaps:          0

US-10-821-670A-36 (1-197) x AAV13819 (1-669)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 44
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
```

skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis and hair loss; infections; dog Parvovirus infection and distemper virus, cat plaque virus infection and feline leukaemia, and allergic diseases, e.g. pollinosis

Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

.gnment Scores:
:d. No.: 2.24e-43 Length: 669
:re: 52.00 Matches: 52
:cent Similarity: 100.0% Conservative: 0
:t Local Similarity: 100.0% Mismatches: 0
:ry Match: 26.4% Indels: 0
2 Gaps: 0

10-821-670A-36 (1-197) x AAX03163 (1-669)

```
 40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

 60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

 80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
    |||||||||||||||||||||||||||||||||||
313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

;ULT 45
(03153
AAX03153 standard; cDNA to mRNA; 669 BP.

AAX03153;

30-MAR-1999 (first entry)

Nucleic acid encoding canine interleukin 12.

Canine; interleukin 12; IL-12; feline; immunological disease; tumour; skin disease; viral infection; allergic disease; breast tumour; oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma; othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour; otitis externa; dermatitis; eczema; fungal skin disease; pyoderma; allergic dermatitis; nettle rash; traumatic dermatitis; hair loss; dog Parvovirus infection; distemper virus; cat plaque virus infection; feline leukaemia; allergy; pollinosis; ds.

Canis sp.

Key	Location/Qualifiers
CDS	1. .669
	/*tag= a
	/product= "interleukin_12"

WO9851327-A1.

19-NOV-1998.

07-MAY-1998; 98WO-JP002031.

16-MAY-1997; 97JP-00127690.

(TORA) TORAY IND INC.

Okano F, Satoh M, Yamada K;

WPI; 1999-070100/06.
P-PSDB; AAW84372.

New therapeutic and prophylactic agents - comprise genetically-engineered canine interleukin 12, used to treat, e.g. canine and feline immunological diseases.

XX
PS Claim 1; Page 26-27; 45pp; Japanese.
XX
CC The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC IL-12 protein can be used in therapeutic or prophylactic agents. The
CC agents can be used to prevent and treat canine and feline immunological
CC diseases including dog and cat tumours, skin diseases, viral infections
CC and allergic diseases, especially tumours, breast tumour, oesinophilic
CC granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC and hair loss; infections; dog Parvovirus infection and distemper virus,
CC cat plaque virus infection and feline leukaemia, and allergic diseases,
CC e.g. pollinosis
XX
SQ Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.24e-43 Length: 669
Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.4% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-36 (1-197) x AAX03153 (1-669)

```
Qy       40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy       60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy       80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
Db      313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

RESULT 46
AAX35616
ID AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC AAX35616;
XX
DT 09-JUL-1999 (first entry)
XX
DE Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .669
FT /*tag= a
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-00133345.
XX
PR 16-MAY-1997; 97JP-00127690.
PR 07-AUG-1997; 97JP-00213755.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR P-PSDB; AAY02340.
XX

A prevention and treating agent containing interleukin 12 (CaIL12) - for prevention and treatment of dog and cat immune diseases.

Claim 1; Page 13; 16pp; Japanese.

The present sequence encodes canine interleukin-12 (IL-12). The specification describes a method for the prevention and treatment of dog and cat immune diseases. The treatment used an agent comprising dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is useful for preventing and treating dog and cat immune diseases, including tumours, skin diseases, infectious diseases and allergic diseases

Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

:gnment Scores:

ed. No.:	2.24e-43	Length:	669
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.4%	Indels:	0
:	2	Gaps:	0

-10-821-670A-36 (1-197) x AAX35616 (1-669)

```
Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

SULT 47
X35626
AAX35626 standard; cDNA to mRNA; 669 BP.

AAX35626;

09-JUL-1999 (first entry)

Nucleic acid encoding canine Interleukin-12 (IL-12).

Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer; tumour; skin disease; infectious disease; allergic disease; ds.

Canis sp.

Key	Location/Qualifiers
CDS	1. .669
	/*tag= a

JP11106350-A.

20-APR-1999.

15-MAY-1998; 98JP-00133345.

16-MAY-1997; 97JP-00127690.
07-AUG-1997; 97JP-00213755.

(TORA) TORAY IND INC.

WPI; 1999-308068/26.
P-PSDB; AAY02343.

A prevention and treating agent containing interleukin 12 (CaIL12) - for prevention and treatment of dog and cat immune diseases.

Claim 1; Page 15-16; 16pp; Japanese.

XX
CC The present sequence encodes canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment of dog
CC and cat immune diseases. The treatment used an agent comprising dog IL-12
CC (CaIL12) proteins to form a heterodimer. The agent is useful for
CC preventing and treating dog and cat immune diseases, including tumours,
CC skin diseases, infectious diseases and allergic diseases
XX
SQ Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.24e-43	Length:	669
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.4%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-36 (1-197) x AAX35626 (1-669)

```
Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

RESULT 48
AAI64389
ID AAI64389 standard; DNA; 669 BP.
XX
AC AAI64389;
XX
DT 23-NOV-2001 (first entry)
XX
DE Canine coding sequence #4.
XX
KW Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS Canis familiaris.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .669
FT		/*tag= a
FT		/product= "Canine protein #4"
FT	sig_peptide	1. .75
FT		/*tag= b
FT	mat_peptide	76. .666
FT		/*tag= c

XX
PN JP2001161378-A.
XX
PD 19-JUN-2001.
XX
PF 26-SEP-2000; 2000JP-00292946.
XX
PR 01-OCT-1999; 99JP-00281234.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 2001-592466/67.
DR P-PSDB; AAG66483.
XX
PT Preparation of a highly pure protein, interleukin 12, a protein
PT inhibiting the activity of interleukin 12, and a treating agent and a
PT treating method for immunopathy of mammalian.
XX
PS Claim 6; Page 18; 21pp; Japanese.

The present invention relates to a method for the preparation of a highly pure protein in which interleukin 12 (IL12) and/or a protein inhibiting the activity of IL12 is contacted to an ion exchanging carrier and/or a pigment carrier to get IL12 and/or a protein inhibiting the activity of IL12. The protein is used as a preventive agent for dog immunopathy. The present sequence was used in the method of the present invention

Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

.gnment Scores:
:d. No.: 2.24e-43 Length: 669
)re: 52.00 Matches: 52
:cent Similarity: 100.0% Conservative: 0
:t Local Similarity: 100.0% Mismatches: 0
:ry Match: 26.4% Indels: 0
: 4 Gaps: 0

·10-821-670A-36 (1-197) x AAI64389 (1-669)

```
        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

SULT 49
:64379
AAI64379 standard; DNA; 669 BP.

AAI64379;

23-NOV-2001 (first entry)

Canine coding sequence #2.

Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.

Canis familiaris.

Key	Location/Qualifiers
CDS	1. .669
	/*tag= a
	/product= "Canine protein #2"
sig_peptide	1. .75
	/*tag= b
mat_peptide	76. .666
	/*tag= c

JP2001161378-A.

19-JUN-2001.

26-SEP-2000; 2000JP-00292946.

01-OCT-1999; 99JP-00281234.

(TORA) TORAY IND INC.

WPI; 2001-592466/67.
P-PSDB; AAG66481.

Preparation of a highly pure protein, interleukin 12, a protein inhibiting the activity of interleukin 12, and a treating agent and a treating method for immunopathy of mammalian.

Claim 6; Page 15; 21pp; Japanese.

XX
CC The present invention relates to a method for the preparation of a highly
CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC IL12. The protein is used as a preventive agent for dog immunopathy. The
CC present sequence was used in the method of the present invention
XX
SQ Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.24e-43 Length: 669
Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.4% Indels: 0
DB: 4 Gaps: 0

US-10-821-670A-36 (1-197) x AAI64379 (1-669)

```
Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

RESULT 50
ADZ25701
ID ADZ25701 standard; cDNA; 669 BP.
XX
AC ADZ25701;
XX
DT 16-JUN-2005 (first entry)
XX
DE Canine interleukin 12 P35 encoding cDNA SEQ ID NO:6.
XX
KW interleukin-12; antiviral; gene; ss.
XX
OS Canis sp.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .669
FT		/*tag= b
FT		/product= "interleukin-12 P40"
FT	sig_peptide	1. .75
FT		/*tag= a
FT	mat_peptide	76. .666
FT		/*tag= c
FT		/product= "interleukin-12 P40"

XX
PN JP2003284585-A.
XX
PD 07-OCT-2003.
XX
PF 28-MAR-2002; 2002JP-00090161.
XX
PR 28-MAR-2002; 2002JP-00090161.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 2003-885430/82.
DR P-PSDB; ADZ25703.
XX
PT Large scale production of interleukin-12 for pharmaceutical applications,
PT comprises infecting an insect cell with a recombinant virus containing
PT gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT of insect cell.

Example; SEQ ID NO 6; 8pp; Japanese.

The invention related to the large scale production of interleukin-12 (IL -12), which involves infecting an insect cell with a recombinant virus containing a gene encoding IL-12, and producing IL-12 by carrying out spinner culture of insect cell. The method is useful for producing IL-12, preferably canine IL-12. IL-12 has pharmaceutical applications. The present sequence encodes canine IL-12 P35, which is used in the exemplification of the present invention.

Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	2.24e-43	Length:	669
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.4%	Indels:	0
:	11	Gaps:	0

-10-821-670A-36 (1-197) x ADZ25701 (1-669)

```
Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

SULT 51
X18178
AAX18178 standard; cDNA; 1282 BP.

AAX18178;

07-MAY-1999 (first entry)

Canine full length CLAF p35 subunit coding sequence.

CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog; viral disease; canine distemper; canine parvovirus; autoimmune disease; canine infectious hepatitis; ds.

Canis sp.

WO9855511-A1.

10-DEC-1998.

26-MAY-1998; 98WO-JP002295.

03-JUN-1997; 97JP-00161936.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Imamura T, Maeda H, Tokiyoshi S, Eda Y;

WPI; 1999-070260/06.
P-PSDB; AAW74324.

Canine cytokine protein which activates canine cytotoxic T lymphocytes - is useful for treatment of viral and autoimmune diseases in dogs.

Claim 8; Page 33-34; 51pp; Japanese.

This sequence encodes the canine lymphocyte activation factor (CLAF) of the invention. CLAF activates lymphocytes, especially canine cytotoxic T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies recognising it may be used in the treatment of viral diseases in dogs (such as canine distemper, canine parvovirus and canine infectious hepatitis). The antibodies may also be used in isolation of CLAF from culture of the transformant host cells by affinity chromatography. The p40 homodimer can be used for the treatment of autoimmune diseases in dogs

Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.2e-43	Length:	1282
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.4%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-36 (1-197) x AAX18178 (1-1282)

```
Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         258 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 317

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         318 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 377

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         378 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 413
```

RESULT 52
ABK99003
ID ABK99003 standard; cDNA; 1455 BP.
XX
AC ABK99003;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p35-1455 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69316.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 4; Page 94-95; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain

proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

.gnment Scores:

ɔd. No.:	4.74e-43	Length:	1455
ɔre:	52.00	Matches:	52
·cent Similarity:	100.0%	Conservative:	0
;t Local Similarity:	100.0%	Mismatches:	0
ɛry Match:	26.4%	Indels:	0
	6	Gaps:	0

·10-821-670A-36 (1-197) x ABK99003 (1-1455)

```
        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579
```

ɜULT 53
‹99004/c
ABK99004 standard; cDNA; 1455 BP.

ABK99004;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12p35-1455 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 4; Page 96; 106pp; English.

CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.74e-43	Length:	1455
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.4%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK99004 (1-1455)

```
Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877
```

RESULT 54
ADV34756/c
ID ADV34756 standard; DNA; 1455 BP.
XX
AC ADV34756;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 1455.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 106; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the canine single chain IL-12p35 subunit complementary DNA.

Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

:gnment Scores:
:d. No.: 4.74e-43 Length: 1455
:ore: 52.00 Matches: 52
:cent Similarity: 100.0% Conservative: 0
:st Local Similarity: 100.0% Mismatches: 0
:ery Match: 26.4% Indels: 0
: 14 Gaps: 0

-10-821-670A-36 (1-197) x ADV34756 (1-1455)

```
        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877
```

SULT 55
V34754
ADV34754 standard; cDNA; 1455 BP.

ADV34754;

24-FEB-2005 (first entry)

Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 1455.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; gene; ss.

Canis familiaris.

Key	Location/Qualifiers
CDS	232. .900
	/*tag= a
	/product= "PCaIL-12p35 222 protein"

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.
P-PSDB; ADV34755.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a

PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 104; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p35 subunit protein
CC encoding cDNA.
XX
SQ Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.74e-43 Length: 1455
Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.4% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-36 (1-197) x ADV34754 (1-1455)

```
Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579
```

RESULT 56
ABK98967
ID ABK98967 standard; cDNA; 1533 BP.
XX
AC ABK98967;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69314.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.

Claim 6; Page 83-85; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

.gnment Scores:

ed. No.:	4.99e-43	Length:	1533
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.4%	Indels:	0
	6	Gaps:	0

-10-821-670A-36 (1-197) x ABK98967 (1-1533)

```
        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
      1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215
```

SULT 57
(98968/c
ABK98968 standard; cDNA; 1533 BP.

ABK98968;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12-1533 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and

PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 86-87; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.99e-43	Length:	1533
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.4%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98968 (1-1533)

```
Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319
```

RESULT 58
ADV34718/c
ID ADV34718 standard; DNA; 1533 BP.
XX
AC ADV34718;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 4; SEQ ID NO 68; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the canine single chain IL-12 complementary DNA.

Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

```
ignment Scores:
ed. No.:              4.99e-43      Length:        1533
ore:                  52.00         Matches:       52
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            26.4%         Indels:        0
:                     14            Gaps:          0

-10-821-670A-36 (1-197) x ADV34718 (1-1533)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 59
V34716
   ADV34716 standard; cDNA; 1533 BP.

   ADV34716;

   24-FEB-2005  (first entry)

   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; gene; ss.

   Canis familiaris.

   Key             Location/Qualifiers
   CDS             1. .1533
                   /*tag= a
                   /product= "PCaIL-12 511 protein"
                   /partial
                   /note= "No start and stop codon"

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;
```

```
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.99e-43      Length:        1533
Score:                  52.00         Matches:       52
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.4%         Indels:        0
DB:                     14            Gaps:          0

US-10-821-670A-36 (1-197) x ADV34716 (1-1533)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 60
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69313.
```

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 79-80; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

.gnment Scores:
ed. No.: 5.2e-43 Length: 1599
ore: 52.00 Matches: 52
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 26.4% Indels: 0
: 6 Gaps: 0

10-821-670A-36 (1-197) x ABK98965 (1-1599)

```
        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
      1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281
```

SULT 61
(98966/c
ABK98966 standard; cDNA; 1599 BP.

ABK98966;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12-1599 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 82-83; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.2e-43 Length: 1599
Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.4% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-36 (1-197) x ABK98966 (1-1599)

```
Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319
```

RESULT 62
ADV34715/c
ID ADV34715 standard; DNA; 1599 BP.
XX
AC ADV34715;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 4; SEQ ID NO 63; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the canine single chain IL-12 complementary DNA.

Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

```
:gnment Scores:
ed. No.:                5.2e-43         Length:         1599
ore:                    52.00           Matches:        52
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              26.4%           Indels:         0
:                       14              Gaps:           0

-10-821-670A-36 (1-197) x ADV34715 (1-1599)

         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 63
V34713
   ADV34713 standard; cDNA; 1599 BP.

   ADV34713;

   24-FEB-2005  (first entry)

   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; gene; ss.

   Canis familiaris.

   Key             Location/Qualifiers
   CDS             1. .1599
                   /*tag=  a
                   /product= "PCaIL-12 533 protein"
                   /partial
                   /note= "No stop codon"

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.2e-43         Length:         1599
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.4%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x ADV34713 (1-1599)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db        1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 64
ADT04852
ID   ADT04852 standard; DNA; 669 BP.
XX
AC   ADT04852;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p35 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
```

Novel gene vector for expression in insect useful for expression of foreign gene such as dog interleukin 12 gene, comprises two promoters.

Claim 4; SEQ ID NO 8; 13pp; Japanese.

The invention relates to a novel gene vector for expression in an insect comprising at least two promoters, particularly the polyhedrin promoter and p10 promoter. The vector contains at least two types of foreign protein expression gene and the gene product of the vector is produced using a gene recombinant baculovirus, particularly a recombinant silkworm nuclear polyhedrosis virus. The baculovirus is proliferated in a silkworm. The vector of the invention may be useful for expression of a foreign gene, such as canine interleukin 12. Within the vector, two types of foreign protein expression genes are integrated simultaneously for their simultaneous expression. The current sequence is that of the canine interleukin-12 (IL-12) p35 DNA of the invention.

Sequence 669 BP; 183 A; 177 C; 145 G; 164 T; 0 U; 0 Other;

.gnment Scores:

;d. No.:	2.5e-41	Length:	669
›re:	50.00	Matches:	50
:cent Similarity:	100.0%	Conservative:	0
;t Local Similarity:	100.0%	Mismatches:	0
;ry Match:	25.4%	Indels:	0
	13	Gaps:	0

-10-821-670A-36 (1-197) x ADT04852 (1-669)

```
        42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAG 258

        62 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 81
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

        82 LeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||
       319 TTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

;ULT 65
)15212
AAD15212 standard; DNA; 666 BP.

AAD15212;

01-NOV-2001 (first entry)

Modified human cytokine p35 encoding DNA from clone R2-146.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p35; mutant; ds.

Homo sapiens.
Synthetic.

Key	Location/Qualifiers
CDS	1. .666
	/*tag= a
	/product= "Modified p35 protein precursor"
sig_peptide	1. .75
	/*tag= b
mat_peptide	76. .663
	/*tag= c
	/product= "Mature modified p35 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08605.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 139; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 666 BP; 186 A; 179 C; 141 G; 160 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.65e-34	Length:	666
Score:	43.00	Matches:	43
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	21.8%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-36 (1-197) x AAD15212 (1-666)

```
Qy         71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

Qy         91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAG 402

Qy        111 MetTyrGln 113
              ||||||||
Db        403 ATGTACCAG 411
```

RESULT 66
AAT50757
ID AAT50757 standard; cDNA; 554 BP.
XX
AC AAT50757;
XX
DT 17-OCT-2003 (revised)
DT 24-SEP-1997 (first entry)
XX
DE Partial sequence of ovine IL-12 35 kD sununit cDNA.
XX
KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW immunosuppression; allergy; reproductive system; growth; early maturity;
KW antibody; diagnosis; immunopotentiator;
KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.
XX
OS Ovis aries.
XX
PN WO9700321-A1.

```
   03-JAN-1997.

   14-JUN-1996;   96WO-AU000360.

   14-JUN-1995;   95AU-00003502.
   27-OCT-1995;   95AU-00006244.

   (CSIR ) COMMONWEALTH SCI & IND RES ORG.

   Seow H,  Wood P;

   WPI; 1997-077528/07.
   P-PSDB; AAW08481.

   Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
   adjuvants and to treat or prevent microbial infections in livestock.

   Claim 8; Page 43-44; 78pp; English.

   The sequences given in AAT50757-59 encode ovine interleukin-12 (IL-12) 35
   kD subunit (partial and full length sequence) and the 40 kD subunit.
   Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
   livestock (esp. cows and sheep), particularly where the animals are
   stressed, e.g. during transport. IL-5 and IL-12 can also be used as
   adjuvants in vaccines for veterinary use (partic. weakly immunogenic
   subunit or synthetic peptide vaccines). They may also be used to treat
   cancer, immunosuppression and allergy, to enhance/suppress the
   reproductive system and to promote growth or early maturity. Optionally
   interleukin can be delivered from constructs or delivery cells and
   antibodies are useful in enzyme immunoassays for rapid diagnosis of
   infection. The interleukins are immunopotentiators, especially IL-5
   promotes growth of early haematopoietic progenitor cells and generation
   of cytotoxic cells from thymocytes, also it stimulates production and
   secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
   induces production of gamma-interferon by, and proliferation of, T and NK
   cells and increases the (non-)specific cytolytic lymphocyte response. The
   genetic constructs can also be used for in vitro production of IL-5 or -
   12. (Updated on 17-OCT-2003 to standardise OS field)

   Sequence 554 BP; 159 A; 144 C; 124 G; 127 T; 0 U; 0 Other;

ignment Scores:
ed. No.:               3.23e-33       Length:        554
ore:                   42.00          Matches:       42
rcent Similarity:      100.0%         Conservative:  0
st Local Similarity:   100.0%         Mismatches:    0
ery Match:             21.3%          Indels:        0
:                      2              Gaps:          0

-10-821-670A-36 (1-197) x AAT50757 (1-554)

        27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        96 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 155

        47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       156 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 215

        67 GluLeu 68
           ||||||
       216 GAATTA 221

SULT 67
A70708
   AAA70708 standard; DNA; 703 BP.

   AAA70708;

   15-DEC-2000  (first entry)

   Bovine interleukin-12 p35 subunit gene.

XX
KW   Antiinfective; bovine; interleukin 12; IL12; heterodimer; infection; ss.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .677
FT                   /*tag=  a
FT                   /product= "IL-12 p35 subunit"
XX
PN   JP2000157274-A.
XX
PD   13-JUN-2000.
XX
PF   20-NOV-1998;   98JP-00331052.
XX
PR   20-NOV-1998;   98JP-00331052.
XX
PA   (DAUC ) DAIICHI PHARM CO LTD.
XX
DR   WPI; 2000-468201/41.
DR   P-PSDB; AAB15391.
XX
PT   Preparation of bovine interleukin 12 comprising using a vector containing
PT   the gene encoding it, useful for the prevention and treatment of chronic
PT   and opportunistic infections.
XX
PS   Example 1; Page 8-9; 11pp; Japanese.
XX
CC   The invention relates to a method for the preparation of bovine
CC   interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35 and p40
CC   subunits. BoIL12 is produced by introducing into a host cell, recombinant
CC   vectors containing genes encoding the p35 and p40 subunits. This sequence
CC   represents the coding region for the bovine IL12 p35 subunit. Interleukin
CC   12 is used for the prevention and treatment of chronic infections and
CC   opportunistic infections
XX
SQ   Sequence 703 BP; 188 A; 194 C; 157 G; 164 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             4.54e-31       Length:        703
Score:                 40.00          Matches:       40
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           20.3%          Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-36 (1-197) x AAA70708 (1-703)

Qy         29 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 ACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 227

Qy         49 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 287

RESULT 68
AAD15213
ID   AAD15213 standard; DNA; 660 BP.
XX
AC   AAD15213;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-796.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
```

```
Key             Location/Qualifiers
CDS             1. .660
                /*tag=  a
                /product= "Modified p35 protein precursor"
sig_peptide     1. .66
                /*tag=  b
mat_peptide     67. .657
                /*tag=  c
                /product= "Mature modified p35 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999;   99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR,  Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08606.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
and p35 polypeptides), useful for treating various diseases e.g. diabetic
retinopathy and cancer.

Claim 87; Page 139; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine
polypeptides (i.e. modified p40 and p35 polypeptides). The modified
cytokine polypeptides have T-cell proliferative and interferon (IFN)-
gamma induction activities. The polypeptides and polynucleotides of the
invention are useful for treating various diseases e.g. bacterial
infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
polynucleotide may also be useful as a vaccine adjuvant, to enhance a
vaccinated host's cell-mediated immunity for protective response to a
pathogen. The present sequence is a modified human p35 protein encoding
DNA

Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

.gnment Scores:
:d. No.:              4.51e-30      Length:         660
)re:                  39.00         Matches:        39
:cent Similarity:     100.0%        Conservative:   0
:t Local Similarity:  100.0%        Mismatches:     0
:ry Match:            19.8%         Indels:         0
                      5             Gaps:           0

 10-821-670A-36 (1-197) x AAD15213 (1-660)

        30 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 49
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

        50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

;ULT 69
)15216
   AAD15216 standard; DNA; 660 BP.

   AAD15216;

   01-NOV-2001  (first entry)

   Modified human cytokine p35 encoding DNA from clone R2-571.

XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08609.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 184 A; 172 C; 141 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.51e-30      Length:         660
Score:                  39.00         Matches:        39
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            19.8%         Indels:         0
DB:                     5             Gaps:           0

US-10-821-670A-36 (1-197) x AAD15216 (1-660)

Qy         30 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 270

RESULT 70
AAD15220
```

AAD15220 standard; DNA; 660 BP.

AAD15220;

01-NOV-2001 (first entry)

Modified human cytokine p35 encoding DNA from clone R1-4-87.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p35; mutant; ds.

Homo sapiens.
Synthetic.

Key	Location/Qualifiers
CDS	1. .660
	/*tag= a
	/product= "Modified p35 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .657
	/*tag= c
	/product= "Mature modified p35 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR, Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08613.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides), useful for treating various diseases e.g. diabetic retinopathy and cancer.

Claim 87; Page 140-141; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is a modified human p35 protein encoding DNA

Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	4.51e-30	Length:	660
ore:	39.00	Matches:	39
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	19.8%	Indels:	0
:	5	Gaps:	0

-10-821-670A-36 (1-197) x AAD15220 (1-660)

```
Qy         30 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270
```

RESULT 71
AAD15217
ID AAD15217 standard; DNA; 660 BP.
XX
AC AAD15217;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-555.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a
FT		/product= "Modified p35 protein precursor"
FT	sig_peptide	1. .66
FT		/*tag= b
FT	mat_peptide	67. .657
FT		/*tag= c
FT		/product= "Mature modified p35 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08610.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 140; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 660 BP; 189 A; 173 C; 136 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.04e-28	Length:	660
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	18.8%	Indels:	0

```
                    5             Gaps:          0

10-821-670A-36 (1-197) x AAD15217 (1-660)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

       179 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       601 GCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

SULT 72
)15211
   AAD15211 standard; DNA; 666 BP.

   AAD15211;

   01-NOV-2001  (first entry)

   Modified human cytokine p35 encoding DNA from clone R2-42.

   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
   p35; mutant; ds.

   Homo sapiens.
   Synthetic.

   Key             Location/Qualifiers
   CDS             1. .666
                   /*tag= a
                   /product= "Modified p35 protein precursor"
   sig_peptide     1. .75
                   /*tag= b
   mat_peptide     76. .663
                   /*tag= c
                   /product= "Mature modified p35 protein"

   WO200140257-A2.

   07-JUN-2001.

   30-NOV-2000; 2000WO-US032664.

   02-DEC-1999;   99US-0169035P.
   28-NOV-2000; 2000US-00725324.

   (MAXY-) MAXYGEN INC.

   Leong SR,  Punnonen J;

   WPI; 2001-502381/55.
   P-PSDB; AAE08604.

   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
   and p35 polypeptides), useful for treating various diseases e.g. diabetic
   retinopathy and cancer.

   Claim 87; Page 139; 223pp; English.

   The invention relates to nucleic acids encoding modified cytokine
   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
   gamma induction activities. The polypeptides and polynucleotides of the
   invention are useful for treating various diseases e.g. bacterial
   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
   vaccinated host's cell-mediated immunity for protective response to a
   pathogen. The present sequence is a modified human p35 protein encoding
   DNA

   Sequence 666 BP; 186 A; 181 C; 141 G; 158 T; 0 U; 0 Other;

   Alignment Scores:
   Pred. No.:              7.07e-22        Length:         666
   Score:                  31.00           Matches:        31
   Percent Similarity:     100.0%          Conservative:   0
   Best Local Similarity:  100.0%          Mismatches:     0
   Query Match:            15.7%           Indels:         0
   DB:                     5               Gaps:           0

   US-10-821-670A-36 (1-197) x AAD15211 (1-666)

   Qy          71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db         283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

   Qy          91 SerArgLysThrSerPheMetThrThrLeuCys 101
               |||||||||||||||||||||||||||||||||
   Db         343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGC 375

   RESULT 73
   ADQ41825
   ID   ADQ41825 standard; DNA; 201 BP.
   XX
   AC   ADQ41825;
   XX
   DT   18-NOV-2004  (first entry)
   XX
   DE   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3488.
   XX
   KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
   KW   cardiant; gene therapy; human; ds.
   XX
   OS   Homo sapiens.
   XX
   PN   WO2004058052-A2.
   XX
   PD   15-JUL-2004.
   XX
   PF   22-DEC-2003; 2003WO-US040978.
   XX
   PR   20-DEC-2002; 2002US-0434778P.
   PR   10-MAR-2003; 2003US-0453135P.
   PR   30-APR-2003; 2003US-0466412P.
   PR   23-SEP-2003; 2003US-0504955P.
   XX
   PA   (APPL-) APPLERA CORP.
   XX
   PI   Cargill M,  Devlin JJ,  Iakoubova O;
   XX
   DR   WPI; 2004-533949/51.
   XX
   PT   Identifying an individual who has an altered risk for developing
   PT   myocardial infarction by detecting a single nucleotide polymorphism in
   PT   the individual's nucleic acids.
   XX
   PS   Claim 7; SEQ ID NO 3488; 145pp; English.
   XX
   CC   The invention relates to a novel method for identifying an individual who
   CC   has an altered risk for developing myocardial infarction. The method
   CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
   CC   the nucleotide sequences given in the specification in the individual's
   CC   nucleic acids, where the presence of the SNP is correlated with an
   CC   altered risk for myocardial infarction in the individual. The invention
   CC   further comprises: an isolated nucleic acid molecule comprising at least
   CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
   CC   the specification or its complement and encoding any one of the amino
   CC   acid sequences given in the specification; an isolated polypeptide
   CC   comprising an amino acid sequence given in the specification; an antibody
   CC   that specifically binds to the polypeptide or its antigen-binding
   CC   fragment; an amplified polynucleotide containing an SNP given in the
   CC   specification and which is between about 16 and 1000 nucleotides in
   CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
   CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
```

nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

gnment Scores:
ed. No.: 2.48e-20 Length: 201
ore: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 14.7% Indels: 0
: 13 Gaps: 0

-10-821-670A-36 (1-197) x ADQ41825 (1-201)

159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

179 AlaPheArgIleArgAlaValThrIle 187
72 GCTTTCAGAATTCGGGCAGTGACTATT 98

SULT 74
Q41824
ADQ41824 standard; DNA; 201 BP.

ADQ41824;

18-NOV-2004 (first entry)

Myocardial infarction-associated SNP flanking transcript, SEQ ID 3487.

Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; ds.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin JJ, Iakoubova O;

WPI; 2004-533949/51.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 7; SEQ ID NO 3487; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method

CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.48e-20 Length: 201
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 13 Gaps: 0

US-10-821-670A-36 (1-197) x ADQ41824 (1-201)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
Db 4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy 179 AlaPheArgIleArgAlaValThrIle 187
Db 64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 75
ADQ41835
ID ADQ41835 standard; DNA; 201 BP.
XX
AC ADQ41835;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3498.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX

(APPL-) APPLERA CORP.

Cargill M, Devlin JJ, Iakoubova O;

WPI; 2004-533949/51.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 7; SEQ ID NO 3498; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

gnment Scores:
d. No.: 2.48e-20 Length: 201
re: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 14.7% Indels: 0
13 Gaps: 0

10-821-670A-36 (1-197) x ADQ41835 (1-201)

159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

179 AlaPheArgIleArgAlaValThrIle 187
72 GCTTTCAGAATTCGGGCAGTGACTATT 98

ULT 76
41829
ADQ41829 standard; DNA; 201 BP.

ADQ41829;

18-NOV-2004 (first entry)

Myocardial infarction-associated SNP flanking transcript, SEQ ID 3492.

Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; ds.

XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3492; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.48e-20 Length: 201
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 13 Gaps: 0

US-10-821-670A-36 (1-197) x ADQ41829 (1-201)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
Db 113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy 179 AlaPheArgIleArgAlaValThrIle 187

173 GCTTTCAGAATTCGGGCAGTGACTATT 199

SULT 77
Q41838
ADQ41838 standard; DNA; 201 BP.

ADQ41838;

18-NOV-2004 (first entry)

Myocardial infarction-associated SNP flanking transcript, SEQ ID 3501.

Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; ds.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin JJ, Iakoubova O;

WPI; 2004-533949/51.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 7; SEQ ID NO 3501; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.48e-20 Length: 201

Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	13	Gaps:	0

US-10-821-670A-36 (1-197) x ADQ41838 (1-201)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199
```

RESULT 78
ADQ41833
ID ADQ41833 standard; DNA; 201 BP.
XX
AC ADQ41833;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3496.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3496; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.

The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

gnment Scores:
d. No.: 2.48e-20 Length: 201
re: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 14.7% Indels: 0
13 Gaps: 0

10-821-670A-36 (1-197) x ADQ41833 (1-201)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              ||||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90
```

ULT 79
77258
ADF77258 standard; DNA; 630 BP.

ADF77258;

26-FEB-2004 (first entry)

Human IL-12 p35 subunit optimised DNA #5.

ds; human; interferon alpha expression plasmid; tumour; IL-12.

Synthetic.
Homo sapiens.

US2003181405-A1.

25-SEP-2003.

29-APR-2002; 2002US-00136837.

12-MAR-1999; 99US-00268135.

(NORD/) NORDSTROM J L.
(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

Nordstrom JL, Pericle F, Rolland A, Ralston RO;

WPI; 2004-020834/02.

A mammalian interferon alpha expression plasmid is useful in gene therapy to deliver interferon alpha to cells to modulate tumor activity in the treatment of cancer.

Disclosure; SEQ ID NO 27; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

SQ Sequence 630 BP; 118 A; 234 C; 141 G; 137 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.47e-20 Length: 630
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 12 Gaps: 0

US-10-821-670A-36 (1-197) x ADF77258 (1-630)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TCCTCCTTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGTTGTGCATCTTGTTGCAC 570

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              ||||||||||||||||||||||||||
Db        571 GCCTTCCGCATCCGCGCCGTCACCATC 597
```

RESULT 80
ADG39431
ID ADG39431 standard; DNA; 657 BP.
XX
AC ADG39431;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human CLMF 35 kDa subunit DNA.
XX
KW human; cytotoxic lymphocyte maturation factor; CLMF;
KW activated T-cell stimulator; natural killer cell stimulator;
KW immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 67. .657
FT /*tag= a
FT /partial
FT /product= "CLMF 35 kDa subunit"
FT /note= "No start or stop codon given"
XX
PN US2003204059-A1.
XX
PD 30-OCT-2003.
XX
PF 08-OCT-2002; 2002US-00267565.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 24-MAR-1992; 92US-00857023.
PR 02-MAR-1994; 94US-00205011.
PR 02-JUN-1995; 95US-00459151.
PR 22-SEP-1999; 99US-00401839.
XX
PA (HOFF) HOFFMANN LA ROCHE & CIE SA F.
XX
PI Gately MK, Gubler UA, Hulmes JD, Podlaski FJ, Stern AS;
PI Chizzonite RA, Pan YE;
XX
DR WPI; 2004-010534/01.
DR P-PSDB; ADG39428.
XX
PT Novel protein comprising cytotoxic lymphocyte maturation factor in
PT substantially pure form or protein which exhibits cytotoxic lymphocyte
PT maturation factor activity, useful as antitumor and immunoenhancing
PT agent.
XX
PS Claim 20; Page 29; 74pp; English.

The invention relates to a protein which comprises a cytotoxic lymphocyte maturation factor (CLMF). The protein is useful for stimulating activated T-cells which involves treating T-cells with the protein. The method further involves treating the activated T-cells with IL2 or its biologically active fragment. The protein is useful for stimulating natural killer cells which involves treating the natural killer cells with the protein. The protein has immunoenhancing and antitumour effects when used as single therapeutic agent in vivo. The present sequence is used in the exemplification of the present invention.

Sequence 657 BP; 186 A; 166 C; 139 G; 166 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.78e-20	Length:	657
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-36 (1-197) x ADG39431 (1-657)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

RESULT 81
AAQ97485
AAQ97485 standard; cDNA; 660 BP.

AAQ97485;

25-MAR-2003 (revised)
22-DEC-1995 (first entry)

Human interleukin-12 35 kD subunit.

Interleukin-12; IL-12; cytokine; gamma-interferon; T cell; natural killer cell; graft vs. host disease; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .660
	/*tag= a

WO9519786-A1.

27-JUL-1995.

20-JAN-1995; 95WO-US000879.

21-JAN-1994; 94US-00186529.

(GEMY) GENETICS INST INC.
(GEHO) GEN HOSPITAL CORP.

Wolf SF, Sykes M;

WPI; 1995-269273/35.
P-PSDB; AAR79187.

Control of graft versus host disease using interleukin 12 - partic. admin. at the time of bone marrow transplant.

Disclosure; Page 23-24; 32pp; English.

AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-12 is a heterodimeric cytokine which was originally identified as a factor which induces gamma-interferon from T cells and natural killer cells as set forth in PCT/US91/06332, published April 2 1992, and incorporated by reference. EP 433827, published June 26 1991, disclosed IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12 is defined as a heterodimeric glycoprotein comprised of two covalently linked subunits having mol. wts of about 40 kD and 35 kD. The two subunits may be disulfide-bonded. IL-12 is administered to prevent or ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily for 3 days, the first dose given 1 hr. after transplant. IL-12 can be used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.82e-20	Length:	660
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-36 (1-197) x AAQ97485 (1-660)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

RESULT 82
AAV07274
ID AAV07274 standard; cDNA; 660 BP.
XX
AC AAV07274;
XX
DT 25-SEP-1998 (first entry)
XX
DE Human Interleukin-12 p35 gene.
XX
KW IL-12 subunit; expression construct; treatment; asthma;
KW microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a
FT		/product= "IL-12 p35"
FT		/transl_except= (pos:58. .60,aa:Ser)

XX
PN WO9817689-A2.
XX
PD 30-APR-1998.
XX
PF 10-OCT-1997; 97WO-US018779.
XX
PR 18-OCT-1996; 96US-0028676P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Freimark B, Deshpande D;
XX
DR WPI; 1998-261428/23.
DR P-PSDB; AAV07274.
XX
PT Constructs for expression of interleukin-12 sub-units - are used for
PT delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT infections and certain cancers.
XX

Claim 1; Page 34-35; 80pp; English.

The IL-12 subunits AAV07273 and AAV07274 can be expressed using an appropriate expression construct engineered into a plasmid. The plasmids can provide for efficient expression of IL-12 subunits. The products can be used for the treatment of asthma, microbial and viral infections and certain cancers

Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

gnment Scores:
d. No.: 7.82e-20 Length: 660
re: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 14.7% Indels: 0
2 Gaps: 0

10-821-670A-36 (1-197) x AAV07274 (1-660)

159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

179 AlaPheArgIleArgAlaValThrIle 187
601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 83
/07218
AAV07218 standard; DNA; 660 BP.

AAV07218;

12-AUG-1998 (first entry)

DNA encoding human interleukin-12 35kDa subunit.

Interleukin-12; IL-12; graft-versus-host disease;
GVHD. bone marrow transplantation; graft-versus-leukemia; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 1. .660
/*tag= a
/product= "Interleukin-12_35kDa_subunit"

US5756085-A.

26-MAY-1998.

30-APR-1996; 96US-00640386.

21-JAN-1994; 94US-00186529.

(GEMY) GENETICS INST INC.
(GEHO) GEN HOSPITAL CORP.

Sykes M, Wolf SF;

WPI; 1998-321459/28.
P-PSDB; AAW51222.

Therapy of graft-versus-host disease - by administration of interleukin-12 to maintain and/or promote graft-versus-leukaemia effects.

Disclosure; Col 23-24; 20pp; English.

The invention relates to a method for the treatment or prevention of graft-versus-host disease (GVHD) which comprises the administration of interleukin-12 (IL-12) at the time of bone-marrow transplantation to maintain or promote graft-versus-leukaemia effects. Preferably, dosage is

CC 0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC the bone marrow transplant. IL-12 is administered daily until there is an
CC improvement in the condition. Administration is oral, cutaneous,
CC subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC intravenous. The present sequence encodes the human interleukin-12 35kDa
CC subunit
XX
SQ Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.82e-20 Length: 660
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-36 (1-197) x AAV07218 (1-660)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
Db 541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy 179 AlaPheArgIleArgAlaValThrIle 187
Db 601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 84
AAZ40408
ID AAZ40408 standard; DNA; 660 BP.
XX
AC AAZ40408;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human interleukin 12 p35 subunit optimised coding sequence.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9947678-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005394.
XX
PR 19-MAR-1998; 98US-0078654P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR P-PSDB; AAY42488.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX
PS Claim 11; Page 38-39; 137pp; English.
XX
CC This sequence represents an optimised coding region for the human
CC interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC untranslated region (UTR). The plasmids can be used for treating a
CC mammalian condition or disease, particularly cancer
XX
SQ Sequence 660 BP; 147 A; 237 C; 180 G; 96 T; 0 U; 0 Other;

Alignment Scores:

ed. No.: 7.82e-20 Length: 660
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 14.7% Indels: 0
: 2 Gaps: 0

-10-821-670A-36 (1-197) x AAZ40408 (1-660)

```
159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

179 AlaPheArgIleArgAlaValThrIle 187
    |||||||||||||||||||||||||
601 GCCTTCCGCATCCGCGCCGTGACCATC 627
```

SULT 85
240407
AAZ40407 standard; DNA; 660 BP.

AAZ40407;

15-FEB-2000 (first entry)

Human interleukin 12 p35 subunit wild type coding sequence.

Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV; promoter; growth hormone; untranslated region; UTR; mammal; disease; cancer; ss.

Homo sapiens.

WO9947678-A2.

23-SEP-1999.

12-MAR-1999; 99WO-US005394.

19-MAR-1998; 98US-0078654P.

(GENE-) GENEMEDICINE INC.

Nordstrom J, Pericle F, Rolland A, Ralston R;

WPI; 1999-562116/47.
P-PSDB; AAY42488.

New plasmids containing an interferon-alpha coding sequence, used for the treatment of a mammalian condition or disease, particularly cancer.

Claim 11; Page 38-39; 137pp; English.

This sequence represents the wild type coding region for the human interleukin 12 p35 subunit. The invention relates to a novel plasmid comprising a cytomegalovirus (CMV) promoter transcriptionally linked with an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-untranslated region (UTR). The plasmids can be used for treating a mammalian condition or disease, particularly cancer

Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 7.82e-20 Length: 660
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 14.7% Indels: 0
: 2 Gaps: 0

-10-821-670A-36 (1-197) x AAZ40407 (1-660)

```
159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy  179 AlaPheArgIleArgAlaValThrIle 187
    |||||||||||||||||||||||||
Db  601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

RESULT 86
AAZ40409
ID AAZ40409 standard; DNA; 660 BP.
XX
AC AAZ40409;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human interleukin 12 p35 subunit semi-optimised coding sequence.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9947678-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005394.
XX
PR 19-MAR-1998; 98US-0078654P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR P-PSDB; AAY42488.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX
PS Claim 11; Page 38-39; 137pp; English.
XX
CC This sequence represents a semi-optimised coding region for the human
CC interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC untranslated region (UTR). The plasmids can be used for treating a
CC mammalian condition or disease, particularly cancer
XX
SQ Sequence 660 BP; 147 A; 242 C; 170 G; 101 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.82e-20 Length: 660
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-36 (1-197) x AAZ40409 (1-660)

```
Qy  159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy  179 AlaPheArgIleArgAlaValThrIle 187
    |||||||||||||||||||||||||
Db  601 GCCTTCCGCATCCGGGCCGTGACCATC 627
```

RESULT 87
AAD15221
ID AAD15221 standard; DNA; 660 BP.

AAD15221;

01-NOV-2001 (first entry)

Human cytokine p35 DNA.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p35; ds.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .660
	/*tag= a
	/product= "p35 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .657
	/*tag= c
	/product= "Mature p35 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR, Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08614.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides), useful for treating various diseases e.g. diabetic retinopathy and cancer.

Claim 91; Page 142; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is human p35 protein encoding DNA

Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

gnment Scores:			
d. No.:	7.82e-20	Length:	660
re:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	14.7%	Indels:	0
	5	Gaps:	0

10-821-670A-36 (1-197) x AAD15221 (1-660)

```
      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

      179 AlaPheArgIleArgAlaValThrIle 187
          |||||||||||||||||||||||||||
```

Db 601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 88
AAL44226
ID AAL44226 standard; DNA; 660 BP.
XX
AC AAL44226;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human interleukin 12A (IL-12A) coding sequence.
XX
KW Human; gene; ds; interleukin 12A; IL-12A; drug screening; AIDS; malaria;
KW tuberculosis; cancer; haplotyping; genotyping; transgenic animal.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a
FT		/product= "Human interleukin 12A (IL-12A)"
FT	variation	replace(142, A)
FT		/*tag= b
FT		/standard_name= "Single nucleotide polymorphism"

XX
PN WO200229115-A1.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031656.
XX
PR 06-OCT-2000; 2000US-0238693P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Armstrong B, Cappola G, Choi JY, Gilson CR, Kliem SE, Koshy B;
PI Parks KE;
XX
DR WPI; 2002-315865/35.
DR P-PSDB; AAO15506.
XX
PT New interleukin 12A (IL-12A) gene polymorphic variants, for studying the
PT expression and function of IL-12A and screening candidate drugs for
PT treating AIDS and cancer.
XX
PS Claim 28; Fig 2; 72pp; English.
XX
CC The invention comprises the amino acid and coding sequence of the human
CC interleukin 12A (IL-12A) protein. Specifically the invention relates to
CC the identification of polymorphisms within the human (IL-12A) gene
CC sequence. The polymorphisms identified in the human IL-12A gene sequence
CC are useful in studying the expression and function of IL-12A, and in
CC screening drugs for the treatment of disorders such as AIDS, malaria,
CC tuberculosis and cancer. The IL-12A polymorphisms may be used to
CC haplotype and genotype the IL-12A gene of an individual. The IL-12A DNA
CC sequences of the invention can be used to create transgenic animals for
CC studying expression of the IL-12A isogenes in vivo. The present DNA
CC sequence represents the coding sequence of the human interleukin 12A (IL-
CC 12A) gene
XX
SQ Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	7.82e-20	Length:	660
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x AAL44226 (1-660)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178

```
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

      179 AlaPheArgIleArgAlaValThrIle 187
          |||||||||||||||||||||||||||
      601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

SULT 89
C47589
ACC47589 standard; DNA; 660 BP.

ACC47589;

12-JUN-2003 (first entry)

Human interleukin 12 (hIL-12) P35 subunit gene.

Human; interleukin 12; hIL-12; baculovirus vector;
recombinant production; AcNPV-hIL12;
Autographa california nuclear polyhedrosis virus; tumour; cancer;
infection; bacterial; viral; cytostatic; P35 subunit; gene; ds.

Homo sapiens.

CN1357622-A.

10-JUL-2002.

02-NOV-2001; 2001CN-00133631.

02-NOV-2001; 2001CN-00133631.

(UYWU-) UNIV WUHAN.

Meng X, Xu J, Yu Z;

WPI; 2002-741792/81.

Human interleukin-12 recombinant insect virus strain and its preparation.

Claim 4; Fig 6; 17pp; Chinese.

The invention relates to a recombinant baculovirus comprising DNA
encoding human interleukin 12 (hIL-12) and methods for its preparation.
The recombinant baculovirus strain is designated Autographa california
nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
(ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
respectively under the control of the viral polyhedrin and P10 promoters.
The baculovirus can be used in the recombinant production of human IL-12
which is suitable for treating tumours and bacterial, viral and other
infections. The present sequence represents the human IL-12 P35 subunit
gene used in construction of the baculovirus vector of the invention

Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

:gnment Scores:			
ed. No.:	7.82e-20	Length:	660
ore:	29.00	Matches:	29
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	14.7%	Indels:	0
:	6	Gaps:	0

-10-821-670A-36 (1-197) x ACC47589 (1-660)

```
      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

      179 AlaPheArgIleArgAlaValThrIle 187
          |||||||||||||||||||||||||||
      601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

RESULT 90
ADF77245
ID ADF77245 standard; DNA; 660 BP.
XX
AC ADF77245;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p35 subunit optimised DNA #1.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; SEQ ID NO 7; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,
CC comprising a promoter and a synthetic 5' intron transcriptionally linked
CC with an interferon alpha coding sequence and a 3' untranslated region.
CC The mammalian interferon alpha expression plasmid is useful for treating
CC tumour growth. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 660 BP; 147 A; 237 C; 180 G; 96 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	7.82e-20	Length:	660
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-36 (1-197) x ADF77245 (1-660)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGCGCCGTGACCATC 627
```

RESULT 91
ADF77257
ID ADF77257 standard; DNA; 660 BP.
XX
AC ADF77257;
XX
DT 26-FEB-2004 (first entry)

Human IL-12 p35 subunit optimised DNA #4.

ds; human; interferon alpha expression plasmid; tumour; IL-12.

Synthetic.
Homo sapiens.

US2003181405-A1.

25-SEP-2003.

29-APR-2002; 2002US-00136837.

12-MAR-1999; 99US-00268135.

(NORD/) NORDSTROM J L.
(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

Nordstrom JL, Pericle F, Rolland A, Ralston RO;

WPI; 2004-020834/02.

A mammalian interferon alpha expression plasmid is useful in gene therapy to deliver interferon alpha to cells to modulate tumor activity in the treatment of cancer.

Disclosure; SEQ ID NO 26; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 660 BP; 197 A; 93 C; 82 G; 288 T; 0 U; 0 Other;

gnment Scores:			
d. No.:	7.82e-20	Length:	660
re:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	14.7%	Indels:	0
	12	Gaps:	0

10-821-670A-36 (1-197) x ADF77257 (1-660)

```
       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 TCTTCTTTAGAAGAACCTGATTTTTATAAAACTAAAATTAAATTATGTATTTTATTACAT 600

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       601 GCTTTTCGTATTCGTGCTGTTACTATT 627
```

ULT 92
77246
ADF77246 standard; DNA; 660 BP.

ADF77246;

26-FEB-2004 (first entry)

Human IL-12 p35 subunit optimised DNA #2.

ds; human; interferon alpha expression plasmid; tumour; IL-12.

Synthetic.
Homo sapiens.

PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; SEQ ID NO 8; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,
CC comprising a promoter and a synthetic 5' intron transcriptionally linked
CC with an interferon alpha coding sequence and a 3' untranslated region.
CC The mammalian interferon alpha expression plasmid is useful for treating
CC tumour growth. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 660 BP; 147 A; 242 C; 170 G; 101 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	7.82e-20	Length:	660
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-36 (1-197) x ADF77246 (1-660)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGGGCCGTGACCATC 627
```

RESULT 93
ADF77244
ID ADF77244 standard; DNA; 660 BP.
XX
AC ADF77244;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p35 subunit DNA.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.

(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

Nordstrom JL, Pericle F, Rolland A, Ralston RO;

WPI; 2004-020834/02.

A mammalian interferon alpha expression plasmid is useful in gene therapy to deliver interferon alpha to cells to modulate tumor activity in the treatment of cancer.

Disclosure; SEQ ID NO 6; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

:gnment Scores:

ed. No.:	7.82e-20	Length:	660
ore:	29.00	Matches:	29
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	14.7%	Indels:	0
:	12	Gaps:	0

-10-821-670A-36 (1-197) x ADF77244 (1-660)

```
        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

SULT 94
F26096
AAF26096 standard; DNA; 683 BP.

AAF26096;

24-APR-2001 (first entry)

Human pG-hIL12p DNA.

Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection; immunostimulant; tumor; antiviral; antitumor; interferon-gamma; Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.

Homo sapiens.

WO200104155-A2.

18-JAN-2001.

08-JUL-2000; 2000WO-DE002263.

08-JUL-1999; 99CH-00001259.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.
(REGC) UNIV CALIFORNIA.

Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;

WPI; 2001-147178/15.

PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Disclosure; Fig 2; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 683 BP; 198 A; 171 C; 142 G; 172 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.08e-20	Length:	683
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-36 (1-197) x AAF26096 (1-683)

```
Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy      179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
Db      601 GCTTTCAGAATACGGGCAGTGACTATT 627
```

RESULT 95
ADP88401
ID ADP88401 standard; cDNA; 702 BP.
XX
AC ADP88401;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human interleukin-12 alpha chain coding sequence.
XX
KW antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW antibacterial; protozoacide; gene therapy; expression vector;
KW interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004052929-A2.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2003; 2003WO-IB006404.
XX
PR 06-DEC-2002; 2002GB-00028465.
XX

(UYBE-) UNIV QUEENS BELFAST.

Vandenbroeck K, Alloza I;

WPI; 2004-487887/46.

New expression vector comprising DNA encoding a subunit of a dimeric form of interleukin under transcriptional control of an ecdysone-inducible promoter, useful in preparing a composition for treating e.g., inflammatory disease.

Disclosure; Page 85-86; 87pp; English.

The present invention relates to an expression vector comprising DNA encoding a subunit of a dimeric form of interleukin under transcriptional control of an ecdysone-inducible promoter. The expression vector is useful in preparing a composition for treating a disease having a pathogenesis which includes endogenous production of cytokine IL-12, IL-23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-induced inflammation, epithelial airway inflammation such as asthma, allergic disease, or autoimmune disease such as multiple sclerosis or inflammatory bowel disease. The present sequence is the coding sequence of the human interleukin-12 alpha chain used in the exemplification of the invention.

Sequence 702 BP; 199 A; 184 C; 147 G; 172 T; 0 U; 0 Other;

gnment Scores:
d. No.: 8.3e-20 Length: 702
re: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 14.7% Indels: 0
12 Gaps: 0

10-821-670A-36 (1-197) x ADP88401 (1-702)

159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
556 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 615

179 AlaPheArgIleArgAlaValThrIle 187
616 GCTTTCAGAATTCGGGCAGTGACTATT 642

ULT 96
67880
AAQ67880 standard; DNA; 721 BP.

AAQ67880;

25-MAR-2003 (revised)
23-MAR-1995 (first entry)

EPV 42 kD promoter/Human IL-12 p35 subunit expression cassette.

Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector; plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response; polymerase chain reaction; poxvirus; pSD542; immunological response; pathogen; human; interferon; IFN; ss.

Synthetic.

Key	Location/Qualifiers
promoter	1. .61
	/*tag= a
	/note= "Vaccinia E3L promoter"
CDS	32. .1018
	/*tag= b
	/product= "Human IL-12 p35"

WO9416716-A1.

XX
PD 04-AUG-1994.
XX
PF 21-JAN-1994; 94WO-US000888.
XX
PR 21-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI Paoletti E, Tartaglia J, Cox WI;
XX
DR WPI; 1994-263767/32.
XX
PT Attenuated recombinant virus used for cancer therapy - comprises DNA
PT encoding cytokine and/or tumour associated antigen.
XX
PS Example 27; Fig 34; 232pp; English.
XX
CC The sequences given in AAQ67879-80 are expression cassettes which contain
CC the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC promoter, respectively. These sequences were used in the construction of
CC an ALVAC-based recombinant virus containing the genes for the two
CC subunits of human IL-12. The p40 subunit was amplified using primers
CC JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC 42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC using primers JP186 and JP201 and placed under the control of the
CC vaccinia E3L promoter using primers JP218 and JP220. The expression
CC cassette was isolated and ligated with pBSSK+ generating plasmid
CC PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC cassettes are orientated head-to-head relative to each other. The
CC combination casette containing the poxvirus promoted genes for both IL-12
CC subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC contains both the human IL-12 genes in the C6 locus. The resulting virus
CC may be used in a composition for inducing an antigenic or immunological
CC response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.52e-20 Length: 721
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-36 (1-197) x AAQ67880 (1-721)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
Db 602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy 179 AlaPheArgIleArgAlaValThrIle 187
Db 662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 97
AAZ08515
ID AAZ08515 standard; DNA; 721 BP.
XX
AC AAZ08515;
XX
DT 19-OCT-1999 (first entry)
XX
DE Vaccinia E3L/human IL-12 P35 expression cassette.
XX
KW Attenuated recombinant virus; cytokine; tumour associated antigen;

NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies; cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF; interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen; carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza; immunological response; immunotherapy; vaccine; Newcastle Disease; ss.

Synthetic.
Homo sapiens.
Vaccinia virus.

US5942235-A.

24-AUG-1999.

02-JUN-1995; 95US-00458356.

24-DEC-1981; 81US-00334456.
08-DEC-1982; 82US-00446824.
19-JUN-1984; 84US-00622135.
27-AUG-1987; 87US-00090209.
28-AUG-1987; 87US-00090711.
20-OCT-1987; 87US-00110335.
25-APR-1988; 88US-00186054.
23-AUG-1988; 88US-00234390.
14-JUN-1990; 90US-00537882.
14-JUN-1990; 90US-00537890.
16-DEC-1991; 91US-00805567.
03-MAR-1992; 92US-00847977.
06-MAR-1992; 92US-00847951.
04-MAY-1992; 92US-00881995.
22-JUL-1992; 92US-00918278.
20-JAN-1993; 93US-00007115.
19-JAN-1994; 94US-00184009.
14-APR-1994; 94US-00228926.
13-SEP-1994; 94US-00306259.

(HEAL-) HEALTH RES INC.

Paoletti E;

WPI; 1999-493494/41.

Recombinant poxviruses comprising exogenous DNA encoding antigenic determinants useful in immunotherapy to immunize against cancers and other diseases such as influenza, Newcastle Disease and rabies.

Example 27; Fig 34; 163pp; English.

The present invention describes a recombinant poxvirus (I), comprising exogenous DNA encoding an antigenic determinant of a pathogen which is then expressed in vivo in infected host cells after administration to a patient and therefore induces an immunological response. (I) may be used to vaccinate patients against a wide range of diseases and disorders depending on the type of antigen encoded by the exogenous DNA. (I) may be used to vaccinate against diseases such as rabies, influenza and Newcastle Disease. It is particularly useful for immunising against cancers. The poxvirus (I) also provides a means of manipulating lymphocytes and tumour cells for use in cell-based immunotherapeutic modalities for cancer. (I) also have enhanced safety compared to unattenuated viruses (attenuation reduces the virulence of the viruses) and known recombinant poxvirus vaccines. This increased level of safety reduces the possibility of a 'runaway' infection in the host and reduces the chance of transmission from vaccinated to unvaccinated individuals and contamination of the environment. The present sequence represents a Vaccinia E3L/human IL-12 P35 expression cassette used in the exemplification of the present invention

Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

..gnment Scores:
..ed. No.: 8.52e-20 Length: 721
..ore: 29.00 Matches: 29
..rcent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-36 (1-197) x AAZ08515 (1-721)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688
```

RESULT 98
ADR21891
ID ADR21891 standard; DNA; 721 BP.
XX
AC ADR21891;
XX
DT 04-NOV-2004 (first entry)
XX
DE Vaccinia E3L/human IL-12 expression cassette.
XX
KW Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW cancer therapy; ds; human; IL-12; interleukin-12; E3L;
KW expression cassette.
XX
OS Vaccinia virus.
OS Homo sapiens.
OS Synthetic.
XX
PN US6780407-B1.
XX
PD 24-AUG-2004.
XX
PF 15-SEP-2000; 2000US-00663667.
XX
PR 08-MAR-1989; 89US-00320471.
PR 14-FEB-1990; 90US-00478179.
PR 07-JAN-1991; 91US-00638080.
PR 07-MAR-1991; 91US-00666056.
PR 11-JUN-1991; 91US-00713967.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 21-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 30-AUG-1995; 95US-00521016.
XX
PA (AVET) AVENTIS PASTEUR.
XX
PI Paoletti E, Tartaglia J, Cox WI;
XX
DR WPI; 2004-601998/58.
XX
PT New recombinant poxvirus which is an attenuated avipox Virus that
PT expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
PS Example 27; SEQ ID NO 199; 181pp; English.
XX
CC The invention describes a recombinant poxvirus containing exogenous DNA
CC in a nonessential region of the poxvirus, where the poxvirus is an
CC attenuated avipox Virus that expresses an exogenous DNA encoding
CC carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC described are: a composition comprising a poxvirus above in admixture
CC with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC vivo comprising administering to a mammal the composition above.
CC Disclosed are: making recombinant poxvirus defined above; recombinant
CC poxvirus vaccine having an increased level of safety compared to known
CC recombinant poxvirus vaccines; and a modified vector for expressing a

gene product in a host. The recombinant poxvirus is useful for providing a recombinant poxvirus vaccine having an increased level of safety compared to known recombinant poxvirus vaccines. The recombinant poxvirus is useful for cancer therapy. This sequence represents a human IL-12 expression cassette used in the creation of NYVAC rescue virus and canarypox virus vector ALVAC comprising the human IL-12 gene.

Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

gnment Scores:
d. No.: 8.52e-20 Length: 721
re: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 14.7% Indels: 0
13 Gaps: 0

10-821-670A-36 (1-197) x ADR21891 (1-721)

159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

179 AlaPheArgIleArgAlaValThrIle 187
662 GCTTTCAGAATTCGGGCAGTGACTATT 688

ULT 99
98708
ADK98708 standard; DNA; 761 BP.

ADK98708;

06-MAY-2004 (first entry)

Human interleukin-12 (IL-12) P35 subunit DNA seqid 3.

human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.

Homo sapiens.

CN1408727-A.

09-APR-2003.

29-SEP-2001; 2001CN-00126923.

29-SEP-2001; 2001CN-00126923.

(ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.

Wan G, Li C;

WPI; 2003-664076/63.

Method for efficiently expressing recombinant human interleukin 12 in eukaryotic cell.

Claim 6; SEQ ID NO 3; 14pp; Chinese.

The invention describes the process of producing human recombinant interleukin-12 (IL-12) includes: providing a nucleotide sequence corresponding to the P35 subunit with the first signal peptide and a nucleotide sequence corresponding to the P40 subunit; inserting the nucleotide sequences into an expression vector; converting the eukaryotic cell with the expression vector; and culturing the transfected eukaryotic cell in condition suitable for recombinant human IL-12 expression. The process balances the expression amount of both P35 and P40 subunits and thus raises the expression amount of IL-12 with bioactivity via raising the expression strength of P35 subunit. This sequence represents the human interleukin-12 (IL-12) P35 subunit polynucleotide.

Sequence 761 BP; 205 A; 204 C; 164 G; 187 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 8.97e-20 Length: 761
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 10 Gaps: 0

US-10-821-670A-36 (1-197) x ADK98708 (1-761)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
Db 642 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 701

Qy 179 AlaPheArgIleArgAlaValThrIle 187
Db 702 GCTTTCAGAATTCGGGCAGTGACTATT 728

RESULT 100
ADK98706
ID ADK98706 standard; DNA; 761 BP.
XX
AC ADK98706;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human interleukin-12 (IL-12) P35 subunit DNA seqid 1.
XX
KW human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS Homo sapiens.
XX
PN CN1408727-A.
XX
PD 09-APR-2003.
XX
PF 29-SEP-2001; 2001CN-00126923.
XX
PR 29-SEP-2001; 2001CN-00126923.
XX
PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI Wan G, Li C;
XX
DR WPI; 2003-664076/63.
XX
PT Method for efficiently expressing recombinant human interleukin 12 in
PT eukaryotic cell.
XX
PS Claim 4; SEQ ID NO 1; 14pp; Chinese.
XX
CC The invention describes the process of producing human recombinant
CC interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC corresponding to the P35 subunit with the first signal peptide and a
CC nucleotide sequence corresponding to the P40 subunit; inserting the
CC nucleotide sequences into an expression vector; converting the eukaryotic
CC cell with the expression vector; and culturing the transfected eukaryotic
CC cell in condition suitable for recombinant human IL-12 expression. The
CC process balances the expression amount of both P35 and P40 subunits and
CC thus raises the expression amount of IL-12 with bioactivity via raising
CC the expression strength of P35 subunit. This sequence represents the
CC human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ Sequence 761 BP; 199 A; 209 C; 167 G; 185 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 8.97e-20 Length: 761
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 10 Gaps: 0

-10-821-670A-36 (1-197) x ADK98706 (1-761)

```
        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        642 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 701

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
        702 GCTTTCAGAATTCGGGCAGTGACTATT 728
```

arch completed: June 10, 2006, 02:27:30
b time : 495.317 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

on: June 10, 2006, 01:35:52 ; Search time 2729.64 Seconds
(without alignments)
6053.601 Million cell updates/sec

le: US-10-821-670A-36
fect score: 197
uence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

ring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

rched: 48236798 seqs, 27959665780 residues

d size: 1

al number of hits satisfying chosen parameters: 96471816

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Listing first 200 summaries

mand line parameters:
DEL=frame+_p2n.model -DEV=xlp
/abss/ABSSWEB_spool/US10821670/runat_07062006_110453_27580/app_query.fasta_1
=EST -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rst -MINMATCH=0.1 -LOOPCL=0
OPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
ST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL
TFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
ER=US10821670_@CGN_1_1_22222_@runat_07062006_110453_27580 -NCPU=6 -ICPU=3
MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
RN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
APOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

abase : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	% Query Match	Length	DB	ID	Description
1	29	14.7	762	14	DQ033872	DQ033872 Homo sapi
2	29	14.7	863	4	CD013916	CD013916 90138296
3	29	14.7	935	4	CD013914	CD013914 90138124
4	29	14.7	1136	4	CD013915	CD013915 90138132
5	29	14.7	1938	6	BC035571	BC035571 Homo sapi
6	28	14.2	762	14	DQ033873	DQ033873 Pan trogl
7	28	14.2	812	2	BG702253	BG702253 602683459
8	28	14.2	832	2	BI523569	BI523569 603175938
9	24	12.2	581	3	BP260963	BP260963 BP260963
10	24	12.2	777	14	CT080894	CT080894 Sus scrof
11	21	10.7	592	12	CE159257	CE159257 tigr-gss-
c 12	21	10.7	778	1	AJ820622	AJ820622 AJ820622
13	20	10.2	342	2	BM257856	BM257856 521721 MA
14	20	10.2	344	14	BX537236	BX537236 INRA porc
15	18	9.1	447	2	BI824638	BI824638 603033580
c 16	17	8.6	1099	2	BI523344	BI523344 603175938
c 17	16	8.1	777	4	CB168830	CB168830 CWI602769
c 18	13	6.6	528	1	AI332701	AI332701 qg19a07.x
19	10	5.1	373	7	BF552757	BF552757 UI-R-C0-i
20	10	5.1	427	10	DT930939	DT930939 S13.1784
21	10	5.1	456	10	DT913216	DT913216 S13.1426
22	10	5.1	561	3	BU699383	BU699383 LL2in1157
23	10	5.1	563	3	BU698113	BU698113 LL2in1206
24	10	5.1	589	1	AI050362	AI050362 ub30a07.r
c 25	10	5.1	614	11	AZ729972	AZ729972 RPCI-24-1
26	10	5.1	692	5	CJ137697	CJ137697 CJ137697
c 27	10	5.1	941	13	CZ271875	CZ271875 ZMMBF0051
28	10	5.1	1299	6	AK153729	AK153729 Mus muscu
29	9	4.6	192	4	BY368866	BY368866 BY368866
c 30	9	4.6	194	7	BF366007	BF366007 PM4-NT007
c 31	9	4.6	234	10	DV345207	DV345207 NABWE87TR
32	9	4.6	294	4	BY364595	BY364595 BY364595
33	9	4.6	304	5	CF799003	CF799003 Lr_PAHCF_
34	9	4.6	343	12	CG422132	CG422132 ZMMBBc003
35	9	4.6	372	12	CG396825	CG396825 ZMMBBc001
36	9	4.6	404	9	DN988885	DN988885 ZEBRA_2F_
37	9	4.6	412	4	CB801533	CB801533 AMGNNUC:S
38	9	4.6	425	5	CF798662	CF798662 Lr_PAHCF_
c 39	9	4.6	437	1	AI750954	AI750954 cn06g05.x
c 40	9	4.6	453	11	AZ215995	AZ215995 Sheared D
41	9	4.6	495	8	CO869708	CO869708 Lr_JV2CF_
c 42	9	4.6	501	9	DA587595	DA587595 DA587595
c 43	9	4.6	502	9	DA599473	DA599473 DA599473
44	9	4.6	512	9	DR008986	DR008986 Lr_Cu2CF_
c 45	9	4.6	519	7	BE294832	BE294832 601177293
c 46	9	4.6	521	9	DA598142	DA598142 DA598142
47	9	4.6	539	14	CR813130	CR813130 GR0AAA37C
c 48	9	4.6	549	9	DA956152	DA956152 DA956152
49	9	4.6	551	10	DT919655	DT919655 PCRS30821
c 50	9	4.6	556	9	DA555731	DA555731 DA555731
c 51	9	4.6	556	10	DY063836	DY063836 000403BPP
52	9	4.6	558	9	CX570753	CX570753 RVL1941 W
c 53	9	4.6	562	9	DA552898	DA552898 DA552898
c 54	9	4.6	565	9	DA557449	DA557449 DA557449
55	9	4.6	568	14	CR795312	CR795312 GR0AAA12D
c 56	9	4.6	572	7	BE296563	BE296563 601174065
c 57	9	4.6	577	4	CA153972	CA153972 SCVPRZ203
c 58	9	4.6	579	4	BY797655	BY797655 BY797655
c 59	9	4.6	585	9	DA541205	DA541205 DA541205
60	9	4.6	610	7	BB194492	BB194492 BB194492
61	9	4.6	610	11	BH488094	BH488094 BOGBX77TR
62	9	4.6	617	13	CZ102767	CZ102767 OM__Ba011
63	9	4.6	663	5	CF809729	CF809729 Lr_LC1ED_
64	9	4.6	671	9	DR008485	DR008485 Lr_Cu2CF_
65	9	4.6	679	8	CO408614	CO408614 Lr_CHECF_
66	9	4.6	680	5	CF810266	CF810266 Lr_LC1ED_
c 67	9	4.6	692	7	BE299956	BE299956 600944512
68	9	4.6	705	11	AZ306792	AZ306792 1M0008F02
69	9	4.6	710	13	CW744074	CW744074 MARC_9128
c 70	9	4.6	713	12	BZ715412	BZ715412 HSC 00419
c 71	9	4.6	731	5	CF934165	CF934165 TrEST-B01
72	9	4.6	731	9	DR009499	DR009499 Lr_Cu2CF_
73	9	4.6	734	13	CL419793	CL419793 ZMMBBb042
74	9	4.6	750	12	CG395353	CG395353 ZMMBBc001
75	9	4.6	753	12	CG875642	CG875642 ZMMBBc028
c 76	9	4.6	765	7	BE298508	BE298508 601119636
c 77	9	4.6	770	7	BE967024	BE967024 601660755

78	9	4.6	773	2	BI524152	BI524152 603051564
79	9	4.6	773	13	CZ119478	CZ119478 OA_BBa000
80	9	4.6	788	9	DR008334	DR008334 Lr_Cu2CF_
81	9	4.6	794	2	BM007478	BM007478 603616745
82	9	4.6	794	4	CB899783	CB899783 tric019xp
83	9	4.6	796	2	BM397339	BM397339 5009-0-31
84	9	4.6	822	4	BX835464	BX835464 BX835464
85	9	4.6	825	12	CG385421	CG385421 OGYBY32TV
86	9	4.6	831	14	CT469425	CT469425 Sus scrof
87	9	4.6	845	5	CD516665	CD516665 AGENCOURT
88	9	4.6	847	12	CG681185	CG681185 ZMMBBc014
89	9	4.6	860	3	BQ707955	BQ707955 AGENCOURT
90	9	4.6	870	3	BQ712265	BQ712265 AGENCOURT
91	9	4.6	909	3	BQ710906	BQ710906 AGENCOURT
92	9	4.6	918	14	CNS01EWE	AL141087 Anopheles
93	9	4.6	928	12	CG396548	CG396548 ZMMBBc001
94	9	4.6	933	13	CZ252347	CZ252347 LQCYI32TV
95	9	4.6	1054	4	BX444783	BX444783 BX444783
96	9	4.6	1083	12	CL092806	CL092806 ISB1-22J9
97	9	4.6	1145	4	BX418555	BX418555 BX418555
98	9	4.6	1215	8	CV123647	CV123647 OSTF30015
99	9	4.6	1470	6	CR607863	CR607863 full-leng
100	9	4.6	2160	6	CR590609	CR590609 full-leng
101	9	4.6	2192	14	DQ041206	DQ041206 Homo sapi
102	9	4.6	2828	6	AK079629	AK079629 Mus muscu
103	9	4.6	3200	6	BC035570	BC035570 Homo sapi
104	8	4.1	108	5	CK549365	CK549365 swkz0_005
105	8	4.1	131	11	AZ818875	AZ818875 2M0089I12
106	8	4.1	136	1	AV088513	AV088513 AV088513
107	8	4.1	144	2	BF751315	BF751315 RC3-BN042
108	8	4.1	154	13	CZ613100	CZ613100 OM__Ba014
109	8	4.1	181	1	AV093643	AV093643 AV093643
110	8	4.1	183	5	CK931475	CK931475 p5rmgc_00
111	8	4.1	191	1	AI996576	AI996576 701667517
112	8	4.1	198	13	CL228836	CL228836 ZMMBBc005
113	8	4.1	200	13	CL227798	CL227798 ZMMBBc002
114	8	4.1	204	5	CF773702	CF773702 AG_FSL_21
115	8	4.1	207	12	CE180687	CE180687 tigr-gss-
116	8	4.1	208	12	CE014974	CE014974 tigr-gss-
117	8	4.1	208	12	CG875289	CG875289 ZMMBBc028
118	8	4.1	212	7	BE398188	BE398188 WHE0002.H
119	8	4.1	212	12	BZ635858	BZ635858 OGAOJ54TC
120	8	4.1	213	12	CL198575	CL198575 ZMMBBc025
121	8	4.1	214	12	CG863507	CG863507 ZMMBBc027
122	8	4.1	216	5	CD957154	CD957154 SCH_190 G
123	8	4.1	218	1	AI523278	AI523278 ar71b08.x
124	8	4.1	218	13	CZ419338	CZ419338 1015041 R
125	8	4.1	219	12	CG832793	CG832793 ZMMBBc012
126	8	4.1	222	13	CL230869	CL230869 ZMMBBc011
127	8	4.1	224	13	CL229028	CL229028 ZMMBBc014
128	8	4.1	226	3	BQ359215	BQ359215 RC3-HN002
129	8	4.1	233	12	CG689981	CG689981 ZMMBBc013
130	8	4.1	233	13	CL232247	CL232247 ZMMBBc018
131	8	4.1	235	12	CG704890	CG704890 ZMMBBc017
132	8	4.1	238	1	AI488162	AI488162 EST246484
133	8	4.1	239	8	CO705025	CO705025 DG32-295b
134	8	4.1	239	12	CG861225	CG861225 ZMMBBc026
135	8	4.1	240	1	AJ464031	AJ464031 AJ464031
136	8	4.1	244	11	BZ123728	BZ123728 CH230-451
137	8	4.1	245	12	CG866219	CG866219 ZMMBBb035
138	8	4.1	246	13	CL231442	CL231442 ZMMBBc017
139	8	4.1	249	12	CG397302	CG397302 ZMMBBc001
140	8	4.1	250	12	CL199220	CL199220 ZMMBBc004
141	8	4.1	252	13	CL223080	CL223080 ZMMBBc050
142	8	4.1	253	8	CO692882	CO692882 DG11-54p6
143	8	4.1	253	12	CG838113	CG838113 ZMMBBc021
144	8	4.1	255	13	CL229509	CL229509 ZMMBBc015
145	8	4.1	256	12	CG871103	CG871103 ZMMBBc027
146	8	4.1	257	13	CL228829	CL228829 ZMMBBc005
147	8	4.1	258	13	CL232488	CL232488 ZMMBBc018
148	8	4.1	260	13	CL230006	CL230006 ZMMBBc016
149	8	4.1	261	12	CG833649	CG833649 ZMMBBc013
150	8	4.1	263	12	CG702086	CG702086 ZMMBBc011
151	8	4.1	264	10	T42005	T42005 5268 Lambda
152	8	4.1	264	13	CL229198	CL229198 ZMMBBc014
153	8	4.1	270	4	BX106716	BX106716 BX106716
154	8	4.1	270	11	AQ313634	AQ313634 RPCI11-96
155	8	4.1	270	12	CG423103	CG423103 ZMMBBc003
156	8	4.1	272	13	CL398698	CL398698 ZMMBBb040
157	8	4.1	274	13	CL233175	CL233175 ZMMBBc019
158	8	4.1	275	12	CG699411	CG699411 ZMMBBc016
159	8	4.1	276	10	DR380792	DR380792 987564 CE
160	8	4.1	278	12	CE383544	CE383544 tigr-gss-
161	8	4.1	280	10	DY123482	DY123482 001212BAM
162	8	4.1	280	12	CG415220	CG415220 ZMMBBc002
163	8	4.1	282	5	CF935745	CF935745 TrEST-B06
164	8	4.1	283	12	CG837368	CG837368 ZMMBBc021
c 165	8	4.1	284	13	CW284805	CW284805 104_761_1
166	8	4.1	287	13	CL232690	CL232690 ZMMBBc018
167	8	4.1	288	1	AV438134	AV438134 AV438134
c 168	8	4.1	289	12	CE344758	CE344758 tigr-gss-
c 169	8	4.1	290	12	CC973001	CC973001 ZUAFD31TH
170	8	4.1	290	12	CG432320	CG432320 ZMMBBc004
171	8	4.1	290	12	CG836142	CG836142 ZMMBBc021
c 172	8	4.1	291	9	DR111969	DR111969 RTS1_25_A
173	8	4.1	292	8	CO698693	CO698693 DG32-143m
174	8	4.1	293	12	CG875068	CG875068 ZMMBBc028
175	8	4.1	296	12	CL198716	CL198716 ZMMBBc008
176	8	4.1	297	12	CG834313	CG834313 ZMMBBc014
177	8	4.1	297	13	CL233069	CL233069 ZMMBBc019
c 178	8	4.1	298	2	BG883630	BG883630 fp27g12.y
179	8	4.1	298	12	CG416332	CG416332 ZMMBBc002
180	8	4.1	298	12	CG681996	CG681996 ZMMBBc014
181	8	4.1	299	12	CG765145	CG765145 ZMMBBc020
182	8	4.1	299	12	CG834124	CG834124 ZMMBBc014
c 183	8	4.1	300	12	CC177028	CC177028 ZMMBBc030
184	8	4.1	301	8	CO698412	CO698412 DG32-136a
185	8	4.1	303	12	CG700904	CG700904 ZMMBBc011
186	8	4.1	305	2	BF947586	BF947586 QV2-NN004
187	8	4.1	305	12	CG687680	CG687680 ZMMBBc016
188	8	4.1	306	12	CG838969	CG838969 ZMMBBc020
189	8	4.1	309	8	CO616608	CO616608 DG9-166k7
c 190	8	4.1	309	10	DY190750	DY190750 000929BEM
191	8	4.1	309	12	CG690895	CG690895 ZMMBBc013
192	8	4.1	310	10	Z43509	Z43509 HSC1EA031 n
193	8	4.1	312	12	CG703018	CG703018 ZMMBBc011
194	8	4.1	312	12	CG740564	CG740564 ZMMBBc019
195	8	4.1	312	12	CG836284	CG836284 ZMMBBc021
196	8	4.1	313	13	CL232602	CL232602 ZMMBBc018
197	8	4.1	315	8	CO619156	CO619156 DG9-193n2
198	8	4.1	315	12	CG423552	CG423552 ZMMBBc004
199	8	4.1	315	12	CG832047	CG832047 ZMMBBc010
c 200	8	4.1	317	4	CA550636	CA550636 C0833C06-

ALIGNMENTS

RESULT 1
DQ033872
LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

```
JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
 PUBMED   15869325
ERENCE    2  (bases 1 to 762)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
          Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
          White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
ITLE      Direct Submission
JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
MENT      This sequence was made by sequencing genomic exons and ordering
          them based on alignment.  Translation starts at the beginning of
          alignment.
ATURES              Location/Qualifiers
   source           1. .762
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /chromosome="3"
   gene             <1. .>762
                    /gene="IL12A"
                    /locus_tag="HC3464"
IGIN

gnment Scores:
d. No.:              2.34e-18        Length:         762
re:                  29.00           Matches:        29
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            14.7%           Indels:         0
                     14              Gaps:           0

10-821-670A-36 (1-197) x DQ033872 (1-762)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||
       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

ULT 2
13916
US        CD013916                  863 bp    mRNA    linear   EST 21-OCT-2003
INITION   90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ESSION    CD013916
SION      CD013916.1  GI:37777446
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 863)
AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
          Au-Young,J. and Stuve,L.L.
ITLE      PCR isolation and cloning of novel splice variant mRNAs from known
          drug target genes
JOURNAL   Genomics 83 (4), 566-571 (2004)
 PUBMED   15028279
MENT      Contact: Jin, P.
          Incyte Corporation
          3160 Porter Drive, Palo Alto, CA 94304, USA
          Tel: 650 621 8639
          Fax: 650 621 8965
          Email: pjin@incyte.com.
ATURES              Location/Qualifiers
   source           1. .863
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone_lib="Single gene library"
                    /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                    using gene-specific primers flanking the open-reading
                    frame. PCR products were subcloned into pDrive Cloning
                    Vector and sequenced completely using M13 forward and
                    reverse primers. Sequencing gaps were closed by
                    re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              2.62e-18        Length:         863
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-36 (1-197) x CD013916 (1-863)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         632 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 691

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||
Db         692 GCTTTCAGAATTCGGGCAGTGACTATT 718

RESULT 3
CD013914
LOCUS       CD013914                  935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES            Location/Qualifiers
     source         1. .935
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone_lib="Single gene library"
                    /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                    using gene-specific primers flanking the open-reading
                    frame. PCR products were subcloned into pDrive Cloning
                    Vector and sequenced completely using M13 forward and
                    reverse primers. Sequencing gaps were closed by
                    re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              2.81e-18        Length:         935
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-36 (1-197) x CD013914 (1-935)
```

```
       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       704 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 763

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       764 GCTTTCAGAATTCGGGCAGTGACTATT 790

ULT 4
13915
US       CD013915                1136 bp    mRNA    linear   EST 21-OCT-2003
INITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ESSION   CD013915
SION     CD013915.1  GI:37777445
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 1136)
UTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
         Au-Young,J. and Stuve,L.L.
ITLE     PCR isolation and cloning of novel splice variant mRNAs from known
         drug target genes
OURNAL   Genomics 83 (4), 566-571 (2004)
PUBMED   15028279
MENT     Contact: Jin, P.
         Incyte Corporation
         3160 Porter Drive, Palo Alto, CA 94304, USA
         Tel: 650 621 8639
         Fax: 650 621 8965
         Email: pjin@incyte.com.
TURES             Location/Qualifiers
  source          1. .1136
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone_lib="Single gene library"
                  /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                  using gene-specific primers flanking the open-reading
                  frame. PCR products were subcloned into pDrive Cloning
                  Vector and sequenced completely using M13 forward and
                  reverse primers. Sequencing gaps were closed by
                  re-sequencig using primers flanking the gapped areas."
GIN

gnment Scores:
d. No.:              3.33e-18       Length:        1136
re:                  29.00          Matches:       29
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            14.7%          Indels:        0
                     4              Gaps:          0

10-821-670A-36 (1-197) x CD013915 (1-1136)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       905 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 964

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       965 GCTTTCAGAATTCGGGCAGTGACTATT 991

ULT 5
35571
US       BC035571                1938 bp    mRNA    linear   HTC 04-MAR-2003
INITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ESSION   BC035571
SION     BC035571.1  GI:23958681
WORDS    HTC.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 1938)
  AUTHORS    Strausberg,R.
  TITLE      Direct Submission
  JOURNAL    Submitted (31-JUL-2002) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
  REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: National Institutes of Health Intramural
             Sequencing Center (NISC),
             Gaithersburg, Maryland;
             Web site: http://www.nisc.nih.gov/
             Contact: nisc_mgc@nhgri.nih.gov
             Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
             Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
             Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
             Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
             Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
             McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
             Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
             Young,A., Zhang,L.-H. and Green,E.D.

             Clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRAK Plate: 69 Row: b Column: 15
             This clone was selected for full length sequencing because it
             passed the following selection criteria: matched mRNA gi: 4504638
             This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:              5.33e-18       Length:        1938
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            14.7%          Indels:        0
DB:                     6              Gaps:          0

US-10-821-670A-36 (1-197) x BC035571 (1-1938)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1385

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db       1386 GCTTTCAGAATTCGGGCAGTGACTATT 1412

RESULT 6
DQ033873
LOCUS        DQ033873                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION   Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
```

```
:ESSION    DQ033873
:SION      DQ033873.1  GI:66885082
:WORDS     GSS.
:RCE       Pan troglodytes (chimpanzee)
:RGANISM   Pan troglodytes
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Pan.
:ERENCE    1  (bases 1 to 762)
:UTHORS    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
           Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
           White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
:ITLE      A Scan for Positively Selected Genes in the Genomes of Humans and
           Chimpanzees
:OURNAL    (er) PLoS Biol. 3 (6), E170 (2005)
 :UBMED    15869325
:ERENCE    2  (bases 1 to 762)
:UTHORS    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
           Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
           White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
:ITLE      Direct Submission
:OURNAL    Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
           Rockville, MD 20850, USA
:MENT      This sequence was made by sequencing genomic exons and ordering
           them based on alignment.  Translation starts at the beginning of
           alignment.
:TURES             Location/Qualifiers
   source          1. .762
                   /organism="Pan troglodytes"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9598"
   gene            <1. .>762
                   /gene="IL12A"
                   /locus_tag="HC3464"
:GIN

:gnment Scores:
:d. No.:              2.38e-17       Length:        762
:re:                  28.00          Matches:       28
:cent Similarity:     100.0%         Conservative:  0
:t Local Similarity:  100.0%         Mismatches:    0
:ry Match:            14.2%          Indels:        0
                      14             Gaps:          0

-10-821-670A-36 (1-197) x DQ033873 (1-762)

        42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       292 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 351

        62 AlaCysLeuProLeuGluLeuThr 69
           |||||||||||||||||||||||
       352 GCCTGTTTACCATTGGAATTAACC 375

:ULT 7
'02253
:US        BG702253                812 bp    mRNA    linear   EST 07-MAY-2001
'INITION   602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
           mRNA sequence.
:ESSION    BG702253
:SION      BG702253.1  GI:13973409
:WORDS     EST.
:RCE       Homo sapiens (human)
:RGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
'ERENCE    1  (bases 1 to 812)
:UTHORS    NIH-MGC http://mgc.nci.nih.gov/.
:ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
:OURNAL    Unpublished (1999)
'MENT      Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
           Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM10714  row: e  column: 15
           High quality sequence stop: 804.
FEATURES           Location/Qualifiers
     source        1. .812
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:4816118"
                   /tissue_type="hippocampus"
                   /lab_host="DH10B"
                   /clone_lib="NIH_MGC_95"
                   /note="Organ: brain; Vector: pBluescriptR (modified
                   pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                   (gtcgag); Oligo-dT primed using primer
                   5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                   insert size 2.5 kb and normalized to ROT 5. This is a
                   primary library enriched for  full-length clones and
                   constructed using the Cap-trapper method (Carninci, in
                   preparation).  Library constructed by M. Brownstein
                   (NIMH/NHGRI, National Institutes of Health).  Note: this
                   is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              2.51e-17       Length:        812
Score:                  28.00          Matches:       28
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            14.2%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x BG702253 (1-812)

Qy          42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         606 TGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 665

Qy          62 AlaCysLeuProLeuGluLeuThr 69
               |||||||||||||||||||||||
Db         666 GCCTGTTTACCATTGGAATTAACC 689

RESULT 8
BI523569
LOCUS       BI523569                832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
```

```
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: LLAM11605  row: 1  column: 09
        High quality sequence start: 23
        High quality sequence stop: 821.
TURES             Location/Qualifiers
  source          1. .832
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:5240216"
                  /lab_host="DH10B"
                  /clone_lib="NIH_MGC_121"
                  /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                  fetal brains, female age 20 weeks, female age 24 weeks,
                  and male age 26 weeks.  Library is oligo-dT primed and
                  directionally cloned (EcoRV site is destroyed  upon
                  cloning).  Average insert size 1.7 kb, insert size range
                  0.7-3.5 kb.  Library is normalized and enriched for
                  full-length clones and  was constructed by C. Gruber
                  (Invitrogen).  Research Genetics  tracking code 017. Note:
                  this is a NIH_MGC Library."
GIN

gnment Scores:
d. No.:              2.57e-17       Length:         832
re:                  28.00          Matches:        28
cent Similarity:     100.0%         Conservative:   0
t Local Similarity:  100.0%         Mismatches:     0
ry Match:            14.2%          Indels:         0
                     2              Gaps:           0

10-821-670A-36 (1-197) x BI523569 (1-832)

        42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       511 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 570

        62 AlaCysLeuProLeuGluLeuThr 69
           |||||||||||||||||||||||
       571 GCCTGTTTACCATTGGAATTAACC 594

ULT 9
60963
US       BP260963                  581 bp    mRNA    linear   EST 16-SEP-2004
INITION  BP260963 Sugano cDNA library, small intestine Homo sapiens cDNA
         clone HSI02082, mRNA sequence.
ESSION   BP260963
SION     BP260963.1  GI:52176194
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 581)
UTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
         Mizushima-Sugano,J., Nakai,K. and Sugano,S.
ITLE     Sequence comparison of human and mouse genes reveals a homologous
         block structure in the promoter regions
OURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED   15342556
MENT     Contact: Yutaka Suzuki
         Department of Virology
         Institute of Medical Science, University of Tokyo
         4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
         Tel: 81-3-5449-5343
         Fax: 81-3-5449-5416
         Email: ysuzuki@hgc.jp.
TURES             Location/Qualifiers
  source          1. .581
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="HSI02082"
                  /tissue_type="small intestine"
                  /clone_lib="Sugano cDNA library, small intestine"
ORIGIN

Alignment Scores:
Pred. No.:              1.97e-13       Length:         581
Score:                  24.00          Matches:        24
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            12.2%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-36 (1-197) x BP260963 (1-581)

Qy          42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         508 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 567

Qy          62 AlaCysLeuPro 65
               ||||||||||||
Db         568 GCCTGTTTACCA 579

RESULT 10
CT080894
LOCUS       CT080894                 777 bp    DNA     linear   GSS 01-NOV-2005
DEFINITION  Sus scrofa genomic clone PigE-253A7, genomic survey sequence.
ACCESSION   CT080894
VERSION     CT080894.1  GI:78647963
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 253A7. 253A7 is
            part of the PigEBAC BAC Library created by Roslin Institute/RFCGR.
            Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="PigE-253A7"
                     /tissue_type="Blood cells"
                     /note="vector pBeloBAC11
                     sex male"
ORIGIN

Alignment Scores:
Pred. No.:              2.55e-13       Length:         777
Score:                  24.00          Matches:        24
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            12.2%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-36 (1-197) x CT080894 (1-777)

Qy         118 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         609 GCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTGGATCAGAACATG 668

Qy         138 LeuThrAlaIle 141
               ||||||||||||
Db         669 CTCACAGCCATC 680
```

```
       669 CTGACAGCTATT 680

;ULT 11
.59257
:US        CE159257                592 bp    DNA     linear   GSS 25-SEP-2003
'INITION   tigr-gss-dog-17000371408491 Dog Library Canis familiaris genomic,
           genomic survey sequence.
:ESSION    CE159257
:SION      CE159257.1  GI:35287296
'WORDS     GSS.
:RCE       Canis familiaris (dog)
)RGANISM   Canis familiaris
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
           Canis.
'ERENCE    1  (bases 1 to 592)
\UTHORS    Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
           Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
           Venter,J.C.
:ITLE      The dog genome: survey sequencing and comparative analysis
'OURNAL    Science 301 (5641), 1898-1903 (2003)
 PUBMED    14512627
'MENT      Contact: Kirkness EF
           The Institute for Genomic Research
           Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
           Rockville, MD 20850, USA
           Tel: 301-838-0200
           Fax: 301-838-0208
           Email: ekirknes@tigr.org
           Class: shotgun.
\TURES              Location/Qualifiers
   source           1. .592
                    /organism="Canis familiaris"
                    /mol_type="genomic DNA"
                    /strain="Standard Poodle"
                    /db_xref="taxon:9615"
                    /clone_lib="Dog Library"
                    /note="Site_1: BstXI; Libraries were prepared from
                    peripheral blood"
:GIN

.gnment Scores:
:d. No.:               2.08e-10       Length:         592
)re:                   21.00          Matches:        21
:cent Similarity:      100.0%         Conservative:   0
:t Local Similarity:   100.0%         Mismatches:     0
:ry Match:             10.7%          Indels:         0
                       12             Gaps:           0

-10-821-670A-36 (1-197) x CE159257 (1-592)

        50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 69
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        51 GAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACC 110

        70 Met 70
           |||
       111 ATG 113

;ULT 12
)20622/c
:US        AJ820622                778 bp    mRNA    linear   EST 12-MAY-2005
'INITION   AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
:ESSION    AJ820622
:SION      AJ820622.1  GI:51888098
'WORDS     EST.
:RCE       Bos sp.
)RGANISM   Bos sp.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
           Pecora; Bovidae; Bovinae; Bos.
'ERENCE    1  (bases 1 to 778)
\UTHORS    McGuire,K. and Glass,E.J.
  TITLE     The expanding role of microarrays in the investigation of
            macrophage responses to pathogens
  JOURNAL   Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT     Contact: McGuire K
            Genomics and Genetics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
            1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
            constructed from pooled monocytes from Bos taurus (Holstein) and
            Bos indicus (Sahiwals) cattle subjected to various stimuli,
            including infection with the protozoan parasite Theileria annulata.
FEATURES              Location/Qualifiers
     source           1. .778
                      /organism="Bos sp."
                      /mol_type="mRNA"
                      /db_xref="taxon:29061"
                      /clone="C0006020h12"
                      /tissue_type="blood"
                      /cell_type="bovine monocyte"
                      /clone_lib="KN206"
                      /note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
                      Site_2: NotI; Normalised library constructed from pooled
                      monocytes from Bos taurus (Holstein) and Bos indicus
                      (Sahiwals) cattle subjected to various stimuli, including
                      infection with the protozoan parasite Theileria annulata"
ORIGIN

Alignment Scores:
Pred. No.:               2.65e-10       Length:         778
Score:                   21.00          Matches:        21
Percent Similarity:      100.0%         Conservative:   0
Best Local Similarity:   100.0%         Mismatches:     0
Query Match:             10.7%          Indels:         0
DB:                      1              Gaps:           0

US-10-821-670A-36 (1-197) x AJ820622 (1-778)

Qy        118 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 GCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAAATCTTTCTAGACCAGAACATG 697

Qy        138 Leu 138
              |||
Db        696 CTG 694

RESULT 13
BM257856
LOCUS       BM257856                342 bp    mRNA    linear   EST 17-DEC-2001
DEFINITION  521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BM257856
VERSION     BM257856.1  GI:17893455
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
```

```
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called and alt_trimmed with phred
        v0.980904.e. Vector identified by cross_match with the -minscore 18
        and -minmatch 12 options.
        PCR PRimers
        FORWARD: AGGAAACAGCTATGACCAT
        BACKWARD: GTTTTCCCAGTCACGACG
        Plate: 125  row: E  column: 18
        Seq primer: ATTTAGGTGACACTATAG.
TURES             Location/Qualifiers
  source          1. .342
                  /organism="Bos taurus"
                  /mol_type="mRNA"
                  /db_xref="taxon:9913"
                  /tissue_type="pooled"
                  /lab_host="DH10B"
                  /clone_lib="MARC 3BOV"
                  /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                  Library made from pooled tissue from marrow, alveolar
                  macrophage, ovary, fetal semitendonosus muscle, and fetal
                  longissimus muscle."
GIN

gnment Scores:
d. No.:               1.3e-09        Length:         342
re:                   20.00          Matches:        20
cent Similarity:      100.0%         Conservative:   0
t Local Similarity:   100.0%         Mismatches:     0
ry Match:             10.2%          Indels:         0
                      2              Gaps:           0

10-821-670A-36 (1-197) x BM257856 (1-342)

        27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       282 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 341

ULT 14
37236
US        BX537236                344 bp    DNA     linear   GSS 05-JUN-2003
INITION   INRA porcine BAC library, clone 0849A01 BAC end sequence (Uni M13),
          genomic survey sequence.
ESSION    BX537236
SION      BX537236.1  GI:31455351
WORDS     GSS; genome survey sequence.
RCE       Sus scrofa (pig)
RGANISM   Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
          Sus.
ERENCE    1
UTHORS    Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
          Chardon,P.
ITLE      Construction of a swine BAC library: application to the
          characterization and mapping of porcine type C endoviral elements
OURNAL    Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
UBMED     10449899
ERENCE    2  (bases 1 to 344)
UTHORS    Robic,A.
ITLE      Direct Submission
OURNAL    Submitted (05-JUN-2003) Robic A., INRA, Laboratoire de Genetique
          Cellulaire, chemin de Borde rouge, BP27, Auzeville, 31626, FRANCE
          Phone : 05 61 28 51 15 Fax : 05 61 28 53 08 Email :
          arobic@toulouse.inra.fr
TURES             Location/Qualifiers
  source          1. .344
                  /organism="Sus scrofa"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9823"
                  /clone="0849A01"
                  /note="library Rogel gaillard et al 1999, clone 0849A01
                  Clone distribution : AGENAE Resource center. Francois
                  PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA
                  Radiobiologie et Etude du genome (LREG), Domaine de
                  Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
ORIGIN

Alignment Scores:
Pred. No.:            1.31e-09       Length:         344
Score:                20.00          Matches:        20
Percent Similarity:   100.0%         Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:          10.2%          Indels:         0
DB:                   14             Gaps:           0

US-10-821-670A-36 (1-197) x BX537236 (1-344)

Qy        122 LysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTGGATCAGAACATGCTGACAGCTATT 60

RESULT 15
BI824638
LOCUS       BI824638                447 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
            mRNA sequence.
ACCESSION   BI824638
VERSION     BI824638.1  GI:15936188
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11435  row: o  column: 19
            High quality sequence start: 3
            High quality sequence stop: 445.
FEATURES              Location/Qualifiers
     source           1. .447
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5175018"
                      /lab_host="DH10B"
                      /clone_lib="NIH_MGC_115"
                      /note="Organ: pooled brain, lung, testis; Vector:
                      pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                      source anonymous pool of 6 male brains, age range 23-27; 1
                      male lung, age 27; and 1 male testis, age 69.  Library is
                      oligo-dT primed and directionally cloned (EcoRV site is
                      destroyed upon  cloning).  Average insert size 1.8 kb,
                      insert size range 1-3 kb. Library is normalized and
                      enriched for full-length clones and was  constructed by C.
                      Gruber (Invitrogen).  Research Genetics tracking  code
                      021. Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:            1.69e-07       Length:         447
Score:                18.00          Matches:        18
Percent Similarity:   100.0%         Conservative:   0
```

```
:t Local Similarity:  100.0%          Mismatches:    0
:ry Match:            9.1%            Indels:        0
                      2               Gaps:          0

10-821-670A-36 (1-197) x BI824638 (1-447)

       170 LysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATT 54

:ULT 16
:23344/c
:US       BI523344              1099 bp    mRNA    linear   EST 29-AUG-2001
'INITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
          mRNA sequence.
:ESSION   BI523344
:SION     BI523344.1  GI:15348136
'WORDS    EST.
'RCE      Homo sapiens (human)
)RGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
'ERENCE   1  (bases 1 to 1099)
\UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
:ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
IOURNAL   Unpublished (1999)
IMENT     Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11605  row: 1  column: 09
          High quality sequence start: 40
          High quality sequence stop: 727.
\TURES              Location/Qualifiers
   source           1. .1099
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5240216"
                    /lab_host="DH10B"
                    /clone_lib="NIH_MGC_121"
                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                    fetal brains, female age 20 weeks, female age 24 weeks,
                    and male age 26 weeks.  Library is oligo-dT primed and
                    directionally cloned (EcoRV site is destroyed  upon
                    cloning).  Average insert size 1.7 kb, insert size range
                    0.7-3.5 kb.  Library is normalized and enriched for
                    full-length clones and  was constructed by C. Gruber
                    (Invitrogen).  Research Genetics  tracking code 017. Note:
                    this is a NIH_MGC Library."
:GIN

.gnment Scores:
:d. No.:              3.78e-06        Length:        1099
)re:                  17.00           Matches:       17
:cent Similarity:     100.0%          Conservative:  0
:t Local Similarity:  100.0%          Mismatches:    0
:ry Match:            8.6%            Indels:        0
                      2               Gaps:          0

10-821-670A-36 (1-197) x BI523344 (1-1099)

       171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
       522 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATT 472

RESULT 17
CB168830/c
LOCUS       CB168830               777 bp    mRNA    linear   EST 30-JAN-2003
DEFINITION  CWI602769160.R1 CSEQFXL41 testes Bos taurus cDNA, mRNA sequence.
ACCESSION   CB168830
VERSION     CB168830.1  GI:28154956
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Bovine ESTs (Adelson and Gill)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="testes"
                     /clone_lib="CSEQFXL41 testes"
                     /note="Organ: testes; Vector: pBluescript SK+; Site_1:
                     NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     non-normalized library, sequenced 3' with M13R primer."
ORIGIN

Alignment Scores:
Pred. No.:            2.83e-05        Length:        777
Score:                16.00           Matches:       16
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          8.1%            Indels:        0
DB:                   4               Gaps:          0

US-10-821-670A-36 (1-197) x CB168830 (1-777)

Qy        172 LysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 AAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATC 572

RESULT 18
AI332701/c
LOCUS       AI332701               528 bp    mRNA    linear   EST 13-FEB-1999
DEFINITION  qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948
            3' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   AI332701
VERSION     AI332701.1  GI:4069260
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1469 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.

TURES Location/Qualifiers
source 1. .528
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1932948"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

GIN

gnment Scores:

d. No.:	0.0209	Length:	528
re:	13.00	Matches:	13
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	6.6%	Indels:	0
	1	Gaps:	0

10-821-670A-36 (1-197) x AI332701 (1-528)

```
       175 IleLeuLeuHisAlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||||||||||||||
       528 ATACTTCTCCATGCTTTCAGAATTCGGGCAGTGACTATT 490
```

ULT 19
52757
US BF552757 373 bp mRNA linear EST 12-DEC-2000
INITION UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ESSION BF552757
SION BF552757.1 GI:11662487
WORDS EST.
RCE Rattus norvegicus (Norway rat)
RGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
ERENCE 1 (bases 1 to 373)
UTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
ITLE Normalization and subtraction: two approaches to facilitate gene discovery
OURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
MENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID= 1782759
Seq primer: M13 Forward.

FEATURES Location/Qualifiers
source 1. .373
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-iz-d-02-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-C0"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"

ORIGIN

Alignment Scores:

Pred. No.:	16	Length:	373
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x BF552757 (1-373)

```
Qy        104 SerIleTyrGluAspLeuLysMetTyrGln 113
              |||||||||||||||||||||||||||||||
Db         98 AGCATCTATGAGGACTTGAAGATGTACCAG 127
```

RESULT 20
DT930939
LOCUS DT930939 427 bp mRNA linear EST 20-SEP-2005
DEFINITION S13.1784 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION DT930939
VERSION DT930939.1 GI:75963455
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 427)
AUTHORS Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and Lemischka,I.R.
TITLE Diversification of Stem Cell Molecular Repertoire by Alternative Splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657

```
         Fax: 609 258 1704
         Email: pritsker@molbio.princeton.edu.
ATURES              Location/Qualifiers
   source           1. .427
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /tissue_type="Hematopoietic stem cells"
                    /cell_type="Hematopoietic stem cells"
                    /clone_lib="Hematopoietic stem cells"
                    /note="cDNA library was made from FACS-purified
                    hematopoietic stem cells"
IGIN

gnment Scores:
d. No.:              18              Length:         427
re:                  10.00           Matches:        10
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            5.1%            Indels:         0
                     10              Gaps:           0

10-821-670A-36 (1-197) x DT930939 (1-427)

       104 SerIleTyrGluAspLeuLysMetTyrGln 113
           ||||||||||||||||||||||||||||||
       382 AGCATCTATGAGGACTTGAAGATGTACCAG 411

ULT 21
13216
US       DT913216                456 bp    mRNA    linear   EST 19-SEP-2005
FINITION  S13.1426 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
CESSION  DT913216
SION     DT913216.1  GI:75893697
WORDS    EST.
RCE      Mus musculus (house mouse)
RGANISM  Mus musculus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
         Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE   1  (bases 1 to 456)
UTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
         Lemischka,I.R.
ITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
         Splicing
OURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
MENT     Contact: Pritsker M
         Lab of Ihor Lemischka, Department of Molecular Biology
         Princeton University
         Princeton, NJ 08544, USA
         Tel: 609 258 5657
         Fax: 609 258 1704
         Email: pritsker@molbio.princeton.edu.
ATURES              Location/Qualifiers
   source           1. .456
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /tissue_type="Hematopoietic stem cells"
                    /cell_type="Hematopoietic stem cells"
                    /clone_lib="Hematopoietic stem cells"
                    /note="cDNA library was made from FACS-purified
                    hematopoietic stem cells"
IGIN

gnment Scores:
d. No.:              19.1            Length:         456
re:                  10.00           Matches:        10
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            5.1%            Indels:         0
                     10              Gaps:           0
```

```
US-10-821-670A-36 (1-197) x DT913216 (1-456)

Qy         104 SerIleTyrGluAspLeuLysMetTyrGln 113
               ||||||||||||||||||||||||||||||
Db         382 AGCATCTATGAGGACTTGAAGATGTACCAG 411

RESULT 22
BU699383
LOCUS       BU699383                561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES                Location/Qualifiers
     source             1. .561
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /tissue_type="Hematopoietic"
                        /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                        Ly6A/E (Sca-1)pos"
                        /dev_stage="Embryonic day 14-14.5"
                        /lab_host="DH10B"
                        /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                        /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                        Site_2: Not I; Two directionally cloned cDNA libraries
                        were made from fetal liver hematopoietic stem cells
                        enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                        (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                        cells. Subtractive hybridization was performed by
                        hybridization of the target, Scapos, single stranded cDNA
                        library in pSport1 to biotinylated RNA transcribed from
                        the driver, AA4.1neg cDNA library in pSport2 with inserts
                        cloned in the complementary orientation. For detailed
                        protocols and additional information please see our
                        website at http://stemcell.princeton.edu."
ORIGIN

Alignment Scores:
Pred. No.:              22.9            Length:         561
Score:                  10.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.1%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x BU699383 (1-561)
```

```
       104 SerIleTyrGluAspLeuLysMetTyrGln 113
           ||||||||||||||||||||||||||||||
       299 AGCATCTATGAGGACTTGAAGATGTACCAG 328

ULT 23
98113
US       BU698113                 563 bp    mRNA    linear   EST 09-OCT-2002
INITION  LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus
         musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
         sequence.
ESSION   BU698113
SION     BU698113.1  GI:23610620
WORDS    EST.
RCE      Mus musculus (house mouse)
RGANISM  Mus musculus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
         Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE   1  (bases 1 to 563)
UTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
         Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
ITLE     The genetic program of hematopoietic stem cells
OURNAL   Science 288 (5471), 1635-1640 (2000)
PUBMED   10834841
MENT     Contact: Lemischka, Ihor R.
         Department of Molecular Biology
         Princeton University
         Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
         Tel: 609 258 2838
         Fax: 609 258 2759
         Email: ilemischka@molbio.princeton.edu
         These ESTs are derived from a subtracted cDNA library enriched for
         gene products expressed in day 14-14.5 fetal liver hematopoietic
         stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
         (Sca-1)pos
         Seq primer: M13Reverse or T7.
TURES             Location/Qualifiers
  source          1. .563
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /tissue_type="Hematopoietic"
                  /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                  Ly6A/E (Sca-1)pos"
                  /dev_stage="Embryonic day 14-14.5"
                  /lab_host="DH10B"
                  /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                  /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                  Site_2: Not I; Two directionally cloned cDNA libraries
                  were made from fetal liver  hematopoietic stem cells
                  enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                  (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                  cells. Subtractive hybridization was  performed by
                  hybridization of the target, Scapos, single stranded cDNA
                  library in pSport1 to  biotinylated RNA transcribed from
                  the driver, AA4.1neg cDNA library in pSport2 with  inserts
                  cloned in the complementary orientation. For detailed
                  protocols and additional  information please see our
                  website at http://stemcell.princeton.edu."
GIN

gnment Scores:
d. No.:              23              Length:         563
re:                  10.00           Matches:        10
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            5.1%            Indels:         0
                     3               Gaps:           0

10-821-670A-36 (1-197) x BU698113 (1-563)
```

```
Qy       104 SerIleTyrGluAspLeuLysMetTyrGln 113
             ||||||||||||||||||||||||||||||
Db       315 AGCATCTATGAGGACTTGAAGATGTACCAG 344

RESULT 24
AI050362
LOCUS       AI050362                 589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:              23.9            Length:         589
Score:                  10.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.1%            Indels:         0
DB:                     1               Gaps:           0

US-10-821-670A-36 (1-197) x AI050362 (1-589)
```

```
       104 SerIleTyrGluAspLeuLysMetTyrGln 113
           ||||||||||||||||||||||||||||||
       324 AGCATCTATGAGGACTTGAAGATGTACCAG 353

ULT 25
29972/c
US       AZ729972                 614 bp    DNA     linear   GSS 25-JAN-2001
INITION  RPCI-24-117G9.TV RPCI-24 Mus musculus genomic clone RPCI-24-117G9,
         genomic survey sequence.
ESSION   AZ729972
SION     AZ729972.1  GI:12488267
WORDS    GSS.
RCE      Mus musculus (house mouse)
RGANISM  Mus musculus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
         Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE   1  (bases 1 to 614)
UTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
         Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
         Russell,D., de Jong,P. and Fraser,C.M.
ITLE     Mouse BAC End Sequences from Library RPCI-24
OURNAL   Unpublished (1999)
MENT     Other_GSSs: RPCI-24-117G9.TJ
         Contact: Shaying Zhao
         Department of Eukaryotic Genomics
         The Institute for Genomic Research
         9712 Medical Center Dr., Rockville, MD 20850, USA
         Tel: 301 838 0200
         Fax: 301 838 0208
         Email: szhao@tigr.org
         Clones are derived from the mouse BAC library RPCI-24. For BAC
         library availability, please contact Pieter de Jong
         (pdejong@mail.cho.org). Clones may be purchased from BACPAC
         Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
         page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
         Plate: 117  row: G  column: 9
         Seq primer: T7
         Class: BAC ends.
TURES              Location/Qualifiers
   source          1. .614
                   /organism="Mus musculus"
                   /mol_type="genomic DNA"
                   /strain="C57BL/6J"
                   /db_xref="taxon:10090"
                   /clone="RPCI-24-117G9"
                   /sex="Male"
                   /cell_type="Spleen/Brain"
                   /clone_lib="RPCI-24"
                   /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                   RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                   library was  cloned in the pTARBAC1 cloning vector at the
                   BamH1 sites using MboI  partially digested male C57BL/6J
                   DNA."
GIN

gnment Scores:
d. No.:              24.8          Length:        614
re:                  10.00         Matches:       10
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            5.1%          Indels:        0
                     11            Gaps:          0

-10-821-670A-36 (1-197) x AZ729972 (1-614)

        74 CysLeuAlaSerArgGluIleSerLeuIle 83
           ||||||||||||||||||||||||||||||
       350 TGTTTAGCTTCTAGAGAAATTAGTCTCATC 321

ULT 26
37697
US       CJ137697                 692 bp    mRNA    linear   EST 23-SEP-2005

DEFINITION  CJ137697 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            thymus 3 days neonate Mus musculus cDNA clone A630064E02 5', mRNA
            sequence.
ACCESSION   CJ137697
VERSION     CJ137697.1  GI:76238025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Dr. John Todd (
            Dept. of Medical Genetics Wellcome Trust Centre for Molecular
            Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes
            Hospital Cambridge ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES              Location/Qualifiers
     source           1. .692
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="A630064E02"
                      /tissue_type="thymus"
                      /dev_stage="3 days neonate"
                      /clone_lib="RIKEN full-length enriched mouse cDNA library,
                      C57BL/6J thymus 3 days neonate"
ORIGIN

Alignment Scores:
Pred. No.:              27.6          Length:        692
Score:                  10.00         Matches:       10
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            5.1%          Indels:        0
DB:                     5             Gaps:          0

US-10-821-670A-36 (1-197) x CJ137697 (1-692)

Qy        104 SerIleTyrGluAspLeuLysMetTyrGln 113
              ||||||||||||||||||||||||||||||
Db        518 AGCATCTATGAGGACTTGAAGATGTACCAG 547

RESULT 27
CZ271875/c
LOCUS       CZ271875                 941 bp    DNA     linear   GSS 14-MAR-2005
DEFINITION  ZMMBF0051D18f ZMMBF Zea mays genomic clone ZMMBF0051D18 5', genomic
            survey sequence.
ACCESSION   CZ271875
VERSION     CZ271875.1  GI:61108687
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

```
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
ERENCE    1  (bases 1 to 941)
UTHORS    Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,G.
          and Messing,J.
ITLE      Construction, Sequencing and Characterization of a Fosmid Library
          of the B73 Maize Genome
OURNAL    Unpublished (2005)
MENT      Contact: Bharti,A.K.
          Dr.Joachim Messing's lab
          The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
          University
          190 Frelinghuysen Road, Piscataway, NJ 08854, USA
          Tel: 732 445 3801
          Fax: 732 445 5735
          Email: bharti@waksman.rutgers.edu
          Seq primer: Fos_F
          Class: fosmid ends.
TURES               Location/Qualifiers
  source            1. .941
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /cultivar="B73"
                    /db_xref="taxon:4577"
                    /clone="ZMMBF0051D18"
                    /lab_host="EPI100-T1"
                    /clone_lib="ZMMBF"
                    /note="Vector: pEpiFOS-5; Site_1: Eco72I"
GIN

gnment Scores:
d. No.:                 36.2            Length:         941
re:                     10.00           Matches:        10
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               5.1%            Indels:         0
                        13              Gaps:           0

10-821-670A-36 (1-197) x CZ271875 (1-941)

        57 ThrSerThrValGluAlaCysLeuProLeu 66
           ||||||||||||||||||||||||||||||
       935 ACATCTACTGTTGAAGCATGTTTGCCATTG 906

ULT 28
53729
US        AK153729                1299 bp    mRNA    linear   HTC 21-SEP-2005
INITION   Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
          library, clone:A630064E02 product:interleukin 12a, full insert
          sequence.
ESSION    AK153729
SION      AK153729.1  GI:74148962
WORDS     HTC; CAP trapper.
RCE       Mus musculus (house mouse)
RGANISM   Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE    1
UTHORS    Carninci,P. and Hayashizaki,Y.
ITLE      High-efficiency full-length cDNA cloning
OURNAL    Meth. Enzymol. 303, 19-44 (1999)
UBMED     10349636
ERENCE    2
UTHORS    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
          Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
ITLE      Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new genes
OURNAL    Genome Res. 10 (10), 1617-1630 (2000)
UBMED     11042159
ERENCE    3
UTHORS    Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
          Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
          Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
          Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
          Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
          Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
          Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer
  JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
  PUBMED  11076861
REFERENCE 4
  AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
          Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
          Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
          Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
          Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
          Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
          Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
          Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
          Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
          Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
          Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
          Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
          Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
          Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
          Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
          Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
          Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
          Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
          and Hayashizaki,Y.
  CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the
          FANTOM Consortium
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL Nature 409 (6821), 685-690 (2001)
  PUBMED  11217851
REFERENCE 5
  AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
          Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
          Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
          Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
          Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
          Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
          Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
          Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
          Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
          Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
          Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
          Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
          Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
          Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
          Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
          Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
          Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
          Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
          Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
          Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
          Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
          Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
          Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
          Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
          Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
          Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
          Rogers,J., Birney,E. and Hayashizaki,Y.
  CONSRTM FANTOM Consortium
  TITLE   Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
  JOURNAL Nature 420 (6915), 563-573 (2002)
  PUBMED  12466851
REFERENCE 6
  AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C.,
          Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R.,
          Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R.,
          Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E.,
          Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L.,
```

```
                Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M.,
                Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R.,
                Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G.,
                di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G.,
                Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M.,
                Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E.,
                Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N.,
                Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T.,
                Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H.,
                Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K.,
                Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J.,
                Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L.,
                Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S.,
                Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H.,
                Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O.,
                Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G.,
                Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z.,
                Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A.,
                Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S.,
                Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D.,
                Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R.,
                Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S.,
                Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R.,
                Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A.,
                Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T.,
                Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A.,
                Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M.,
                Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M.,
                Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M.,
                Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M.,
                Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
                Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
:ONSRTM         FANTOM Consortium
:ITLE           The transcriptional landscape of the mammalian genome
:OURNAL         Science 309 (5740), 1559-1563 (2005)
 PUBMED         16141072
:ERENCE         7
:UTHORS         Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
                Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
                Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
                Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
                Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
                Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
                Wahlestedt,C.
:ONSRTM         RIKEN Genome Exploration Research Group
:ITLE           Antisense transcription in the mammalian transcriptome
:OURNAL         Science 309 (5740), 1564-1566 (2005)
 PUBMED         16141073
:ERENCE         8  (bases 1 to 1299)
:UTHORS         Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
                Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
                Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
                Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
                Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
                Muramatsu,M. and Hayashizaki,Y.
:ITLE           Direct Submission
:OURNAL         Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
                Physical and Chemical Research (RIKEN), Laboratory for Genome
                Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
                URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                Fax:81-45-503-9216)
:MENT           cDNA library was prepared and sequenced in Mouse Genome
                Encyclopedia Project of Genome Exploration Research Group in Riken
                Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                Division of Experimental Animal Research in Riken contributed to
                prepare mouse tissues.
                Please visit our web site for further details.
                URL:http://genome.gsc.riken.jp/
                URL:http://fantom.gsc.riken.jp/.
:TURES                  Location/Qualifiers
   source               1. .1299
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="FANTOM_DB:A630064E02"
                        /db_xref="taxon:10090"
                        /clone="A630064E02"
                        /tissue_type="thymus"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="3 days neonate"
      misc_feature      1. .1299
                        /note="interleukin 12a (MGD|MGI:96539 GB|NM_008351,
                        evidence: BLASTN, 100%, match=776)
                        putative"
ORIGIN

Alignment Scores:
Pred. No.:                  48          Length:          1299
Score:                      10.00       Matches:         10
Percent Similarity:         100.0%      Conservative:    0
Best Local Similarity:      100.0%      Mismatches:      0
Query Match:                5.1%        Indels:          0
DB:                         6           Gaps:            0

US-10-821-670A-36 (1-197) x AK153729 (1-1299)

Qy        104 SerIleTyrGluAspLeuLysMetTyrGln 113
              ||||||||||||||||||||||||||||||
Db        518 AGCATCTATGAGGACTTGAAGATGTACCAG 547

RESULT 29
BY368866
LOCUS       BY368866                192 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  BY368866 RIKEN full-length enriched, 6 days neonate spleen Mus
            musculus cDNA clone F430208H13 3', mRNA sequence.
ACCESSION   BY368866
VERSION     BY368866.1  GI:26598354
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 192)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
```

```
PUBMED   12466851
MENT     Contact: Yoshihide Hayashizaki
         Laboratory for Genome Exploration Research Group, RIKEN Genomic
         Sciences Center(GSC), Yokohama Institute
         The Institute of Physical and Chemical Research (RIKEN)
         1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
         Tel: 81-45-503-9222
         Fax: 81-45-503-9216
         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
         Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
         Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
         Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
         Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
         Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
         Hayashizaki,Y. Direct Submission
          Computational Analysis of Full-Length Mouse cDNAs Compared with
         Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
          Normalization and subtraction of cap-trapper-selected cDNAs to
         prepare full-length cDNA libraries for rapid discovery of new
         genes. Genome Res. 10 (10), 1617-1630 (2000)
          RIKEN integrated sequence analysis (RISA) system--384-format
         sequencing pipeline with 384 multicapillary sequencer. Genome Res.
         10 (11), 1757-1771 (2000)
          Computer-based methods for the mouse full-length cDNA
         encyclopedia: real-time sequence clustering for construction of a
         nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
          cDNA library was prepared and sequenced in Mouse Genome
         Encyclopedia Project of Genome Exploration Research Group in Riken
         Genomic Sciences Center and Genome Science Laboratory in RIKEN.
         Division of Experimental Animal Research in Riken contributed to
         prepare mouse tissues.
          Please visit our web site (http://genome.gsc.riken.go.jp) for
         further details.
TURES             Location/Qualifiers
  source          1. .192
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="F430208H13"
                  /tissue_type="spleen"
                  /dev_stage="6 days neonate"
                  /clone_lib="RIKEN full-length enriched, 6 days neonate
                  spleen"
IN

gnment Scores:
d. No.:              90.4          Length:        192
re:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            4.6%          Indels:        0
                     4             Gaps:          0

10-821-670A-36 (1-197) x BY368866 (1-192)

       170 LysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||
       161 AAAATAAAGTTGTGTATTCTATTACAT 187

ULT 30
66007/c
US       BF366007                 194 bp    mRNA    linear   EST 24-NOV-2000
INITION  PM4-NT0073-230500-002-a01 NT0073 Homo sapiens cDNA, mRNA sequence.
ESSION   BF366007
SION     BF366007.1  GI:11328032
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 194)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM4&t2=PM4-NT0073-
            230500-002-a01&t3=2000-05-23&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 16
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .194
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NT0073"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              91.3          Length:        194
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.6%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-36 (1-197) x BF366007 (1-194)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db         93 CCGACACCAACTCCAAGTCCAGGGATG 67

RESULT 31
DV345207/c
LOCUS       DV345207                 234 bp    mRNA    linear   EST 17-OCT-2005
DEFINITION  NABWE87TR Aedes aegypti infected with Brugia Malayi Aedes aegypti
            cDNA clone NABWE87, mRNA sequence.
ACCESSION   DV345207
VERSION     DV345207.1  GI:77794432
KEYWORDS    EST.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
REFERENCE   1  (bases 1 to 234)
  AUTHORS   Loftus,B., Utterback,T., Pertea,G., Koo,H., Mori,A., Schneider,J.,
            Lovin,D., deBruyn,B., Song,Z., Raikhel,A., de Fatima,B.M.,
            Casavant,T., Soares,B. and Severson,D.
  TITLE     Aedes aegypti cDNA sequencing
```

```
JOURNAL   Unpublished (2005)
MENT      Contact: David Severson
          The Institute for Genomic Research (TIGR; www.tigr.org); University
          of Notre Dame, Department of Biological Sciences
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Sequencing performed at TIGR (http://www.tigr.org) Venter
          Institute/JTC (JCVIJTC; http://venterinstitute.org) NABWE87TR
          Seq primer: REVERSE-CAGGAAACAGCTATGACC.
TURES               Location/Qualifiers
   source           1. .234
                    /organism="Aedes aegypti"
                    /mol_type="mRNA"
                    /db_xref="taxon:7159"
                    /clone="NABWE87"
                    /sex="Female"
                    /tissue_type="adult females at 24 h, 3 days and 12 days
                    post feeding on a Brugia malayi infected blood meal"
                    /dev_stage="Adult"
                    /clone_lib="Aedes aegypti infected with Brugia Malayi"
GIN

gnment Scores:
d. No.:              108          Length:        234
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            4.6%         Indels:        0
                     10           Gaps:          0

10-821-670A-36 (1-197) x DV345207 (1-234)

        21 ThrLeuLeuArgAlaIleSerAsnThr 29
           ||||||||||||||||||||||||||||
        28 ACACTTTTGAGAGCCATATCGAACACA 2

ULT 32
64595
US        BY364595                294 bp    mRNA    linear   EST 12-DEC-2002
INITION   BY364595 RIKEN full-length enriched, 8 cells embryo Mus musculus
          cDNA clone E860025O10 3', mRNA sequence.
ESSION    BY364595
SION      BY364595.1  GI:26594083
WORDS     EST.
RCE       Mus musculus (house mouse)
RGANISM   Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE    1  (bases 1 to 294)
UTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
          Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
          Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
          Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
          Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
          Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
          Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
          Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
          Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
          Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
          Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
          Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
          Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
          Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
          Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
          Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
          Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
          Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
          Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
          Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
          Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
          Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
          Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
          Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
          Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
          Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
          Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
  JOURNAL Nature 420, 563-573 (2002)
   PUBMED 12466851
COMMENT   Contact: Yoshihide Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center(GSC), Yokohama Institute
          The Institute of Physical and Chemical Research (RIKEN)
          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel: 81-45-503-9222
          Fax: 81-45-503-9216
          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
          Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
          Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
          Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
          Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
          Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
          Hayashizaki,Y. Direct Submission
           Computational Analysis of Full-Length Mouse cDNAs Compared with
          Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
           Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new
          genes. Genome Res. 10 (10), 1617-1630 (2000)
           RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer. Genome Res.
          10 (11), 1757-1771 (2000)
           Computer-based methods for the mouse full-length cDNA
          encyclopedia: real-time sequence clustering for construction of a
          nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
           cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
           Please visit our web site (http://genome.gsc.riken.go.jp) for
          further details.
FEATURES            Location/Qualifiers
     source         1. .294
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="E860025O10"
                    /cell_type="8 cells"
                    /dev_stage="8 cells embryo"
                    /clone_lib="RIKEN full-length enriched, 8 cells embryo"
ORIGIN

Alignment Scores:
Pred. No.:              132          Length:        294
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            4.6%         Indels:        0
DB:                     4            Gaps:          0

US-10-821-670A-36 (1-197) x BY364595 (1-294)

Qy          3 LeuProThrProThrProSerProGly 11
              |||||||||||||||||||||||||||
Db        165 CTCCCCACCCCCACCCCCAGCCCGGGC 191

RESULT 33
CF799003
LOCUS       CF799003                304 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  Lr_PAHCF_12D05_M13R Earthworm Fluorantene Exposure Library
            Lumbricus rubellus cDNA clone Lr_PAHCF_12D05 5' similar to
            ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
            terrestris, mRNA sequence.
ACCESSION   CF799003
```

```
SION      CF799003.1  GI:37803573
WORDS     EST.
RCE       Lumbricus rubellus (humus earthworm)
RGANISM   Lumbricus rubellus
          Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
          Lumbricina; Lumbricidae; Lumbricus.
ERENCE    1  (bases 1 to 304)
UTHORS    Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S., Kille,P. and
          Blaxter,M.
ITLE      The Lumbricus rubellus EST program - Sequences from a Fluorantene
          Exposure library
OURNAL    Unpublished (2003)
MENT      Contact: Jennifer Chaseley
          BIOSI 1
          Cardiff University
          Main College, Museum Avenue, Cardiff, CF11 3TL, UK
          Tel: +44 2920876680
          Fax: +44 2920874305
          Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
          Sequencing was performed in Cardiff using the pBluescriptII XR cDNA
          library (Stratagene) protocol.
          PCR PRimers
          FORWARD: gttttcccagtcacgacg
          BACKWARD: caggaaacagctatgaccatg
          Plate: 12  row: D  column: 05
          Seq primer: caggaaacagctatgaccatg
          High quality sequence stop: 304.
TURES               Location/Qualifiers
  source            1. .304
                    /organism="Lumbricus rubellus"
                    /mol_type="mRNA"
                    /db_xref="taxon:35632"
                    /clone="Lr_PAHCF_12D05"
                    /tissue_type="Whole worm"
                    /dev_stage="Adult"
                    /clone_lib="Earthworm Fluorantene Exposure Library"
                    /note="Vector: pBluescript II SK+; The library was
                    prepared using protocols given by the supplier
                    (Stratagene)."
GIN

gnment Scores:
d. No.:               136            Length:        304
re:                   9.00           Matches:       9
cent Similarity:      100.0%         Conservative:  0
t Local Similarity:   100.0%         Mismatches:    0
ry Match:             4.6%           Indels:        0
                      5              Gaps:          0

10-821-670A-36 (1-197) x CF799003 (1-304)

        15 CysLeuAsnHisSerGlnThrLeuLeu 23
           ||||||||||||||||||||||||||
       107 TGCCTCAACCATTCGCAGACGCTATTA 133

ULT 34
22132
US        CG422132                 343 bp    DNA     linear   GSS 22-SEP-2003
INITION   ZMMBBc0037M17f ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0037M17
          5', genomic survey sequence.
ESSION    CG422132
SION      CG422132.1  GI:34566977
WORDS     GSS.
RCE       Zea mays
RGANISM   Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
ERENCE    1  (bases 1 to 343)
UTHORS    Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
          Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
ITLE      Sequencing of the maize genome at PGIR (2003c)
OURNAL    Unpublished (2003)
COMMENT   Contact: Bharti,A.K.
          Dr.Joachim Messing's lab
          The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
          University
          190 Frelinghuysen Road, Piscataway, NJ 08854, USA
          Tel: 732 445 3801
          Fax: 732 445 5735
          Email: bharti@waksman.rutgers.edu
          Seq primer: T7
          Class: BAC ends
          High quality sequence start: 137.
FEATURES            Location/Qualifiers
     source         1. .343
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /cultivar="B73"
                    /db_xref="taxon:4577"
                    /clone="ZMMBBc0037M17"
                    /lab_host="E. coli DH10B"
                    /clone_lib="ZMMBBc (EcoRI)"
                    /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:            151            Length:        343
Score:                9.00           Matches:       9
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          4.6%           Indels:        0
DB:                   12             Gaps:          0

US-10-821-670A-36 (1-197) x CG422132 (1-343)

Qy          3 LeuProThrProThrProSerProGly 11
              |||||||||||||||||||||||||||
Db        182 CTGCCAACCCCGACACCATCACCTGGG 208

RESULT 35
CG396825
LOCUS     CG396825                 372 bp    DNA     linear   GSS 22-SEP-2003
DEFINITION ZMMBBc0014O04r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0014O04
          3', genomic survey sequence.
ACCESSION CG396825
VERSION   CG396825.1  GI:34340050
KEYWORDS  GSS.
SOURCE    Zea mays
  ORGANISM Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1  (bases 1 to 372)
  AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
          Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE   Sequencing of the maize genome at PGIR (2003b)
  JOURNAL Unpublished (2003)
COMMENT   Contact: Bharti,A.K.
          Dr.Joachim Messing's lab
          The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
          University
          190 Frelinghuysen Road, Piscataway, NJ 08854, USA
          Tel: 732 445 3801
          Fax: 732 445 5735
          Email: bharti@waksman.rutgers.edu
          Seq primer: SP6
          Class: BAC ends
          High quality sequence start: 154.
FEATURES            Location/Qualifiers
     source         1. .372
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /cultivar="B73"
                    /db_xref="taxon:4577"
                    /clone="ZMMBBc0014O04"
```

/lab_host="E. coli DH10B"
/clone_lib="ZMMBBc (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
:GIN

:gnment Scores:
:d. No.: 162 Length: 372
:re: 9.00 Matches: 9
:cent Similarity: 100.0% Conservative: 0
:t Local Similarity: 100.0% Mismatches: 0
:ry Match: 4.6% Indels: 0
12 Gaps: 0

-10-821-670A-36 (1-197) x CG396825 (1-372)

3 LeuProThrProThrProSerProGly 11
149 CTGCCCACCCCGACACCATCACCTGGG 175

:ULT 36
:38885
:JS DN988885 404 bp mRNA linear EST 17-MAY-2005
'INITION ZEBRA_2F_2-II_05_ZEBRA_2F_2-II_05_G04.ab1 Bermudagrass line Zebra subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone ZEBRA_2F_2-II_05_ZEBRA_2F_2-II_05_G04.ab1, mRNA sequence.
:ESSION DN988885
:SION DN988885.1 GI:66248712
'WORDS EST.
:RCE Cynodon dactylon (Bermuda grass)
)RGANISM Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Chloridoideae; Cynodonteae; Cynodon.
'ERENCE 1 (bases 1 to 404)
\UTHORS Melmaiee,K., Elavarthi,S. and Guenzi,A.C.
'ITLE Identification of differentially expressed genes associated with cold acclimation using suppression subtraction hybridization (SSH) and cDNA microarrays
'OURNAL Unpublished (2005)
'MENT Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR PRimers
FORWARD: M13 forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.
\TURES Location/Qualifiers
source 1. .404
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="Zebra"
/db_xref="taxon:28909"
/clone="ZEBRA_2F_2-II_05_ZEBRA_2F_2-II_05_G04.ab1"
/tissue_type="Crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass line Zebra subtracted cold acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was extracted from control and cold acclimated bermudagrass crown tissue at 2 and 28 days after acclimation and cDNA library was constructed following Clontech PCR- select cDNA subtraction procedure."
:GIN

:gnment Scores:
:d. No.: 174 Length: 404
:re: 9.00 Matches: 9
:cent Similarity: 100.0% Conservative: 0
:t Local Similarity: 100.0% Mismatches: 0
Query Match: 4.6% Indels: 0
DB: 9 Gaps: 0

US-10-821-670A-36 (1-197) x DN988885 (1-404)

Qy 4 ProThrProThrProSerProGlyMet 12
Db 368 CCCACCCCCACCCCCTCGCCGGGGATG 394

RESULT 37
CB801533
LOCUS CB801533 412 bp mRNA linear EST 16-MAY-2003
DEFINITION AMGNNUC:SRPB2-00244-H1-A srpb2 (10220) Rattus norvegicus cDNA clone srpb2-00244-h1 5', mRNA sequence.
ACCESSION CB801533
VERSION CB801533.1 GI:29914888
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 412)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00244 row: h column: 1.
FEATURES Location/Qualifiers
source 1. .412
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srpb2-00244-h1"
/tissue_type="prostate tissue"
/clone_lib="srpb2 (10220)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; rat prostate normalized double selected poly(A+) mRNA size fraction > 1 kb"
ORIGIN

Alignment Scores:
Pred. No.: 177 Length: 412
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.6% Indels: 0
DB: 4 Gaps: 0

US-10-821-670A-36 (1-197) x CB801533 (1-412)

Qy 172 LysLeuCysIleLeuLeuHisAlaPhe 180
Db 283 AAGCTCTGTATCCTGCTCCATGCCTTC 309

RESULT 38
CF798662
LOCUS CF798662 425 bp mRNA linear EST 21-OCT-2003
DEFINITION Lr_PAHCF_05D11_M13R Earthworm Fluorantene Exposure Library Lumbricus rubellus cDNA clone Lr_PAHCF_05D11 5' similar to ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus terrestris, mRNA sequence.
ACCESSION CF798662
VERSION CF798662.1 GI:37803232
KEYWORDS EST.
SOURCE Lumbricus rubellus (humus earthworm)
ORGANISM Lumbricus rubellus
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida; Lumbricina; Lumbricidae; Lumbricus.
REFERENCE 1 (bases 1 to 425)

```
UTHORS   Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S., Kille,P. and
         Blaxter,M.
ITLE     The Lumbricus rubellus EST program - Sequences from a Fluorantene
         Exposure library
OURNAL   Unpublished (2003)
MENT     Contact: Jennifer Chaseley
         BIOSI 1
         Cardiff University
         Main College, Museum Avenue, Cardiff, CF11 3TL, UK
         Tel: +44 2920876680
         Fax: +44 2920874305
         Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
         Sequencing was performed in Cardiff using the pBluescriptII XR cDNA
         library (Stratagene) protocol.
         PCR PRimers
         FORWARD: gttttcccagtcacgacg
         BACKWARD: caggaaacagctatgaccatg
         Plate: 05  row: D  column: 11
         Seq primer: caggaaacagctatgaccatg
         High quality sequence stop: 374.
TURES             Location/Qualifiers
  source          1. .425
                  /organism="Lumbricus rubellus"
                  /mol_type="mRNA"
                  /db_xref="taxon:35632"
                  /clone="Lr_PAHCF_05D11"
                  /tissue_type="Whole worm"
                  /dev_stage="Adult"
                  /clone_lib="Earthworm Fluorantene Exposure Library"
                  /note="Vector: pBluescript II SK+; The library was
                  prepared using protocols given by the supplier
                  (Stratagene)."
GIN

gnment Scores:
d. No.:              182          Length:        425
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            4.6%         Indels:        0
                     5            Gaps:          0

10-821-670A-36 (1-197) x CF798662 (1-425)

        15 CysLeuAsnHisSerGlnThrLeuLeu 23
           |||||||||||||||||||||||||||
       109 TGCCTCAACCATTCGCAGACGCTATTA 135

ULT 39
50954/c
US       AI750954                437 bp    mRNA    linear   EST 20-JUN-2002
INITION  cn06g05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA
         clone NHTBC_cn06g05 random, mRNA sequence.
ESSION   AI750954
SION     AI750954.1  GI:5129218
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 437)
UTHORS   Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
         Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M.,
         Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.
ITLE     SGAP: The Skeletal Genome Anatomy Project
OURNAL   Unpublished (1997)
MENT     Contact: Libin Jia
         Medical Genetics Branch
         National Human Genome Research Institute
         10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
         Tel: 301-402-4877
         Fax: 301-496-7157
         Email: libin@helix.nih.gov
         DNA Sequencing and analyses by National Institutes of Health
         Intramural Sequencing Center (NISC).
         Plate: 06  row: g  column: 05
         Seq primer: -21M13 forward primer (ABI).
FEATURES          Location/Qualifiers
     source       1. .437
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="NHTBC_cn06g05"
                  /sex="Female"
                  /tissue_type="Bone"
                  /cell_type="Trabecular Bone Cells"
                  /lab_host="SURE"
                  /clone_lib="Normal Human Trabecular Bone Cells"
                  /note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI;
                  Library constructed by Dr. Marian Young and Dr. Pamela
                  Gehron Robey (NIDCR)"
ORIGIN

Alignment Scores:
Pred. No.:              187          Length:        437
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            4.6%         Indels:        0
DB:                     1            Gaps:          0

US-10-821-670A-36 (1-197) x AI750954 (1-437)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        295 CCGACACCAACTCCAAGTCCAGGGATG 269

RESULT 40
AZ215995/c
LOCUS       AZ215995                453 bp    DNA     linear   GSS 09-JUN-2000
DEFINITION  Sheared DNA-84C4.TF Sheared DNA Trypanosoma brucei genomic clone
            Sheared DNA-84C4, genomic survey sequence.
ACCESSION   AZ215995
VERSION     AZ215995.1  GI:8433795
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 453)
  AUTHORS   El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
            Donelson,J., Fraser,C. and Adams,M.
  TITLE     Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: Sheared DNA-84C4.TR
            Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through Research Genetics, Alabama, USA. Sheared DNA
            end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
            Seq primer: M13-Forward
            Class: shotgun.
FEATURES          Location/Qualifiers
     source       1. .453
                  /organism="Trypanosoma brucei"
                  /mol_type="genomic DNA"
                  /strain="TREU927/4 GUTat 10.1"
```

```
                /db_xref="taxon:5691"
                /clone="Sheared DNA-84C4"
                /clone_lib="Sheared DNA"
                /note="Vector: pUC18; Site_1: SmaI; Constructed at The
                Institute for Genomic Research (TIGR), Rockville, MD.
                Genomic DNA isolated from a cloned population of
                Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                sheared to give a tight size distribution (approx 2 kb).
                The v + i method used for the library construction is
                described in detail in Smith, H.O. and Venter, J.C.
                (Making small insert libraries for whole genome shotgun
                sequencing projects.  In Genome Sequencing: A Practical
                Approach, eds. M. Vaudin and B. Barell, Oxford University
                Press, 1999)."
:GIN

:gnment Scores:
:d. No.:                193             Length:         453
:re:                    9.00            Matches:        9
:cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              4.6%            Indels:         0
                        11              Gaps:           0

·10-821-670A-36 (1-197) x AZ215995 (1-453)

         86 GlySerCysLeuAlaSerArgLysThr 94
            |||||||||||||||||||||||||
        332 GGGAGCTGTCTCGCCTCGCGAAAAACG 306

:ULT 41
:69708
:US        CO869708                495 bp    mRNA    linear   EST 10-AUG-2004
'INITION   Lr_JV2CF_06B01_SKplus Juvenile Earthworm Library Lumbricus rubellus
           cDNA clone Lr_JV2CF_06B01 similar to
           gi|3122450|sp|Q37546|NU1M_LUMTE NADH-UBIQUINONE OXIDOREDUCTASE.
           Score = 263 bits (671), Expect = 2e-70, mRNA sequence.
:ESSION    CO869708
:SION      CO869708.1  GI:51099550
'WORDS     EST.
:RCE       Lumbricus rubellus (humus earthworm)
:RGANISM   Lumbricus rubellus
           Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
           Lumbricina; Lumbricidae; Lumbricus.
'ERENCE    1  (bases 1 to 495)
\UTHORS    Chaseley,J., Hedley,B.A., Morgan,A.J., Sturzenbaum,S., Kille,P. and
           Blaxter,M.
'ITLE      The Lumbricus rubellus EST program - Sequences from a Juvenile
           library
/OURNAL    Unpublished (2004)
!MENT      Contact: Jennifer Chaseley
           BIOSI 1
           Cardiff University
           Main College, Museum Avenue, Cardiff, CF11 3TL, UK
           Tel: +44 2920876680
           Fax: +44 2920874305
           Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
           Sequencing was performed in Edinburgh using the pBluescript II XR
           cDNA library (Stratagene) protocol.
           PCR PRimers
           FORWARD: M13F (gttttcccagtcacgacg)
           BACKWARD: M13R (caggaaacagctatgaccatg)
           Plate: 06  row: B  column: 01
           Seq primer: SKplus
           High quality sequence start: 3
           High quality sequence stop: 474.
\TURES                Location/Qualifiers
   source              1. .495
                       /organism="Lumbricus rubellus"
                       /mol_type="mRNA"
                       /db_xref="taxon:35632"
                       /clone="Lr_JV2CF_06B01"
                       /sex="mixed"
                       /tissue_type="Whole worm"
                       /dev_stage="Juvenile"
                       /clone_lib="Juvenile Earthworm Library"
                       /note="Organ: Whole worm"
ORIGIN

Alignment Scores:
Pred. No.:              208             Length:         495
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.6%            Indels:         0
DB:                     8               Gaps:           0

US-10-821-670A-36 (1-197) x CO869708 (1-495)

Qy          15 CysLeuAsnHisSerGlnThrLeuLeu 23
               |||||||||||||||||||||||||||
Db         117 TGCCTCAACCATTCGCAGACGCTATTA 143

RESULT 42
DA587595/c
LOCUS       DA587595                501 bp    mRNA    linear   EST 06-NOV-2005
DEFINITION  DA587595 HLUNG2 Homo sapiens cDNA clone HLUNG2008655 5', mRNA
            sequence.
ACCESSION   DA587595
VERSION     DA587595.1  GI:80880623
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES              Location/Qualifiers
     source           1. .501
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="HLUNG2008655"
                      /tissue_type="lung"
                      /clone_lib="HLUNG2"
                      /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              210             Length:         501
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
```

```
t Local Similarity:  100.0%          Mismatches:    0
ry Match:            4.6%            Indels:        0
                     9               Gaps:          0

10-821-670A-36 (1-197) x DA587595 (1-501)

         4 ProThrProThrProSerProGlyMet 12
           |||||||||||||||||||||||||||
       427 CCGACACCAACTCCAAGTCCAGGGATG 401

ULT 43
99473/c
US       DA599473                 502 bp    mRNA    linear   EST 07-NOV-2005
INITION  DA599473 HSYRA2 Homo sapiens cDNA clone HSYRA2004329 5', mRNA
         sequence.
ESSION   DA599473
SION     DA599473.1  GI:81141689
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
RRENCE   1  (bases 1 to 502)
:THORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
         Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
         Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
         Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
         Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
         Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
ITLE     Diversification of Transcriptional Modulation: Large-scale
         Identification and Characterization of Putative Alternative
         Promoters of Human Genes
OURNAL   Genome Res. 16 (1), 55-65 (2006)
PUBMED   16344560
MENT     Contact: Takao Isogai
         FLJ Project (HRI Team)
         Helix Research Institute
         2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
         Tel: 81-438-52-3975
         Fax: 81-438-52-3986
         Email: flj-cdna@nifty.com
         NEDO human cDNA project (New Energy and Industrial Technology
         Developmental Organization, Japan); cDNA library construction:
         Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
         Research Association for Biotechnology (RAB) and Biotechnology
         Center, National Institute of Technology and Evaluation; 3'-end one
         pass sequencing: RAB.
TURES              Location/Qualifiers
  source           1. .502
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="HSYRA2004329"
                   /cell_type="synoviocytes from rheumatioid arthritis
                   (HS-RA)"
                   /clone_lib="HSYRA2"
                   /note="Vector: pME18SFL3; primary culture, synoviocytes
                   from rheumatioid arthritis"
IN

gnment Scores:
d. No.:              211             Length:        502
re:                  9.00            Matches:       9
ent Similarity:      100.0%          Conservative:  0
t Local Similarity:  100.0%          Mismatches:    0
ry Match:            4.6%            Indels:        0
                     9               Gaps:          0

10-821-670A-36 (1-197) x DA599473 (1-502)

         4 ProThrProThrProSerProGlyMet 12
           |||||||||||||||||||||||||||
```

```
Db       265 CCGACACCAACTCCAAGTCCAGGGATG 239

RESULT 44
DR008986
LOCUS       DR008986                 512 bp    mRNA    linear   EST 18-MAY-2005
DEFINITION  Lr_Cu2CF_12A07 Earthworm Copper Exposure Library Lumbricus rubellus
            cDNA clone Lr_Cu2CF_12A07 similar to UniRef100_Q37546
            NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
            Score = 250 bits (638), Expect = 1e-65, mRNA sequence.
ACCESSION   DR008986
VERSION     DR008986.1  GI:66273130
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 512)
  AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
            Sturzenbaum,S., Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Copper
            exposure library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Cardiff using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13(gttttcccagtcacgacgtt)
            BACKWARD: M13R(caggaaacagctatgaccatg)
            Plate: 12  row: A  column: 07
            Seq primer: caggaaacagctatgaccatg
            High quality sequence start: 17
            High quality sequence stop: 323.
FEATURES             Location/Qualifiers
     source          1. .512
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
                     /db_xref="taxon:35632"
                     /clone="Lr_Cu2CF_12A07"
                     /sex="mixed"
                     /tissue_type="whole worm"
                     /dev_stage="Adult"
                     /clone_lib="Earthworm Copper Exposure Library"
                     /note="Vector: pbluescript II SK; The library was prepared
                     using protocols given by the supplier (Clontech)."
ORIGIN

Alignment Scores:
Pred. No.:           214             Length:        512
Score:               9.00            Matches:       9
Percent Similarity:  100.0%          Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:         4.6%            Indels:        0
DB:                  9               Gaps:          0

US-10-821-670A-36 (1-197) x DR008986 (1-512)

Qy          15 CysLeuAsnHisSerGlnThrLeuLeu 23
               |||||||||||||||||||||||||
Db         135 TGCCTCAACCATTCGCAGACGCTATTA 161

RESULT 45
BE294832/c
LOCUS       BE294832                 519 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  601177293F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532535 5',
            mRNA sequence.
ACCESSION   BE294832
VERSION     BE294832.1  GI:9178374
```

```
:WORDS     EST.
'RCE       Homo sapiens (human)
)RGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
'ERENCE    1  (bases 1 to 519)
\UTHORS    NIH-MGC http://mgc.nci.nih.gov/.
:ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
)URNAL     Unpublished (1999)
!MENT      Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
           Plate: LLCM208  row: j  column: 24
           High quality sequence stop: 517.
\TURES                Location/Qualifiers
   source             1. .519
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3532535"
                      /tissue_type="rhabdomyosarcoma"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_17"
                      /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                      Site_2: XhoI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                      for average insert size 1.8kb.  Library constructed by
                      Ling Hong in the laboratory of Gerald M. Rubin (University
                      of California, Berkeley) using ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
:GIN

.gnment Scores:
)d. No.:                217             Length:         519
)re:                    9.00            Matches:        9
:cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              4.6%            Indels:         0
                        7               Gaps:           0

·10-821-670A-36 (1-197) x BE294832 (1-519)

          4 ProThrProThrProSerProGlyMet 12
            |||||||||||||||||||||||||||
        363 CCGACACCAACTCCAAGTCCAGGGATG 337

:ULT 46
;98142/c
:US        DA598142                 521 bp    mRNA    linear   EST 07-NOV-2005
'INITION   DA598142 HSYRA2 Homo sapiens cDNA clone HSYRA2002676 5', mRNA
           sequence.
:ESSION    DA598142
:SION      DA598142.1  GI:81116153
:WORDS     EST.
:RCE       Homo sapiens (human)
)RGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
'ERENCE    1  (bases 1 to 521)
\UTHORS    Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
           Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
           Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
           Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
           Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
           Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE    Diversification of Transcriptional Modulation: Large-scale
           Identification and Characterization of Putative Alternative
           Promoters of Human Genes
  JOURNAL  Genome Res. 16 (1), 55-65 (2006)
   PUBMED  16344560
COMMENT    Contact: Takao Isogai
           FLJ Project (HRI Team)
           Helix Research Institute
           2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
           Tel: 81-438-52-3975
           Fax: 81-438-52-3986
           Email: flj-cdna@nifty.com
           NEDO human cDNA project (New Energy and Industrial Technology
           Developmental Organization, Japan); cDNA library construction:
           Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
           Research Association for Biotechnology (RAB) and Biotechnology
           Center, National Institute of Technology and Evaluation; 3'-end one
           pass sequencing: RAB.
FEATURES              Location/Qualifiers
     source           1. .521
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="HSYRA2002676"
                      /cell_type="synoviocytes from rheumatioid arthritis
                      (HS-RA)"
                      /clone_lib="HSYRA2"
                      /note="Vector: pME18SFL3; primary culture, synoviocytes
                      from rheumatioid arthritis"
ORIGIN

Alignment Scores:
Pred. No.:                218             Length:         521
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.6%            Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-36 (1-197) x DA598142 (1-521)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        454 CCGACACCAACTCCAAGTCCAGGGATG 428

RESULT 47
CR813130
LOCUS       CR813130                 539 bp    DNA     linear   GSS 27-SEP-2004
DEFINITION  GR0AAA37CD06RM1 INRA BAC Bos taurus genomic clone INRAb_622G01, DNA
            sequence, genomic survey sequence.
ACCESSION   CR813130
VERSION     CR813130.1  GI:52749218
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 539)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
```

```
          Fax: 33 1 34 65 24 78
          Email: eggen@jouy.inra.fr
          Clones are derived from the INRA bovine BAC library
          (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
          availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
          work  was undertaken as part of the International Bovine BAC
          Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
          (Evry) Plate: 622 row: G column: 01
          Seq primer: M13 Reverse
          Class: BAC ends.
TURES               Location/Qualifiers
  source            1. .539
                    /organism="Bos taurus"
                    /mol_type="genomic DNA"
                    /strain="breed: Holstein"
                    /db_xref="taxon:9913"
                    /clone="INRAb_622G01"
                    /sex="Male"
                    /cell_type="fibroblast"
                    /clone_lib="INRA bovine BAC"
                    /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                    INRA Bovine BAC library (Male) produced by Andre Eggen
                    Genoscope sequence ID : GR0AAA37CD06RM1"
GIN

gnment Scores:
d. No.:                 224             Length:         539
re:                     9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               4.6%            Indels:         0
                        14              Gaps:           0

10-821-670A-36 (1-197) x CR813130 (1-539)

        71 AsnGluSerCysLeuAlaSerArgGlu 79
           |||||||||||||||||||||||||||
       331 AATGAGAGTTGCCTGGCTTCCAGAGAG 357

ULT 48
56152/c
US        DA956152                549 bp    mRNA    linear   EST 09-NOV-2005
INITION   DA956152 SPLEN2 Homo sapiens cDNA clone SPLEN2035001 5', mRNA
          sequence.
SSION     DA956152
SION      DA956152.1  GI:81288557
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 549)
UTHORS    Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
ITLE      Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
OURNAL    Genome Res. 16 (1), 55-65 (2006)
PUBMED    16344560
MENT      Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
FEATURES            Location/Qualifiers
     source         1. .549
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="SPLEN2035001"
                    /tissue_type="spleen"
                    /clone_lib="SPLEN2"
                    /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              228             Length:         549
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.6%            Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-36 (1-197) x DA956152 (1-549)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        539 CCGACACCAACTCCAAGTCCAGGGATG 513

RESULT 49
DT919655
LOCUS       DT919655                551 bp    mRNA    linear   EST 19-SEP-2005
DEFINITION  PCRS30821 Hematopoietic stem cells Mus musculus cDNA, mRNA
            sequence.
ACCESSION   DT919655
VERSION     DT919655.1  GI:75900136
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES            Location/Qualifiers
     source         1. .551
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /tissue_type="Hematopoietic stem cells"
                    /cell_type="Hematopoietic stem cells"
                    /clone_lib="Hematopoietic stem cells"
                    /note="cDNA library was made from FACS-purified
                    hematopoietic stem cells"
ORIGIN

Alignment Scores:
Pred. No.:              229             Length:         551
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.6%            Indels:         0
```

```
                    10              Gaps:          0

10-821-670A-36 (1-197) x DT919655 (1-551)

       172 LysLeuCysIleLeuLeuHisAlaPhe 180
             ||||||||||||||||||||||||||
       180 AAGCTCTGCATCCTGCTTCACGCCTTC 206

ULT 50
55731/c
US        DA555731                  556 bp    mRNA    linear   EST 06-NOV-2005
INITION   DA555731 HCHON2 Homo sapiens cDNA clone HCHON2006006 5', mRNA
          sequence.
ESSION    DA555731
SION      DA555731.1  GI:80908037
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 556)
UTHORS    Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
ITLE      Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
OURNAL    Genome Res. 16 (1), 55-65 (2006)
 PUBMED   16344560
MENT      Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
TURES               Location/Qualifiers
   source           1. .556
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="HCHON2006006"
                    /cell_type="chondrocytes (HC)"
                    /clone_lib="HCHON2"
                    /note="Vector: pME18SFL3; primary culture, chondrocytes"
GIN

gnment Scores:
d. No.:               231           Length:        556
re:                   9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
t Local Similarity:   100.0%        Mismatches:    0
ry Match:             4.6%          Indels:        0
                      9             Gaps:          0

10-821-670A-36 (1-197) x DA555731 (1-556)

         4 ProThrProThrProSerProGlyMet 12
             |||||||||||||||||||||||||||
       468 CCGACACCAACTCCAAGTCCAGGGATG 442

ULT 51
63836/c
```

```
LOCUS       DY063836                  556 bp    mRNA    linear   EST 31-JAN-2006
DEFINITION  000403BPPA001687HT BPPA Bos taurus cDNA, mRNA sequence.
ACCESSION   DY063836
VERSION     DY063836.1  GI:86208958
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
            Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
            Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C.,
            McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
            Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
            Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
            Atkinson,P.
  TITLE     AgResearch, Genesis and Primary Industry Victoria Bovine EST
            project
  JOURNAL   Unpublished (2006)
COMMENT     Contact: Maqbool N
            AgResearch Ltd.
            Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
            Mosgiel, New Zealand
            Email: nauman.maqbool@agresearch.co.nz.
FEATURES             Location/Qualifiers
     source          1. .556
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="Peyers Patch"
                     /clone_lib="BPPA"
                     /note="Vector: pBK-CMV; Bovine peyers patch cDNA library
                     derived from tissue harvested from a Friesian cross animal
                     by Wayne Hein on 27/01/00"
ORIGIN

Alignment Scores:
Pred. No.:               231           Length:        556
Score:                   9.00          Matches:       9
Percent Similarity:      100.0%        Conservative:  0
Best Local Similarity:   100.0%        Mismatches:    0
Query Match:             4.6%          Indels:        0
DB:                      10            Gaps:          0

US-10-821-670A-36 (1-197) x DY063836 (1-556)

Qy          3 LeuProThrProThrProSerProGly 11
              |||||||||||||||||||||||||||
Db        414 CTACCAACTCCCACTCCCTCTCCTGGC 388

RESULT 52
CX570753
LOCUS       CX570753                  558 bp    mRNA    linear   EST 12-JAN-2005
DEFINITION  RVL1941 Wackym-Soares normalized rat vestibular cDNA library Rattus
            norvegicus cDNA 5', mRNA sequence.
ACCESSION   CX570753
VERSION     CX570753.1  GI:57597784
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Wackym,P.A. and Cioffi,J.A.
  TITLE     In silico analysis of the rat vestibular periphery transcriptome
            using a normalized cDNA library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Wackym, P.A.
            Department of Otolaryngology and Communication Sciences
            9200 W. Wisconsin Ave, Milwaukee, WI, 53226, USA
```

```
        Tel: 414.266.3750
        Fax: 414.266.2693
        Email: wackym@mcw.edu
        Insert Length: 559   Std Error: 0.00
        Seq primer: T7.
TURES           Location/Qualifiers
  source        1. .558
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /db_xref="taxon:10116"
                /tissue_type="Vestibular end organs, primary afferent
                neurons"
                /clone_lib="Wackym-Soares normalized rat vestibular cDNA
                library"
                /note="Vector: pT7T3Pac; The library was constructed and
                normalized according Bonaldo and Soares, Genome Analysis -
                A Laboratory Manual, Vol. 2: 49 - 157.  Inserts are
                directionally cloned into the EcoRI and NotI sites.  The
                library tag located between the NotI site and the polyA
                tail is TAGGTTACAC."
GIN

gnment Scores:
d. No.:             231          Length:        558
re:                 9.00         Matches:       9
cent Similarity:    100.0%       Conservative:  0
t Local Similarity: 100.0%       Mismatches:    0
ry Match:           4.6%         Indels:        0
                    9            Gaps:          0

10-821-670A-36 (1-197) x CX570753 (1-558)

       172 LysLeuCysIleLeuLeuHisAlaPhe 180
           |||||||||||||||||||||||||
        68 AAGCTCTGTATCCTGCTCCATGCCTTC 94

ULT 53
52898/c
US        DA552898                562 bp    mRNA    linear   EST 05-NOV-2005
INITION   DA552898 HCHON2 Homo sapiens cDNA clone HCHON2002588 5', mRNA
          sequence.
ESSION    DA552898
SION      DA552898.1  GI:80836243
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 562)
UTHORS    Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
ITLE      Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
OURNAL    Genome Res. 16 (1), 55-65 (2006)
PUBMED    16344560
MENT      Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
FEATURES        Location/Qualifiers
     source     1. .562
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="HCHON2002588"
                /cell_type="chondrocytes (HC)"
                /clone_lib="HCHON2"
                /note="Vector: pME18SFL3; primary culture, chondrocytes"
ORIGIN

Alignment Scores:
Pred. No.:              233          Length:        562
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            4.6%         Indels:        0
DB:                     9            Gaps:          0

US-10-821-670A-36 (1-197) x DA552898 (1-562)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        390 CCGACACCAACTCCAAGTCCAGGGATG 364

RESULT 54
DA557449/c
LOCUS       DA557449                565 bp    mRNA    linear   EST 06-NOV-2005
DEFINITION  DA557449 HCHON2 Homo sapiens cDNA clone HCHON2008119 5', mRNA
            sequence.
ACCESSION   DA557449
VERSION     DA557449.1  GI:80952829
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 565)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
  PUBMED    16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES        Location/Qualifiers
     source     1. .565
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="HCHON2008119"
                /cell_type="chondrocytes (HC)"
                /clone_lib="HCHON2"
                /note="Vector: pME18SFL3; primary culture, chondrocytes"
```

```
:GIN

.gnment Scores:
:d. No.:                234             Length:         565
)re:                    9.00            Matches:        9
:cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              4.6%            Indels:         0
                        9               Gaps:           0

-10-821-670A-36 (1-197) x DA557449 (1-565)

          4 ProThrProThrProSerProGlyMet 12
            |||||||||||||||||||||||||||
        473 CCGACACCAACTCCAAGTCCAGGGATG 447

:ULT 55
'95312
:US        CR795312                568 bp    DNA     linear   GSS 24-SEP-2004
'INITION   GR0AAA12DG09RM1 INRA BAC Bos taurus genomic clone INRAb_238E06, DNA
           sequence, genomic survey sequence.
:ESSION    CR795312
:SION      CR795312.1  GI:52676311
'WORDS     GSS.
)RCE       Bos taurus (cattle)
)RGANISM   Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
           Pecora; Bovidae; Bovinae; Bos.
'ERENCE    1  (bases 1 to 568)
\UTHORS    Eggen,A., Schibler,L. and Roy,A.
:ITLE      Bovine BAC End Sequences from the INRA bovine BAC library
'OURNAL    Unpublished
'ERENCE    2  (bases 1 to 568)
\UTHORS    Genoscope.
:ITLE      Direct Submission
'OURNAL    Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
           BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
           - Web : www.genoscope.cns.fr)
'MENT      Contact: Andre Eggen
           Department of Animal Genetics - LGbC
           INRA
           78350 Jouy-en-Josas, France
           Tel: 33 1 34 65 24 24
           Fax: 33 1 34 65 24 78
           Email: eggen@jouy.inra.fr
           Clones are derived from the INRA bovine BAC library
           (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
           availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
           work  was undertaken as part of the International Bovine BAC
           Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
           (Evry) Plate: 238 row: E column: 06
           Seq primer: M13 Reverse
           Class: BAC ends.
\TURES                Location/Qualifiers
   source             1. .568
                      /organism="Bos taurus"
                      /mol_type="genomic DNA"
                      /strain="breed: Holstein"
                      /db_xref="taxon:9913"
                      /clone="INRAb_238E06"
                      /sex="Male"
                      /cell_type="fibroblast"
                      /clone_lib="INRA bovine BAC"
                      /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                      INRA Bovine BAC library (Male) produced by Andre Eggen
                      Genoscope sequence ID : GR0AAA12DG09RM1"
:GIN

.gnment Scores:
:d. No.:                235             Length:         568
)re:                    9.00            Matches:        9
:cent Similarity:       100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.6%            Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x CR795312 (1-568)

Qy          71 AsnGluSerCysLeuAlaSerArgGlu 79
               |||||||||||||||||||||||||||
Db         330 AATGAGAGTTGCCTGGCTTCCAGAGAG 356

RESULT 56
BE296563/c
LOCUS       BE296563                572 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  601174065F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529265 5',
            mRNA sequence.
ACCESSION   BE296563
VERSION     BE296563.1  GI:9180127
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM200  row: b  column: 18
            High quality sequence start: 18
            High quality sequence stop: 572.
FEATURES              Location/Qualifiers
     source           1. .572
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3529265"
                      /tissue_type="rhabdomyosarcoma"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_17"
                      /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                      Site_2: XhoI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                      for average insert size 1.8kb.  Library constructed by
                      Ling Hong in the laboratory of Gerald M. Rubin (University
                      of California, Berkeley) using ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Alignment Scores:
Pred. No.:              236             Length:         572
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.6%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-36 (1-197) x BE296563 (1-572)

Qy           4 ProThrProThrProSerProGlyMet 12
                |||||||||||||||||||||||||||
Db         456 CCGACACCAACTCCAAGTCCAGGGATG 430

RESULT 57
CA153972/c
```

```
US       CA153972                 577 bp    mRNA    linear   EST 24-SEP-2003
INITION  SCVPRZ2038B02.g RZ2 Saccharum officinarum cDNA clone SCVPRZ2038B02
         5', mRNA sequence.
ESSION   CA153972
SION     CA153972.1  GI:35060583
WORDS    EST.
RCE      Saccharum officinarum
RGANISM  Saccharum officinarum
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
         clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
         complex.
ERENCE   1  (bases 1 to 577)
UTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
ITLE     The libraries that made SUCEST
OURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
MENT     Contact: Arruda P
         Centro de Biologia Molecular e Engenharia Genetica
         Universidade Estadual de Campinas
         Caixa Postal 6010, 13083-970, Campinas SP, Brazil
         Tel: 55 19 3788 1137
         Fax: 55 19 3788 1089
         Email: parruda@unicamp.br
         Clone distribution: clone distribution information can be found
         through the Brazilian Clone Collection Center (BCCC) at
         http://www.bcccenter.fcav.unesp.br
         Plate: 038  row: B  column: 02
         Seq primer: T7 Promoter Primer.
TURES             Location/Qualifiers
  source          1. .577
                  /organism="Saccharum officinarum"
                  /mol_type="mRNA"
                  /db_xref="taxon:4547"
                  /clone="SCVPRZ2038B02"
                  /lab_host="DH10B"
                  /clone_lib="RZ2"
                  /note="Organ: Shoot-root transition zone from young plants
                  (small insert library); Vector: pSport1; Site_1: SalI;
                  Site_2: NotI; An unidirectional cDNA library generated
                  from [Shoot-root transition zone  from young plants (small
                  insert library)]. cDNA was prepared from polyA+  mRNA
                  using SuperScript Plasmid System Kit (Invitrogen). The
                  double-strand  cDNAs were fractionated in a sepharose
                  CL-2B 40cm-columns and fragments  sizing between 0.8 and
                  1.5 Kb were directionally cloned into the vector.  Details
                  of each source of RNA and library construction can be
                  obtained at  http://sucest.lad.ic.unicamp.br/public"
GIN

gnment Scores:
d. No.:               238            Length:        577
re:                   9.00           Matches:       9
cent Similarity:      100.0%         Conservative:  0
t Local Similarity:   100.0%         Mismatches:    0
ry Match:             4.6%           Indels:        0
                      4              Gaps:          0

10-821-670A-36 (1-197) x CA153972 (1-577)

       144 LeuLeuGlnAlaLeuAsnValAsnSer 152
             |||||||||||||||||||||||||
        51 CTTCTCCAAGCTCTCAACGTCAACTCC 25

ULT 58
97655/c
US       BY797655                 579 bp    mRNA    linear   EST 16-AUG-2005
INITION  BY797655 Homo sapiens eye Homo sapiens cDNA clone
         HEmEye2086A07_049.ab1 5', mRNA sequence.
ESSION   BY797655
SION     BY797655.1  GI:73475674
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
REFERENCE  1  (bases 1 to 579)
  AUTHORS  Choy,K., Wang,C., Ogura,A., Lau,T., Rogers,M., Ikeo,K.,
           Gojobori,T., Lam,D. and Pang,C.
  TITLE    Comparative annotation of 15,809 ESTs identified from pooled early
           gestation human eyes
  JOURNAL  Unpublished (2005)
COMMENT    Contact: Kw Choy
           National Institute of Genetics, Center for Information Biology and
           DDBJ
           Yata1111, Mishima, 411-8540, Japan
           Tel: 852-2632-3099
           Email: richardchoy@cuhk.edu.hk
           This sequence is assembled via IDEA. This clone was obtained from
           National Institute of Genetics and Chinese University of HongKong.
FEATURES             Location/Qualifiers
     source          1. .579
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HEmEye2086A07_049.ab1"
                     /tissue_type="eye"
                     /clone_lib="Homo sapiens eye"
ORIGIN

Alignment Scores:
Pred. No.:                239            Length:        579
Score:                    9.00           Matches:       9
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              4.6%           Indels:        0
DB:                       4              Gaps:          0

US-10-821-670A-36 (1-197) x BY797655 (1-579)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        240 CCGACACCAACTCCAAGTCCAGGGATG 214

RESULT 59
DA541205/c
LOCUS       DA541205                 585 bp    mRNA    linear   EST 04-NOV-2005
DEFINITION  DA541205 FELNG2 Homo sapiens cDNA clone FELNG2001238 5', mRNA
            sequence.
ACCESSION   DA541205
VERSION     DA541205.1  GI:80523474
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
```

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES Location/Qualifiers
source 1. .585
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FELNG2001238"
/tissue_type="lung"
/dev_stage="fetal"
/clone_lib="FELNG2"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.:	241	Length:	585
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.6%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-36 (1-197) x DA541205 (1-585)

```
Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        456 CCGACACCAACTCCAAGTCCAGGGATG 430
```

RESULT 60
BH194492
LOCUS BB194492 610 bp mRNA linear EST 19-OCT-2001
DEFINITION BB194492 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330083H15 3', mRNA sequence.
ACCESSION BB194492
VERSION BB194492.2 GI:16270905
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 610)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT On Jun 30, 2000 this sequence version replaced gi:8855111.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES Location/Qualifiers
source 1. .610
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A330083H15"
/sex="male"
/tissue_type="spinal cord"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male spinal cord"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "

ORIGIN

Alignment Scores:

Pred. No.:	250	Length:	610
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.6%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x BB194492 (1-610)

```
Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        222 CCCACCCCCACCCCCTCTCCTGGCATG 248
```

RESULT 61
BH488094
LOCUS BH488094 610 bp DNA linear GSS 13-DEC-2001
DEFINITION BOGBX77TR BOGB Brassica oleracea genomic clone BOGBX77, genomic survey sequence.
ACCESSION BH488094
VERSION BH488094.1 GI:17696198
KEYWORDS GSS.

```
RCE      Brassica oleracea
RGANISM  Brassica oleracea
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
         rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
ERENCE   1  (bases 1 to 610)
UTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
         Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
ITLE     Whole genome shotgun sequencing of Brassica oleracea and its
         application to gene discovery and annotation in Arabidopsis
OURNAL   Genome Res. 15 (4), 487-495 (2005)
PUBMED   15805490
MENT     Other_GSSs: BOGBX77TF
         Contact: Chris Town
         TIGR
         9712 Medical Center Drive, Rockville, MD 20850, USA.
         Tel: 301-838-3523
         Fax: 301-838-0208
         Email: cdtown@tigr.org
         DNA is from a doubled haploid provided by Tom Osborn.
         Seq primer: TR
         Class: sheared ends.
TURES             Location/Qualifiers
  source          1. .610
                  /organism="Brassica oleracea"
                  /mol_type="genomic DNA"
                  /strain="TO1000DH3"
                  /db_xref="taxon:3712"
                  /clone="BOGBX77"
                  /clone_lib="BOGB"
                  /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                  genomic DNA inserted into pHOS1 using BstXI linkers"
GIN

gnment Scores:
d. No.:              250            Length:        610
re:                  9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            4.6%           Indels:        0
                     11             Gaps:          0

10-821-670A-36 (1-197) x BH488094 (1-610)

        87 SerCysLeuAlaSerArgLysThrSer 95
           |||||||||||||||||||||||||||
       430 TCTTGTCTCGCATCCCGAAAGACGTCA 456

ULT 62
02767
US       CZ102767                617 bp    DNA     linear   GSS 13-JAN-2005
INITION  OM__Ba0111B06.f OM__Ba Oryza minuta genomic clone OM__Ba0111B06 5',
         genomic survey sequence.
ESSION   CZ102767
SION     CZ102767.1  GI:57677146
WORDS    GSS.
RCE      Oryza minuta
RGANISM  Oryza minuta
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
         clade; Ehrhartoideae; Oryzeae; Oryza.
ERENCE   1  (bases 1 to 617)
UTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
         Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
         Wing,R.
ITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
OURNAL   Unpublished (2005)
MENT     Contact: Rod A. Wing
         Arizona Genomics Institute
         University of Arizona
         Forbes Building Room 303, Tucson, AZ 85721-0036, USA
         Tel: 520 626 9595
         Fax: 520 621 1259
         Email: rwing@genome.arizona.edu
         Plate: 0111  row: B  column: 06
         Class: BAC ends.
FEATURES          Location/Qualifiers
     source       1. .617
                  /organism="Oryza minuta"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:63629"
                  /clone="OM__Ba0111B06"
                  /tissue_type="leaves"
                  /lab_host="DH10B"
                  /clone_lib="OM__Ba"
                  /note="Vector: pCUGIBAC1; Site_1: HindIII; Site_2:
                  HindIII"
ORIGIN

Alignment Scores:
Pred. No.:              253           Length:        617
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.6%          Indels:        0
DB:                     13            Gaps:          0

US-10-821-670A-36 (1-197) x CZ102767 (1-617)

Qy         60 ValGluAlaCysLeuProLeuGluLeu 68
              |||||||||||||||||||||||||||
Db        540 GTCGAAGCATGTTTGCCACTAGAGTTG 566

RESULT 63
CF809729
LOCUS       CF809729                663 bp    mRNA    linear   EST 27-OCT-2003
DEFINITION  Lr_LC1ED_30H01_SAC Lumbricus rubellus Late Cocoon Library 1
            Lumbricus rubellus cDNA clone Lr_LC1ED_30H01 5' similar to
            ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
            terrestris, mRNA sequence.
ACCESSION   CF809729
VERSION     CF809729.1  GI:37998060
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Jones,M., Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S.,
            Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a cocoon
            library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK.
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            The library was prepared using protocols given by the supplier
            (Stratagene).
            PCR PRimers
            FORWARD: M13R(AGCGGATAACAATTTCACACAGGA)
            BACKWARD: T7PL(CTCACTATAGGGCGAATTGG)
            Plate: 30  row: H  column: 01
            Seq primer: SAC(GGGAACAAAAGCTGGAG)
            High quality sequence stop: 503.
FEATURES          Location/Qualifiers
     source       1. .663
                  /organism="Lumbricus rubellus"
                  /mol_type="mRNA"
                  /db_xref="taxon:35632"
                  /clone="Lr_LC1ED_30H01"
                  /tissue_type="Whole worm"
```

/dev_stage="Late Cocoon"
/clone_lib="Lumbricus rubellus Late Cocoon Library 1"
/note="Vector: pBluescript II SK+; The library was prepared using protocols given by the supplier (Stratagene)."

GIN

gnment Scores:

d. No.:	269	Length:	663
re:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.6%	Indels:	0
	5	Gaps:	0

10-821-670A-36 (1-197) x CF809729 (1-663)

```
        15 CysLeuAsnHisSerGlnThrLeuLeu 23
           ||||||||||||||||||||||||||||
       179 TGCCTCAACCATTCGCAGACGCTATTA 205
```

ULT 64
08485
US DR008485 671 bp mRNA linear EST 18-MAY-2005
INITION Lr_Cu2CF_09D10 Earthworm Copper Exposure Library Lumbricus rubellus cDNA clone Lr_Cu2CF_09D10 similar to UniRef100_Q37546 NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris. Score = 362 bits (928), Expect = 6e-99, mRNA sequence.
ESSION DR008485
SION DR008485.1 GI:66272629
WORDS EST.
RCE Lumbricus rubellus (humus earthworm)
RGANISM Lumbricus rubellus
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida; Lumbricina; Lumbricidae; Lumbricus.
ERENCE 1 (bases 1 to 671)
UTHORS Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J., Sturzenbaum,S., Kille,P. and Blaxter,M.
ITLE The Lumbricus rubellus EST program - Sequences from a Copper exposure library
OURNAL Unpublished (2005)
MENT Contact: Jennifer Chaseley
BIOSI 1
Cardiff University
Main College, Museum Avenue, Cardiff, CF11 3TL, UK
Tel: +44 2920876680
Fax: +44 2920874305
Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
Sequencing was performed in Cardiff using the pBluescript II XR cDNA library (Stratagene) protocol.
PCR PRimers
FORWARD: M13(gttttcccagtcacgacgtt)
BACKWARD: M13R(caggaaacagctatgaccatg)
Plate: 09 row: D column: 10
Seq primer: caggaaacagctatgaccatg
High quality sequence start: 9
High quality sequence stop: 531.

TURES	Location/Qualifiers
source	1. .671
	/organism="Lumbricus rubellus"
	/mol_type="mRNA"
	/db_xref="taxon:35632"
	/clone="Lr_Cu2CF_09D10"
	/sex="mixed"
	/tissue_type="whole worm"
	/dev_stage="Adult"
	/clone_lib="Earthworm Copper Exposure Library"
	/note="Vector: pbluescript II SK; The library was prepared using protocols given by the supplier (Clontech)."

GIN

gnment Scores:

d. No.:	272	Length:	671
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.6%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-36 (1-197) x DR008485 (1-671)

```
Qy          15 CysLeuAsnHisSerGlnThrLeuLeu 23
               ||||||||||||||||||||||||||||
Db         120 TGCCTCAACCATTCGCAGACGCTATTA 146
```

RESULT 65
CO408614
LOCUS CO408614 679 bp mRNA linear EST 02-JUL-2004
DEFINITION Lr_CHECF_02E05_M13R Earthworm Head Enriched library Lumbricus rubellus cDNA clone Lr_CHECF_02E05 similar to NU1M_LUMTE (Q37546) NADH-ubiquinone oxidoreductase chain 1 (EC. Score = 365 bits (936), Expect = e-100, mRNA sequence.
ACCESSION CO408614
VERSION CO408614.1 GI:49624861
KEYWORDS EST.
SOURCE Lumbricus rubellus (humus earthworm)
ORGANISM Lumbricus rubellus
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida; Lumbricina; Lumbricidae; Lumbricus.
REFERENCE 1 (bases 1 to 679)
AUTHORS Chaseley,J., Hedley,B.A., Morgan,A.J., Sturzenbaum,S., Kille,P. and Blaxter,M.
TITLE The Lumbricus rubellus EST program - Sequences from a Head enriched library
JOURNAL Unpublished (2004)
COMMENT Contact: Jennifer Chaseley
BIOSI 1
Cardiff University
Main College, Museum Avenue, Cardiff, CF11 3TL, UK
Tel: +44 2920876680
Fax: +44 2920874305
Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
PCR PRimers
FORWARD: gttttcccagtcacgacg
BACKWARD: caggaaacagctatgaccatg
Plate: 02 row: E column: 05
Seq primer: M13R (caggaaacagctatgaccatg)
High quality sequence start: 4
High quality sequence stop: 528.

FEATURES	Location/Qualifiers
source	1. .679
	/organism="Lumbricus rubellus"
	/mol_type="mRNA"
	/db_xref="taxon:35632"
	/clone="Lr_CHECF_02E05"
	/sex="Mixed"
	/clone_lib="Earthworm Head Enriched library"

ORIGIN

Alignment Scores:

Pred. No.:	275	Length:	679
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.6%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-36 (1-197) x CO408614 (1-679)

```
Qy          15 CysLeuAsnHisSerGlnThrLeuLeu 23
               ||||||||||||||||||||||||||||
Db         117 TGCCTCAACCATTCGCAGACGCTATTA 143
```

RESULT 66
CF810266
LOCUS CF810266 680 bp mRNA linear EST 27-OCT-2003

```
INITION  Lr_LC1ED_39A02_SAC Lumbricus rubellus Late Cocoon Library 1
         Lumbricus rubellus cDNA clone Lr_LC1ED_39A02 5' similar to
         ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
         terrestris, mRNA sequence.
ESSION   CF810266
SION     CF810266.1  GI:37998597
WORDS    EST.
RCE      Lumbricus rubellus (humus earthworm)
RGANISM  Lumbricus rubellus
         Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
         Lumbricina; Lumbricidae; Lumbricus.
FERENCE  1  (bases 1 to 680)
UTHORS   Jones,M., Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S.,
         Kille,P. and Blaxter,M.
ITLE     The Lumbricus rubellus EST program - Sequences from a cocoon
         library
OURNAL   Unpublished (2003)
MENT     Contact: Blaxter ML
         Institute of Cell, Animal and Population Biology
         University of Edinburgh
         Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
         3JT, UK.
         Tel: +44 131 650 6760
         Fax: +44 131 670 5450
         Email: mark.blaxter@ed.ac.uk
         The library was prepared using protocols given by the supplier
         (Stratagene).
         PCR PRimers
         FORWARD: M13R(AGCGGATAACAATTTCACACAGGA)
         BACKWARD: T7PL(CTCACTATAGGGCGAATTGG)
         Plate: 39  row: A  column: 02
         Seq primer: SAC(GGGAACAAAAGCTGGAG)
         High quality sequence stop: 503.
TURES              Location/Qualifiers
  source           1. .680
                   /organism="Lumbricus rubellus"
                   /mol_type="mRNA"
                   /db_xref="taxon:35632"
                   /clone="Lr_LC1ED_39A02"
                   /tissue_type="Whole worm"
                   /dev_stage="Late Cocoon"
                   /clone_lib="Lumbricus rubellus Late Cocoon Library 1"
                   /note="Vector: pBluescript II SK+; The library was
                   prepared using protocols given by the supplier
                   (Stratagene)."
IN

mment Scores:
d. No.:              275            Length:        680
re:                  9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            4.6%           Indels:        0
                     5              Gaps:          0

10-821-670A-36 (1-197) x CF810266 (1-680)

        15 CysLeuAsnHisSerGlnThrLeuLeu 23
           ||||||||||||||||||||||||||||
       119 TGCCTCAACCATTCGCAGACGCTATTA 145

ULT 67
99956/c
US       BE299956                692 bp    mRNA    linear   EST 20-JUL-2000
INITION  600944512F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960667 5',
         mRNA sequence.
ESSION   BE299956
SION     BE299956.1  GI:9183704
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
REFERENCE  1  (bases 1 to 692)
  AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
           Plate: LLCM54  row: g  column: 04
           High quality sequence stop: 676.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2960667"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_17"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Alignment Scores:
Pred. No.:              280            Length:        692
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.6%           Indels:        0
DB:                     7              Gaps:          0

US-10-821-670A-36 (1-197) x BE299956 (1-692)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        451 CCGACACCAACTCCAAGTCCAGGGATG 425

RESULT 68
AZ306792
LOCUS       AZ306792                705 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0008F02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0008F02 F, genomic survey sequence.
ACCESSION   AZ306792
VERSION     AZ306792.1  GI:10345148
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 705)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
```

```
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000   Std Error: 0.00
          Plate: 0008  row: F  column: 02
          Seq primer: CGTTGTAAAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 705.
TURES             Location/Qualifiers
   source         1. .705
                  /organism="Mus musculus"
                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="UUGC1M0008F02"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained  from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high  molar excess. The
                  adaptored DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                  inducible derivative of plasmid R1. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adaptored mouse DNA was annealed to
                  adaptored vector DNA, and transformed into
                  chemically-competent E. coli XL10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."
IGIN

gnment Scores:
d. No.:              284            Length:        705
re:                  9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            4.6%           Indels:        0
                     11             Gaps:          0

10-821-670A-36 (1-197) x AZ306792 (1-705)

       155 ValProGlnAsnSerSerLeuGluGlu 163
           |||||||||||||||||||||||||||
       344 GTTCCCCAAAATAGCTCTTTAGAAGAG 370

ULT 69
44074
US        CW744074                 710 bp    DNA     linear   GSS 05-NOV-2004
INITION   MARC_912850 CHORI-240-314A10 Bos taurus genomic clone 1H2, genomic
          survey sequence.
ESSION    CW744074
SION      CW744074.1  GI:55459493
WORDS     GSS.
RCE       Bos taurus (cattle)
RGANISM   Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bos.
ERENCE    1  (bases 1 to 710)
UTHORS    Smith,T.P.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Harhay,G.P.
ITLE      SNP discovery in cattle based on low coverage sequencing of BAC
          clones
OURNAL    Unpublished (2004)
MENT      Other_GSSs: MARC_912466
          Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called with phred v0.020425.c and
          trimmed with the aid of the trim_alt option. Vector identified with
          cross_match v0.990329.
          Seq primer: GTAATACGACTCACTATAGGG
          Class: BAC subclone.
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
                     /clone="1H2"
                     /sex="Male"
                     /tissue_type="Blood"
                     /clone_lib="CHORI-240-314A10"
                     /note="Vector: pBLUESCRIPT SK-; Site_1: BamHI; Site_2:
                     BamHI; BAC DNA was digested with Sau3A.  Fragments were
                     sized to 800-1200 bases and subcloned into pBLUESCRIPT
                     SK-."
ORIGIN

Alignment Scores:
Pred. No.:               286            Length:        710
Score:                   9.00           Matches:       9
Percent Similarity:      100.0%         Conservative:  0
Best Local Similarity:   100.0%         Mismatches:    0
Query Match:             4.6%           Indels:        0
DB:                      13             Gaps:          0

US-10-821-670A-36 (1-197) x CW744074 (1-710)

Qy          86 GlySerCysLeuAlaSerArgLysThr 94
               |||||||||||||||||||||||||
Db          80 GGCTCCTGTCTAGCTAGCAGGAAGACT 106

RESULT 70
BZ715412/c
LOCUS       BZ715412                 713 bp    DNA     linear   GSS 15-JUL-2005
DEFINITION  HSC 00419 LL07NC01-96 well Homo sapiens genomic clone cos34b3,
            genomic survey sequence.
ACCESSION   BZ715412
VERSION     BZ715412.2  GI:70908397
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   Scherer,S.W., Rommens,J.M., Tsui,L.C. and Kwasnicka,D.A.
  TITLE     Gene Identification on Human Chromosome 7 (Feb 13/03)
  JOURNAL   Unpublished (2003)
COMMENT     On Jul 15, 2005 this sequence version replaced gi:28436671.
            Contact: Scherer, S.W.; Rommens, J.M.; Tsui, L.C.
            The Human Chromosome 7 Project
            Department of Genetics, The Hospital for Sick Children
            555 University Avenue, Toronto, Ontario M5G 1X8, Canada
            Tel: 416 813 7613
            Fax: 416 813 8319
            Email: steve@genet.sickkids.on.ca
            Maps to human chromosome 7q11.23
            Seq primer: T3
            Class: cosmid ends
            High quality sequence stop: 893.
FEATURES             Location/Qualifiers
     source          1. .713
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
```

```
                /db_xref="taxon:9606"
                /clone="cos34b3"
                /clone_lib="LL07NC01-96 well"
                /note="Vector: LAWRIST 16; Site_1: BamHI; Site_2: BamHI;
                Individual chromosomes were flow sorted from a
                rodent/hybrid cell line  containing the single human
                chromosome of interest."
GIN

gnment Scores:
d. No.:              287          Length:        713
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            4.6%         Indels:        0
                     12           Gaps:          0

10-821-670A-36 (1-197) x BZ715412 (1-713)

         4 ProThrProThrProSerProGlyMet 12
           |||||||||||||||||||||||||||
       488 CCGACACCAACTCCAAGTCCAGGGATG 462

ULT 71
34165/c
US       CF934165                 731 bp    mRNA    linear   EST 17-NOV-2003
INITION  TrEST-B01G07.g TrEST-B Hypocrea jecorina cDNA clone Tr-B01G07.g 5',
         mRNA sequence.
ESSION   CF934165
SION     CF934165.1  GI:38353994
WORDS    EST.
RCE      Hypocrea jecorina (anamorph: Trichoderma reesei)
RGANISM  Hypocrea jecorina
         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
         Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
ERENCE   1  (bases 1 to 731)
UTHORS   Bonaccorsi,E.D., Chambergo,F.S. and El-Dorry,H.
ITLE     TrEST-B
OURNAL   Unpublished (2003)
MENT     Contact: El-Dorry, Hamza
         Department of Biochemistry
         Institute of Chemistry. University of Sao Paulo
         Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,
         BRASIL
         Tel: (55) 11-38183848
         Fax: (55) 11-38183848
         Email: dorry@iq.usp.br
         PCR PRimers
         FORWARD: Universal M13 forward primer
         BACKWARD: Universal M13 reverse primer
         Plate: 01  row: G  column: 07
         Seq primer: M13 reverse primer
         High quality sequence stop: 518
         POLYA=No.
TURES              Location/Qualifiers
  source           1. .731
                   /organism="Hypocrea jecorina"
                   /mol_type="mRNA"
                   /strain="QM9414 (ATCC26921)"
                   /db_xref="taxon:51453"
                   /clone="Tr-B01G07.g"
                   /sex="Asexual"
                   /tissue_type="Mycelia"
                   /dev_stage="Mycelial culture grown from 100 mM and
                   harvested to 80 mM glicose concentrations."
                   /lab_host="E. coli DH10B cells (streptomycin resistant)"
                   /clone_lib="TrEST-B"
                   /note="Vector: pUC18; cDNA cloned into SmaI site of pUC18.
                   Average insert size: 1 kb"
GIN

gnment Scores:
d. No.:              293          Length:        731
Score:               9.00         Matches:       9
Percent Similarity:  100.0%       Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:         4.6%         Indels:        0
DB:                  5            Gaps:          0

US-10-821-670A-36 (1-197) x CF934165 (1-731)

Qy          2 AsnLeuProThrProThrProSerPro 10
              |||||||||||||||||||||||||||
Db        552 AACCTTCCAACTCCAACTCCAAGTCCA 526

RESULT 72
DR009499
LOCUS       DR009499                 731 bp    mRNA    linear   EST 18-MAY-2005
DEFINITION  Lr_Cu2CF_36D11 Earthworm Copper Exposure Library Lumbricus rubellus
            cDNA clone Lr_Cu2CF_36D11 similar to UniRef100_Q37546
            NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
            Score = 380 bits (975), Expect = e-104, mRNA sequence.
ACCESSION   DR009499
VERSION     DR009499.1  GI:66273643
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
            Sturzenbaum,S., Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Copper
            exposure library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Cardiff using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13(gttttcccagtcacgacgtt)
            BACKWARD: M13R(caggaaacagctatgaccatg)
            Plate: 36  row: D  column: 11
            Seq primer: caggaaacagctatgaccatg
            High quality sequence start: 2
            High quality sequence stop: 525.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
                     /db_xref="taxon:35632"
                     /clone="Lr_Cu2CF_36D11"
                     /sex="mixed"
                     /tissue_type="whole worm"
                     /dev_stage="Adult"
                     /clone_lib="Earthworm Copper Exposure Library"
                     /note="Vector: pbluescript II SK; The library was prepared
                     using protocols given by the supplier (Clontech)."
ORIGIN

Alignment Scores:
Pred. No.:           293          Length:        731
Score:               9.00         Matches:       9
Percent Similarity:  100.0%       Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:         4.6%         Indels:        0
DB:                  9            Gaps:          0

US-10-821-670A-36 (1-197) x DR009499 (1-731)

Qy          15 CysLeuAsnHisSerGlnThrLeuLeu 23
```

```
                 ||||||||||||||||||||||||||||
        111 TGCCTCAACCATTCGCAGACGCTATTA 137

ULT 73
19793
US        CL419793                  734 bp    DNA     linear   GSS 09-MAR-2004
INITION   ZMMBBb0423N02f ZMMBBb (HindIII) Zea mays genomic clone
          ZMMBBb0423N02 5', genomic survey sequence.
ESSION    CL419793
SION      CL419793.1  GI:45280509
WORDS     GSS.
RCE       Zea mays
RGANISM   Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
ERENCE    1  (bases 1 to 734)
UTHORS    Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
          Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
ITLE      Sequencing of the maize genome at PGIR (2003c)
OURNAL    Unpublished (2003)
MENT      Contact: Bharti,A.K.
          Dr.Joachim Messing's lab
          The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
          University
          190 Frelinghuysen Road, Piscataway, NJ 08854, USA
          Tel: 732 445 3801
          Fax: 732 445 5735
          Email: bharti@waksman.rutgers.edu
          Seq primer: T7
          Class: BAC ends
          High quality sequence start: 126.
TURES               Location/Qualifiers
   source           1. .734
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /cultivar="B73"
                    /db_xref="taxon:4577"
                    /clone="ZMMBBb0423N02"
                    /lab_host="E. coli DH10B"
                    /clone_lib="ZMMBBb (HindIII)"
                    /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
GIN

gnment Scores:
d. No.:              294            Length:        734
re:                  9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            4.6%           Indels:        0
                     13             Gaps:          0

10-821-670A-36 (1-197) x CL419793 (1-734)

          3 LeuProThrProThrProSerProGly 11
            ||||||||||||||||||||||||||||
        491 TTGCCAACCCCGACACCATCACCTGGG 517

ULT 74
95353
US        CG395353                  750 bp    DNA     linear   GSS 22-SEP-2003
INITION   ZMMBBc0010N12r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0010N12
          3', genomic survey sequence.
ESSION    CG395353
SION      CG395353.1  GI:34338578
WORDS     GSS.
RCE       Zea mays
RGANISM   Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
ERENCE    1  (bases 1 to 750)
UTHORS    Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
          Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003b)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
          Dr.Joachim Messing's lab
          The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
          University
          190 Frelinghuysen Road, Piscataway, NJ 08854, USA
          Tel: 732 445 3801
          Fax: 732 445 5735
          Email: bharti@waksman.rutgers.edu
          Seq primer: SP6
          Class: BAC ends
          High quality sequence start: 420.
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0010N12"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc (EcoRI)"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:              300            Length:        750
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.6%           Indels:        0
DB:                     12             Gaps:          0

US-10-821-670A-36 (1-197) x CG395353 (1-750)

Qy          3 LeuProThrProThrProSerProGly 11
              ||||||||||||||||||||||||||||
Db        179 CTGCCAACCCCGACACCATCACCTGGG 205

RESULT 75
CG875642
LOCUS       CG875642                  753 bp    DNA     linear   GSS 26-NOV-2003
DEFINITION  ZMMBBc0286L13r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0286L13
            3', genomic survey sequence.
ACCESSION   CG875642
VERSION     CG875642.1  GI:38540698
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003c)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
            Class: BAC ends
            High quality sequence start: 478.
FEATURES             Location/Qualifiers
     source          1. .753
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
```

```
                /cultivar="B73"
                /db_xref="taxon:4577"
                /clone="ZMMBBc0286L13"
                /lab_host="E. coli DH10B"
                /clone_lib="ZMMBBc (EcoRI)"
                /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
IN

nment Scores:
. No.:              301           Length:        753
e:                  9.00          Matches:       9
cent Similarity:    100.0%        Conservative:  0
t Local Similarity: 100.0%        Mismatches:    0
y Match:            4.6%          Indels:        0
                    12            Gaps:          0

10-821-670A-36 (1-197) x CG875642 (1-753)

         3 LeuProThrProThrProSerProGly 11
           ||||||||||||||||||||||||||||
       313 TTACCAACCCCGACGCCATCACCTGGG 339

ULT 76
98508/c
US        BE298508                765 bp    mRNA    linear   EST 20-JUL-2000
INITION   601119636F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029409 5',
          mRNA sequence.
ESSION    BE298508
SION      BE298508.1  GI:9182251
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 765)
UTHORS    NIH-MGC http://mgc.nci.nih.gov/.
ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL    Unpublished (1999)
MENT      Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          Plate: LLCM89  row: g  column: 10
          High quality sequence stop: 636.
TURES               Location/Qualifiers
  source            1. .765
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:3029409"
                    /tissue_type="rhabdomyosarcoma"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_17"
                    /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                    Site_2: XhoI; cDNA made by oligo-dT priming.
                    Directionally cloned into EcoRI/XhoI sites using the
                    following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                    for average insert size 1.8kb.  Library constructed by
                    Ling Hong in the laboratory of Gerald M. Rubin (University
                    of California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."
IN

gnment Scores:
d. No.:             305           Length:        765
re:                 9.00          Matches:       9
cent Similarity:    100.0%        Conservative:  0
t Local Similarity: 100.0%        Mismatches:    0
```

```
Query Match:        4.6%          Indels:        0
DB:                 7             Gaps:          0

US-10-821-670A-36 (1-197) x BE298508 (1-765)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        458 CCGACACCTACTCCAAGTCCAGGGATG 432

RESULT 77
BE967024/c
LOCUS       BE967024                770 bp    mRNA    linear   EST 14-DEC-2000
DEFINITION  601660755R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915829 3',
            mRNA sequence.
ACCESSION   BE967024
VERSION     BE967024.2  GI:11773043
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 770)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Oct 3, 2000 this sequence version replaced gi:10577729.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM726  row: m  column: 14
            High quality sequence stop: 479.
FEATURES              Location/Qualifiers
     source           1. .770
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3915829"
                      /tissue_type="melanotic melanoma"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_72"
                      /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 2 kb.   Library constructed by Life
                      Technologies."
ORIGIN

Alignment Scores:
Pred. No.:              307           Length:        770
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.6%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-36 (1-197) x BE967024 (1-770)

Qy          3 LeuProThrProThrProSerProGly 11
              ||||||||||||||||||||||||||||
Db        543 CTGCCCACCCCAACCCCCAGCCCCGGG 517

RESULT 78
BI524152/c
LOCUS       BI524152                773 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603051564F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201510 5',
            mRNA sequence.
ACCESSION   BI524152
```

```
SION      BI524152.1  GI:15348944
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 773)
UTHORS    NIH-MGC http://mgc.nci.nih.gov/.
ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL    Unpublished (1999)
MENT      Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11504  row: o  column: 15
          High quality sequence stop: 759.
TURES               Location/Qualifiers
   source           1. .773
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5201510"
                    /lab_host="DH10B"
                    /clone_lib="NIH_MGC_122"
                    /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                    Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                    anonymous pool of 24 week female lung, 16 week female
                    spleen, and 20-22 week male spleens.  Library is oligo-dT
                    primed and directionally cloned (EcoRV site is destroyed
                    upon  cloning).  Average insert size 1.4 kb, insert size
                    range 1-3 kb. Library is normalized and enriched for
                    full-length clones and was  constructed by C. Gruber
                    (Invitrogen).  Research Genetics tracking  code 026. Note:
                    this is a NIH_MGC Library."
GIN

gnment Scores:
d. No.:                308            Length:        773
re:                    9.00           Matches:       9
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              4.6%           Indels:        0
                       2              Gaps:          0

10-821-670A-36 (1-197) x BI524152 (1-773)

          4 ProThrProThrProSerProGlyMet 12
            |||||||||||||||||||||||||||
        241 CCGACACCAACTCCAAGTCCAGGGATG 215

ULT 79
.19478/c
US        CZ119478                 773 bp    DNA     linear   GSS 13-JAN-2005
INITION   OA_BBa0005O19.f OA_BBa Oryza alta genomic clone OA_BBa0005O19 5',
          genomic survey sequence.
ESSION    CZ119478
SION      CZ119478.1  GI:57710300
WORDS     GSS.
RCE       Oryza alta
RGANISM   Oryza alta
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzeae; Oryza.
ERENCE    1  (bases 1 to 773)
UTHORS    Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
          Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
          Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            Plate: 0005  row: O  column: 19
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .773
                      /organism="Oryza alta"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:52545"
                      /clone="OA_BBa0005O19"
                      /tissue_type="young leaves"
                      /lab_host="DH10B-T1 phage resistant"
                      /clone_lib="OA_BBa"
                      /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Alignment Scores:
Pred. No.:                308            Length:        773
Score:                    9.00           Matches:       9
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              4.6%           Indels:        0
DB:                       13             Gaps:          0

US-10-821-670A-36 (1-197) x CZ119478 (1-773)

Qy          87 SerCysLeuAlaSerArgLysThrSer 95
               |||||||||||||||||||||||||||
Db         561 AGCTGCTTAGCAAGCAGGAAAACAAGT 535

RESULT 80
DR008334
LOCUS       DR008334                 788 bp    mRNA    linear   EST 18-MAY-2005
DEFINITION  Lr_Cu2CF_02G12 Earthworm Copper Exposure Library Lumbricus rubellus
            cDNA clone Lr_Cu2CF_02G12 similar to UniRef100_Q37546
            NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
            Score = 403 bits (1035), Expect = e-111, mRNA sequence.
ACCESSION   DR008334
VERSION     DR008334.1  GI:66272478
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
            Sturzenbaum,S., Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Copper
            exposure library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Cardiff using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13(gttttcccagtcacgacgtt)
            BACKWARD: M13R(caggaaacagctatgaccatg)
            Plate: 02  row: G  column: 12
            Seq primer: caggaaacagctatgaccatg
            High quality sequence start: 20
            High quality sequence stop: 514.
```

```
TURES             Location/Qualifiers
  source          1. .788
                  /organism="Lumbricus rubellus"
                  /mol_type="mRNA"
                  /db_xref="taxon:35632"
                  /clone="Lr_Cu2CF_02G12"
                  /sex="mixed"
                  /tissue_type="whole worm"
                  /dev_stage="Adult"
                  /clone_lib="Earthworm Copper Exposure Library"
                  /note="Vector: pbluescript II SK; The library was prepared
                  using protocols given by the supplier (Clontech)."
GIN

gnment Scores:
d. No.:              313            Length:        788
re:                  9.00           Matches:       9
ent Similarity:      100.0%         Conservative:  0
 Local Similarity:   100.0%         Mismatches:    0
y Match:             4.6%           Indels:        0
                     9              Gaps:          0

0-821-670A-36 (1-197) x DR008334 (1-788)

        15 CysLeuAsnHisSerGlnThrLeuLeu 23
           ||||||||||||||||||||||||||||
       116 TGCCTCAACCATTCGCAGACGCTATTA 142

ULT 81
07478/c
US       BM007478                 794 bp    mRNA    linear   EST 30-OCT-2001
INITION  603616745F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440619 5',
         mRNA sequence.
ESSION   BM007478
SION     BM007478.1  GI:16521832
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 794)
UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL   Unpublished (1999)
MENT     Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Dr. Mark Watson
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLCM1913  row: j  column: 12
         High quality sequence start: 7
         High quality sequence stop: 397.
TURES             Location/Qualifiers
  source          1. .794
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:5440619"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH_MGC_113"
                  /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                  EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                  into EcoRI/XhoI sites using the following 5' adaptor:
                  GGCACGAG(G). Library constructed  by Ling Hong in the
                  laboratory of Gerald M. Rubin (University of  California,
                  Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                  Superscript II RT (Life Technologies). Note: this is a
                  NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              315            Length:        794
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.6%           Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-36 (1-197) x BM007478 (1-794)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        208 CCGACACCAACGCCAAGTCCAGGGATG 182

RESULT 82
CB899783/c
LOCUS       CB899783                 794 bp    mRNA    linear   EST 02-JUL-2003
DEFINITION  tric019xp13 T.reesei mycelial culture, Version 3 april Hypocrea
            jecorina cDNA clone tric019xp13, mRNA sequence.
ACCESSION   CB899783
VERSION     CB899783.1  GI:30114441
KEYWORDS    EST.
SOURCE      Hypocrea jecorina (anamorph: Trichoderma reesei)
  ORGANISM  Hypocrea jecorina
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE   1  (bases 1 to 794)
  AUTHORS   Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
            Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
            Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
            Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
  TITLE     Transcriptional regulation of biomass-degrading enzymes in the
            filamentous fungus Trichoderma reesei
  JOURNAL   J. Biol. Chem. 278 (34), 31988-31997 (2003)
   PUBMED   12788920
COMMENT     Contact: Pamela K. Foreman
            Genencor Intl.
            925 Page Mill Road, Palo Alto, CA 94304, USA
            Tel: (650) 846-7635
            Fax: (650) 621-7817
            Email: Pforeman@genencor.com
            Seq primer: LT-F1 primer.
FEATURES             Location/Qualifiers
     source          1. .794
                     /organism="Hypocrea jecorina"
                     /mol_type="mRNA"
                     /strain="QM6a"
                     /db_xref="taxon:51453"
                     /clone="tric019xp13"
                     /dev_stage="mycelia"
                     /clone_lib="T.reesei mycelial culture, Version 3 april"
                     /note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
                     culture grown from 24 hrs to 6 days with varying Carbon
                     and Nitrogen sources and concentrations."
ORIGIN

Alignment Scores:
Pred. No.:              315            Length:        794
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.6%           Indels:        0
DB:                     4              Gaps:          0

US-10-821-670A-36 (1-197) x CB899783 (1-794)

Qy          2 AsnLeuProThrProThrProSerPro 10
              |||||||||||||||||||||||||||
Db        633 AACCTTCCAACTCCAACTCCAAGTCCA 607

RESULT 83
```

```
397339
:US       BM397339                  796 bp    mRNA    linear   EST 17-JAN-2002
'INITION  5009-0-31-C08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
          Tetrahymena thermophila cDNA, mRNA sequence.
:ESSION   BM397339
:SION     BM397339.1  GI:18197392
'WORDS    EST.
IRCE      Tetrahymena thermophila
)RGANISM  Tetrahymena thermophila
          Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
          Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
'ERENCE   1  (bases 1 to 796)
\UTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
          Frankel,J. and Klobutcher,L.
'ITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
'OURNAL   Unpublished (2002)
;MENT     Contact: Turkewitz AP
          Molecular Genetics and Cell Biology
          University of Chicago
          920 E. 58th Street, Chicago, IL 60637, USA
          Tel: 773 702 4374
          Fax: 773 702 3172
          Email: apturkew@midway.uchicago.edu
          Seq primer: T3.
\TURES              Location/Qualifiers
   source           1. .796
                    /organism="Tetrahymena thermophila"
                    /mol_type="mRNA"
                    /strain="CU428.1"
                    /db_xref="taxon:5911"
                    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                    /note="Vector: BlueScript2 SK+; Details on library
                    preparation can be found in Chilcoat and Turkewitz (2001)
                    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
:GIN

.gnment Scores:
:d. No.:              316           Length:         796
)re:                  9.00          Matches:        9
:cent Similarity:     100.0%        Conservative:   0
:t Local Similarity:  100.0%        Mismatches:     0
:ry Match:            4.6%          Indels:         0
                      2             Gaps:           0

-10-821-670A-36 (1-197) x BM397339 (1-796)

        138 LeuThrAlaIleAspGluLeuLeuGln 146
            ||||||||||||||||||||||||||||
        527 TTGACAGCAATTGACGAATTATTACAG 553

:ULT 84
:35464
:US       BX835464                  822 bp    mRNA    linear   EST 11-FEB-2004
'INITION  BX835464 Arabidopsis thaliana Adult vegetative tissue Col-0
          Arabidopsis thaliana cDNA clone GSLTLS14ZC06 3PRIM, mRNA sequence.
:ESSION   BX835464
:SION     BX835464.1  GI:42529547
'WORDS    EST.
IRCE      Arabidopsis thaliana (thale cress)
)RGANISM  Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
'ERENCE   1  (bases 1 to 822)
\UTHORS   Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
          Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
          Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
:ITLE     Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
          A Combined Approach to Evaluate and Improve Arabidopsis Genome
          Annotation
'OURNAL   Unpublished (2004)
;MENT     Contact: Genoscope
          Genoscope - Centre National de Sequencage
          2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          The sequences are based on single pass reads.
          Life Technologies (a division of Invitrogen) members carried out
          full-length librairies construction : Temple G.
          Genoscope members carried out sequencing and annotation : Castelli
          V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
          Schachter V., Weissenbach J., Salanoubat M.
          URGV INRA : Clepet C., Caboche M.
          Annotation is based on the June 2003 version of the Arabidopsis
          genome released by MIPS (Munich Information center for Protein
          Sequences).
          http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
          http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES            Location/Qualifiers
     source         1. .822
                    /organism="Arabidopsis thaliana"
                    /mol_type="mRNA"
                    /ecotype="Col-0"
                    /db_xref="taxon:3702"
                    /clone="GSLTLS14ZC06"
                    /tissue_type="Adult vegetative tissue"
                    /clone_lib="Arabidopsis thaliana Adult vegetative tissue
                    Col-0"
ORIGIN

Alignment Scores:
Pred. No.:              325           Length:         822
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.6%          Indels:         0
DB:                     4             Gaps:           0

US-10-821-670A-36 (1-197) x BX835464 (1-822)

Qy        183 ArgAlaValThrIleAsnArgMetMet 191
              |||||||||||||||||||||||||||
Db        581 AGAGCAGTGACGATCAACAGGATGATG 607

RESULT 85
CG385421
LOCUS       CG385421                  825 bp    DNA     linear   GSS 26-AUG-2003
DEFINITION  OGYBY32TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0644F15,
            genomic survey sequence.
ACCESSION   CG385421
VERSION     CG385421.1  GI:34302688
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 825)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OGYBY32TH
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: methylation filtered.
FEATURES            Location/Qualifiers
     source         1. .825
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /strain="B73"
```

```
                /db_xref="taxon:4577"
                /clone="ZMMBMa0644F15"
                /clone_lib="ZM_0.7_1.5_KB"
                /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                methylation filtered genomic DNA library"
GIN

gnment Scores:
d. No.:              326           Length:        825
re:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            4.6%          Indels:        0
                     12            Gaps:          0

10-821-670A-36 (1-197) x CG385421 (1-825)

        84 ThrAsnGlySerCysLeuAlaSerArg 92
           |||||||||||||||||||||||||
       268 ACAAATGGGTCGTGTCTGGCGAGCCGA 294

ULT 86
69425/c
US       CT469425                831 bp    DNA     linear   GSS 03-NOV-2005
INITION  Sus scrofa genomic clone CH242-415C18, genomic survey sequence.
ESSION   CT469425
SION     CT469425.1  GI:80205278
WORDS    GSS.
RCE      Sus scrofa (pig)
RGANISM  Sus scrofa
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
         Sus.
ERENCE   1  (bases 1 to 831)
UTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
ITLE     Direct Submission
URNAL    Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
         Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
         humquery@sanger.ac.uk Unpublished
MENT     This sequence was generated from the T7 end of BAC 415C18. 415C18
         is part of the CHORI-242 BAC Library created by P. de Jong. Further
         details: http://www.sanger.ac.uk/Projects/S_scrofa/.
TURES              Location/Qualifiers
  source           1. .831
                   /organism="Sus scrofa"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9823"
                   /clone="CH242-415C18"
                   /tissue_type="White blood cells"
                   /note="vector pTARBAC1.3_BamHI
                   sex female"
GIN

gnment Scores:
d. No.:              328           Length:        831
re:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            4.6%          Indels:        0
                     14            Gaps:          0

10-821-670A-36 (1-197) x CT469425 (1-831)

       168 LysThrLysIleLysLeuCysIleLeu 176
           ||||||||||||||||||||||||||
       805 AAGACGAAGATCAAGCTATGCATTCTA 779

ULT 87
16665/c
US       CD516665                845 bp    mRNA    linear   EST 06-JUN-2003
INITION  AGENCOURT_14371243 NIH_MGC_181 Homo sapiens cDNA clone
         IMAGE:30407983 5', mRNA sequence.
ESSION   CD516665
```

```
VERSION     CD516665.1  GI:31448383
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 845)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM490  row: d  column: 08
            High quality sequence stop: 707.
FEATURES             Location/Qualifiers
     source          1. .845
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30407983"
                     /tissue_type="White Matter"
                     /dev_stage="Unknown"
                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_181"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV
                     (destroyed); Library is oligo-dT primed and directionally
                     cloned (EcoRV site is destroyed upon cloning). Average
                     insert size 1.42 kb. Library was constructed by
                     (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              333           Length:        845
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.6%          Indels:        0
DB:                     5             Gaps:          0

US-10-821-670A-36 (1-197) x CD516665 (1-845)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        542 CCGACACCAACTCCAAGTCCAGGGATG 516

RESULT 88
CG681185
LOCUS       CG681185                847 bp    DNA     linear   GSS 08-OCT-2003
DEFINITION  ZMMBBc0149O20f ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0149O20
            5', genomic survey sequence.
ACCESSION   CG681185
VERSION     CG681185.1  GI:37578022
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 847)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003c)
```

```
'OURNAL   Unpublished (2003)
:MENT     Contact: Bharti,A.K.
          Dr.Joachim Messing's lab
          The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
          University
          190 Frelinghuysen Road, Piscataway, NJ 08854, USA
          Tel: 732 445 3801
          Fax: 732 445 5735
          Email: bharti@waksman.rutgers.edu
          Seq primer: T7
          Class: BAC ends
          High quality sequence start: 404.
\TURES              Location/Qualifiers
   source           1. .847
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /cultivar="B73"
                    /db_xref="taxon:4577"
                    /clone="ZMMBBc0149O20"
                    /lab_host="E. coli DH10B"
                    /clone_lib="ZMMBBc (EcoRI)"
                    /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
:GIN

gnment Scores:
:d. No.:            334             Length:         847
)re:                9.00            Matches:        9
:cent Similarity:   100.0%          Conservative:   0
:t Local Similarity: 100.0%         Mismatches:     0
:ry Match:          4.6%            Indels:         0
                    12              Gaps:           0

10-821-670A-36 (1-197) x CG681185 (1-847)

          4 ProThrProThrProSerProGlyMet 12
            |||||||||||||||||||||||||||
        488 CCAACCCCGACGCCATCACCTGGGATG 514

:ULT 89
'07955/c
:US       BQ707955                860 bp    mRNA    linear   EST 16-JUL-2002
'INITION  AGENCOURT_8347291 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279270
          5', mRNA sequence.
:ESSION   BQ707955
:SION     BQ707955.1  GI:21846854
'WORDS    EST.
)RCE      Homo sapiens (human)
)RGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
'ERENCE   1  (bases 1 to 860)
\UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
:ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
'OURNAL   Unpublished (1999)
)MENT     Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Mark Watson
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM2468  row: j  column: 07
          High quality sequence stop: 664.
\TURES              Location/Qualifiers
   source           1. .860
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6279270"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_113"
                    /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCACGAG(G). Library constructed  by Ling Hong in the
                    laboratory of Gerald M. Rubin (University of  California,
                    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                    Superscript II RT (Life Technologies). Note: this is a
                    NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              338             Length:         860
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.6%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x BQ707955 (1-860)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        203 CCGACACCAACTCCAAGTCCAGGGATG 177

RESULT 90
BQ712265/c
LOCUS       BQ712265                870 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8347466 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279305
            5', mRNA sequence.
ACCESSION   BQ712265
VERSION     BQ712265.1  GI:21851164
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 870)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2468  row: k  column: 18
            High quality sequence stop: 501.
FEATURES              Location/Qualifiers
     source           1. .870
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6279305"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_113"
                      /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                      into EcoRI/XhoI sites using the following 5' adaptor:
                      GGCACGAG(G). Library constructed  by Ling Hong in the
                      laboratory of Gerald M. Rubin (University of  California,
                      Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                      Superscript II RT (Life Technologies). Note: this is a
                      NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              342             Length:         870
```

```
re:                 9.00            Matches:        9
cent Similarity:    100.0%          Conservative:   0
t Local Similarity: 100.0%          Mismatches:     0
ry Match:           4.6%            Indels:         0
                    3               Gaps:           0

10-821-670A-36 (1-197) x BQ712265 (1-870)

         4 ProThrProThrProSerProGlyMet 12
           |||||||||||||||||||||||||||
       203 CCGACACCAACTCCAAGTCCAGGGATG 177

ULT 91
10906/c
US       BQ710906                909 bp    mRNA    linear   EST 16-JUL-2002
INITION  AGENCOURT_8501087 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6303144
         5', mRNA sequence.
ESSION   BQ710906
SION     BQ710906.1  GI:21849805
'ORDS    EST.
:CE      Homo sapiens (human)
:GANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 909)
UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL   Unpublished (1999)
MENT     Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Dr. Mark Watson
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLCM2521  row: m  column: 01
         High quality sequence stop: 582.
TURES              Location/Qualifiers
  source           1. .909
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:6303144"
                   /lab_host="DH10B (phage-resistant)"
                   /clone_lib="NIH_MGC_113"
                   /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                   EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                   into EcoRI/XhoI sites using the following 5' adaptor:
                   GGCACGAG(G). Library constructed  by Ling Hong in the
                   laboratory of Gerald M. Rubin (University of  California,
                   Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                   Superscript II RT (Life Technologies). Note: this is a
                   NIH_MGC Library."
IN

nment Scores:
i. No.:             355             Length:         909
re:                 9.00            Matches:        9
ent Similarity:     100.0%          Conservative:   0
t Local Similarity: 100.0%          Mismatches:     0
ry Match:           4.6%            Indels:         0
                    3               Gaps:           0

10-821-670A-36 (1-197) x BQ710906 (1-909)

         4 ProThrProThrProSerProGlyMet 12
           |||||||||||||||||||||||||||
       203 CCGACACCAACTCCAAGTCCAGGGATG 177

ULT 92
```

```
CNS01EWE
LOCUS       CNS01EWE                  918 bp    DNA     linear   GSS 30-MAY-2001
DEFINITION  Anopheles gambiae GSS T7 end of clone 03C11 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL141087
VERSION     AL141087.1  GI:6999205
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 918)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 918)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .918
                     /organism="Anopheles gambiae"
                     /mol_type="genomic DNA"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="03C11"
                     /clone_lib="NotreDame1"
                     /note="end : T7"
ORIGIN

Alignment Scores:
Pred. No.:              358             Length:         918
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.6%            Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x CNS01EWE (1-918)

Qy        172 LysLeuCysIleLeuLeuHisAlaPhe 180
              |||||||||||||||||||||||||||
Db        497 AAGCTTTGCATATTGCTTCATGCTTTT 523

RESULT 93
CG396548
LOCUS       CG396548                  928 bp    DNA     linear   GSS 22-SEP-2003
DEFINITION  ZMMBBc0013J24r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0013J24
            3', genomic survey sequence.
ACCESSION   CG396548
VERSION     CG396548.1  GI:34339773
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003b)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
```

```
         The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
         University
         190 Frelinghuysen Road, Piscataway, NJ 08854, USA
         Tel: 732 445 3801
         Fax: 732 445 5735
         Email: bharti@waksman.rutgers.edu
         Seq primer: SP6
         Class: BAC ends
         High quality sequence start: 411.
TURES             Location/Qualifiers
   source         1. .928
                  /organism="Zea mays"
                  /mol_type="genomic DNA"
                  /cultivar="B73"
                  /db_xref="taxon:4577"
                  /clone="ZMMBBc0013J24"
                  /lab_host="E. coli DH10B"
                  /clone_lib="ZMMBBc (EcoRI)"
                  /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
GIN

gnment Scores:
d. No.:              362          Length:        928
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            4.6%         Indels:        0
                     12           Gaps:          0

10-821-670A-36 (1-197) x CG396548 (1-928)

          4 ProThrProThrProSerProGlyMet 12
            |||||||||||||||||||||||||||
        502 CCGACCCCGACACCATCACCTGGGATG 528

ULT 94
52347/c
US       CZ252347                 933 bp    DNA     linear   GSS 31-DEC-2005
INITION  LQCYI32TV American Alligator BAC Library Alligator mississippiensis
         genomic, genomic survey sequence.
ESSION   CZ252347
SION     CZ252347.1  GI:84107514
WORDS    GSS.
RCE      Alligator mississippiensis (American alligator)
RGANISM  Alligator mississippiensis
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Archosauria; Crocodylidae; Alligatorinae; Alligator.
ERENCE   1  (bases 1 to 933)
UTHORS   Shedlock,A.M., Botka,C.W., Zhao,S., Shetty,J., Zhang,T., Liu,J.S.,
         Deschavanne,P. and Edwards,E.P.
ITLE     Genomic trends in amniotes inferred from BAC-end sequence analysis
         of non-avian reptiles
OURNAL   Unpublished (2005)
MENT     Contact: Christopher W Botka
         Center for Genomics Research
         Harvard University
         Bauer Laboratory, 7 Divinity Avenue, Cambridge, MA 02138, USA
         Tel: 617 496 5419
         Fax: 617 495 2196
         Email: botka@cgr.harvard.edu
         Class: BAC ends.
TURES             Location/Qualifiers
   source         1. .933
                  /organism="Alligator mississippiensis"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:8496"
                  /clone_lib="American Alligator BAC Library"
GIN

gnment Scores:
d. No.:              364          Length:        933
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%    Mismatches:    0
Query Match:            4.6%      Indels:        0
DB:                     13        Gaps:          0

US-10-821-670A-36 (1-197) x CZ252347 (1-933)

Qy          3 LeuProThrProThrProSerProGly 11
              |||||||||||||||||||||||||||
Db        259 CTGCCAACTCCAACCCCCTCCCCAGGA 233

RESULT 95
BX444783/c
LOCUS       BX444783                1054 bp    mRNA    linear   EST 04-MAY-2004
DEFINITION  BX444783 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF007YA14 5-PRIME, mRNA sequence.
ACCESSION   BX444783
VERSION     BX444783.2  GI:47013734
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1054)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 15, 2003 this sequence version replaced gi:30786261.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 4332.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS1AF002ZE08QP1&c=4332.f.
FEATURES              Location/Qualifiers
     source           1. .1054
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DF007YA14"
                      /tissue_type="FETAL BRAIN"
                      /dev_stage="fetal"
                      /clone_lib="Homo sapiens FETAL BRAIN"
                      /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                      was primed with a NotI-oligo(dT) primer. Five prime end
                      enriched, double-strand cDNA was digested with Not I and
                      cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                      vector. Library was not normalized."
ORIGIN

Alignment Scores:
Pred. No.:              405          Length:        1054
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            4.6%         Indels:        0
DB:                     4            Gaps:          0

US-10-821-670A-36 (1-197) x BX444783 (1-1054)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        519 CCGACACCAACTCCAAGTCCAGGGATG 493

RESULT 96
CL092806/c
LOCUS       CL092806                1083 bp    DNA     linear   GSS 05-JAN-2004
```

```
NITION  ISB1-22J9_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-22J9,
        genomic survey sequence.
SSION   CL092806
ION     CL092806.1  GI:40586441
ORDS    GSS.
CE      Xenopus tropicalis (western clawed frog)
GANISM  Xenopus tropicalis
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
        Xenopodinae; Xenopus; Silurana.
ERENCE  1  (bases 1 to 1083)
UTHORS  Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
        Mardis,E. and Wilson,R.
ITLE    A physical map of the xenopus tropicalis genome
OURNAL  Unpublished (2003)
MENT    Contact: Richard K Wilson
        Genome Sequencing Center
        Washington University School of Medicine
        Email: submissions@watson.wustl.edu
        Insert Length: 75000   Std Error: 0.00
        Seq primer: T7 TAATACGACTCACTATAGGG
        Class: BAC ends
        High quality sequence start: 33
        High quality sequence stop: 811.
TURES           Location/Qualifiers
  source        1. .1083
                /organism="Xenopus tropicalis"
                /mol_type="genomic DNA"
                /db_xref="taxon:8364"
                /clone="ISB1-22J9"
                /clone_lib="ISB1"
                /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
                Library Segment 1"
IN

gnment Scores:
d. No.:             415          Length:       1083
e:                  9.00         Matches:      9
ent Similarity:     100.0%       Conservative: 0
 Local Similarity:  100.0%       Mismatches:   0
y Match:            4.6%         Indels:       0
                    12           Gaps:         0

0-821-670A-36 (1-197) x CL092806 (1-1083)

      170 LysIleLysLeuCysIleLeuLeuHis 178
          |||||||||||||||||||||||||||
      798 AAAATAAAGCTGTGTATATTGTTACAT 772

ULT 97
18555/c
US      BX418555               1145 bp    mRNA    linear   EST 01-MAY-2004
INITION BX418555 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
        CS0DF007YA14 5-PRIME, mRNA sequence.
ESSION  BX418555
SION    BX418555.2  GI:46932321
WORDS   EST.
RCE     Homo sapiens (human)
RGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
ERENCE  1  (bases 1 to 1145)
UTHORS  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
ITLE    Full-length cDNA libraries and normalization
OURNAL  Unpublished (2001)
MENT    On May 13, 2003 this sequence version replaced gi:30654596.
        Contact: Genoscope
        Genoscope - Centre National de Sequencage
        2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
        Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
        1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
        end enriched, double-strand cDNA was digested with Not I and cloned
        into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
        was not normalized. Library was constructed by Life Technologies, a
        division of Invitrogen.
        This sequence belongs to sequence cluster 4332.f
        For more information about this cluster, see
        http://www.genoscope.cns.fr/cdna?s=CS0DF007BA07QP1&c=4332.f.
FEATURES        Location/Qualifiers
     source     1. .1145
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DF007YA14"
                /tissue_type="FETAL BRAIN"
                /dev_stage="fetal"
                /clone_lib="Homo sapiens FETAL BRAIN"
                /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                was primed with a NotI-oligo(dT) primer. Five prime end
                enriched, double-strand cDNA was digested with Not I and
                cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                vector. Library was not normalized."
ORIGIN

Alignment Scores:
Pred. No.:              435          Length:       1145
Score:                  9.00         Matches:      9
Percent Similarity:     100.0%       Conservative: 0
Best Local Similarity:  100.0%       Mismatches:   0
Query Match:            4.6%         Indels:       0
DB:                     4            Gaps:         0

US-10-821-670A-36 (1-197) x BX418555 (1-1145)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        520 CCGACACCAACTCCAAGTCCAGGGATG 494

RESULT 98
CV123647/c
LOCUS       CV123647               1215 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  OSTF30015B11 pDONR201 Entry vector Caenorhabditis elegans cDNA,
            mRNA sequence.
ACCESSION   CV123647
VERSION     CV123647.1  GI:51714819
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 1215)
  AUTHORS   Lamesch,P., Milstein,S., Hao,T., Rosenberg,J., Li,N., Sequerra,R.,
            Bosak,S., Doucette-Stamm,L., Vandenhaute,J., Hill,D.E. and Vidal,M.
  TITLE     C. elegans ORFeome Version 3.1: Increasing the coverage of ORFeome
            resources with improved gene predictions
  JOURNAL   Genome Res. (ORFeome issue) (2004) In press
COMMENT     Contact: Philippe Lamesch and Tong Hao
            Marc Vidal Lab
            DFCI
            44, Binney Street, Boston, MA 02115, USA
            Tel: 6176323910
            Fax: 6176325739
            Email: philippe_lamesch@dfci.harvard.edu
            PCR PRimers
            FORWARD: TGTCGGACGAAAAGATTTCAAT
            BACKWARD: TAGTCGCTGGTATCTTGTT.
FEATURES        Location/Qualifiers
     source     1. .1215
                /organism="Caenorhabditis elegans"
                /mol_type="mRNA"
                /strain="N2"
                /db_xref="taxon:6239"
                /sex="male and hermaphrodite"
                /tissue_type="all tissues"
                /cell_type="all cells"
```

```
                /dev_stage="all stages"
                /clone_lib="pDONR201 Entry vector"
:GIN

:gnment Scores:
:d. No.:                459             Length:         1215
:re:                    9.00            Matches:        9
:cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              4.6%            Indels:         0
                        8               Gaps:           0

10-821-670A-36 (1-197) x CV123647 (1-1215)

        19 SerGlnThrLeuLeuArgAlaIleSer 27
           |||||||||||||||||||||||||
       373 TCCCAAACATTGCTTCGAGCAATATCA 347

:ULT 99
:07863/c
:US       CR607863                1470 bp    mRNA    linear   HTC 21-JUL-2004
:INITION  full-length cDNA clone CS0DI010YO02 of Placenta Cot 25-normalized
          of Homo sapiens (human).
:ESSION   CR607863
:SION     CR607863.1  GI:50488670
:WORDS    HTC; CNSLT_cDNA.
:RCE      Homo sapiens (human)
:RGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
:ERENCE   1  (bases 1 to 1470)
:UTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
:ITLE     Full-length cDNA libraries and normalization
:OURNAL   Unpublished
:EMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue
:ERENCE   2  (bases 1 to 1470)
:UTHORS   Genoscope.
:ITLE     Direct Submission
:OURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
:MENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
:TURES              Location/Qualifiers
   source           1. .1470
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="CS0DI010YO02"
                    /tissue_type="Placenta Cot 25-normalized"
                    /plasmid="pCMVSPORT_6"
:GIN

:gnment Scores:
:d. No.:                542             Length:         1470
:re:                    9.00            Matches:        9
:cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              4.6%            Indels:         0
                        6               Gaps:           0

10-821-670A-36 (1-197) x CR607863 (1-1470)

         4 ProThrProThrProSerProGlyMet 12
           |||||||||||||||||||||||||||
        47 CCGACACCAACTCCAAGTCCAGGGATG 21
```

```
RESULT 100
CR590609/c
LOCUS       CR590609                2160 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DF007YA14 of Fetal brain of Homo sapiens
            (human).
ACCESSION   CR590609
VERSION     CR590609.1  GI:50471416
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2160)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2160)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES              Location/Qualifiers
     source           1. .2160
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DF007YA14"
                      /tissue_type="Petal brain"
                      /plasmid="pCMVSPORT_6"
ORIGIN

Alignment Scores:
Pred. No.:              761             Length:         2160
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.6%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-36 (1-197) x CR590609 (1-2160)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db        520 CCGACACCAACTCCAAGTCCAGGGATG 494


Search completed: June 10, 2006, 16:33:37
Job time : 2744.64 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 01:43:45 ; Search time 112.303 Seconds
(without alignments)
4923.420 Million cell updates/sec

le: US-10-821-670A-36
fect score: 197
quence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 1403666 seqs, 935554401 residues

d size: 1

al number of hits satisfying chosen parameters: 2800942

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mand line parameters:
)DEL=frame+_p2n.model -DEV=xlp
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110458_27682/app_query.fasta_1
B=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rni
NMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
RANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
LIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
AXLEN=2000000000 -HOST=abss05p
SER=US10821670_@CGN_1_1_677_@runat_07062006_110458_27682 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	197	100.0	591	3	US-09-917-265A-35	Sequence 35, Appl
2	197	100.0	591	3	US-09-917-265A-37	Sequence 37, Appl
3	197	100.0	666	3	US-09-917-265A-32	Sequence 32, Appl
4	197	100.0	666	3	US-09-917-265A-34	Sequence 34, Appl
5	197	100.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
6	197	100.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
7	197	100.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c 8	197	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
9	195	99.0	591	3	US-09-011-143-9	Sequence 9, Appli
10	195	99.0	591	3	US-09-302-495-9	Sequence 9, Appli
11	195	99.0	591	3	US-10-079-616-9	Sequence 9, Appli
12	195	99.0	689	3	US-09-011-143-26	Sequence 26, Appl
13	195	99.0	689	3	US-09-302-495-26	Sequence 26, Appl
14	195	99.0	689	3	US-10-079-616-26	Sequence 26, Appl
15	195	99.0	1441	3	US-09-011-143-8	Sequence 8, Appli
16	195	99.0	1441	3	US-09-302-495-8	Sequence 8, Appli
17	195	99.0	1441	3	US-10-079-616-8	Sequence 8, Appli
18	187	94.9	561	3	US-09-917-265A-101	Sequence 101, App
c 19	187	94.9	561	3	US-09-917-265A-103	Sequence 103, App
20	52	26.4	591	3	US-09-917-265A-49	Sequence 49, Appl
c 21	52	26.4	591	3	US-09-917-265A-51	Sequence 51, Appl
22	52	26.4	666	3	US-09-917-265A-46	Sequence 46, Appl
c 23	52	26.4	666	3	US-09-917-265A-48	Sequence 48, Appl
24	52	26.4	669	3	US-09-079-984A-2	Sequence 2, Appli
25	52	26.4	669	3	US-09-079-984A-12	Sequence 12, Appl
26	52	26.4	669	3	US-09-390-729-2	Sequence 2, Appli
27	52	26.4	669	3	US-09-390-729-12	Sequence 12, Appl
28	52	26.4	1455	3	US-09-917-265A-104	Sequence 104, App
c 29	52	26.4	1455	3	US-09-917-265A-106	Sequence 106, App
30	52	26.4	1533	3	US-09-917-265A-66	Sequence 66, Appl
c 31	52	26.4	1533	3	US-09-917-265A-68	Sequence 68, Appl
32	52	26.4	1599	3	US-09-917-265A-61	Sequence 61, Appl
c 33	52	26.4	1599	3	US-09-917-265A-63	Sequence 63, Appl
34	29	14.7	601	3	US-09-949-016-20385	Sequence 20385, A
35	29	14.7	601	3	US-09-949-016-87352	Sequence 87352, A
36	29	14.7	660	2	US-08-186-529-3	Sequence 3, Appli
37	29	14.7	660	2	US-08-640-386A-3	Sequence 3, Appli
38	29	14.7	721	2	US-08-184-009-199	Sequence 199, App
39	29	14.7	721	2	US-08-458-356-199	Sequence 199, App
40	29	14.7	721	3	US-08-460-736-199	Sequence 199, App
41	29	14.7	721	3	US-09-535-370-199	Sequence 199, App
42	29	14.7	721	3	US-09-663-667-199	Sequence 199, App
43	29	14.7	762	3	US-08-848-760B-21	Sequence 21, Appl
44	29	14.7	762	3	US-09-826-025-21	Sequence 21, Appl
45	29	14.7	762	5	US-09-543-679A-2890	Sequence 2890, Ap
46	29	14.7	1019	3	US-09-949-016-2462	Sequence 2462, Ap
47	29	14.7	1026	2	US-08-751-767A-1	Sequence 1, Appli
48	29	14.7	1026	3	US-09-023-655-1041	Sequence 1041, Ap
49	29	14.7	1026	3	US-09-949-016-130	Sequence 130, App
50	29	14.7	1287	3	US-09-634-368-6	Sequence 6, Appli
51	29	14.7	1316	2	US-08-684-687-3	Sequence 3, Appli
52	29	14.7	1316	3	US-09-851-520-3	Sequence 3, Appli
53	29	14.7	1364	2	US-08-265-087-3	Sequence 3, Appli
54	29	14.7	1364	2	US-08-621-493-3	Sequence 3, Appli
55	29	14.7	1364	2	US-08-965-688-3	Sequence 3, Appli
56	29	14.7	1364	3	US-09-260-173-3	Sequence 3, Appli
57	29	14.7	1395	3	US-09-924-703-5	Sequence 5, Appli
58	29	14.7	1560	2	US-08-751-767A-11	Sequence 11, Appl
59	29	14.7	1623	2	US-08-751-767A-9	Sequence 9, Appli
60	29	14.7	1645	3	US-09-310-842-2	Sequence 2, Appli
61	29	14.7	4521	5	US-09-543-679A-2893	Sequence 2893, Ap
62	29	14.7	6139	2	US-08-751-767A-7	Sequence 7, Appli
63	29	14.7	10764	3	US-09-949-016-11872	Sequence 11872, A
64	29	14.7	10765	3	US-09-949-016-14204	Sequence 14204, A
65	28	14.2	601	3	US-09-949-016-20381	Sequence 20381, A
66	28	14.2	601	3	US-09-949-016-87348	Sequence 87348, A
67	26	13.2	79	3	US-09-011-143-24	Sequence 24, Appl
68	26	13.2	79	3	US-09-302-495-24	Sequence 24, Appl
69	26	13.2	79	3	US-10-079-616-24	Sequence 24, Appl
c 70	12	6.1	36	3	US-09-011-143-25	Sequence 25, Appl
c 71	12	6.1	36	3	US-09-302-495-25	Sequence 25, Appl
c 72	12	6.1	36	3	US-10-079-616-25	Sequence 25, Appl
73	11	5.6	39	3	US-09-917-265A-91	Sequence 91, Appl
74	10	5.1	60	3	US-09-917-265A-83	Sequence 83, Appl
c 75	10	5.1	60	3	US-09-917-265A-84	Sequence 84, Appl
76	10	5.1	582	3	US-09-634-368-1	Sequence 1, Appli
77	10	5.1	713	2	US-08-385-335A-10	Sequence 10, Appl
78	10	5.1	1278	3	US-09-634-368-5	Sequence 5, Appli
79	10	5.1	1569	3	US-09-634-368-12	Sequence 12, Appl
80	10	5.1	2013	3	US-09-634-368-11	Sequence 11, Appl

81	10	5.1	2709	3	US-09-634-368-13	Sequence 13, Appl
82	10	5.1	6295	2	US-08-659-206A-4	Sequence 4, Appli
83	10	5.1	7287	2	US-08-659-206A-1	Sequence 1, Appli
84	9	4.6	51	3	US-09-917-265A-96	Sequence 96, Appl
85	9	4.6	2210	3	US-08-464-700-53	Sequence 53, Appl
86	9	4.6	2242	2	US-08-641-627A-37	Sequence 37, Appl
87	9	4.6	2427	2	US-08-678-039A-39	Sequence 39, Appl
88	9	4.6	2845	3	US-10-104-047-945	Sequence 945, App
89	8	4.1	25	3	US-09-396-196G-121547	Sequence 121547,
90	8	4.1	27	3	US-09-917-265A-90	Sequence 90, Appl
91	8	4.1	41	3	US-09-917-265A-92	Sequence 92, Appl
92	8	4.1	452	3	US-09-621-976-13237	Sequence 13237, A
93	8	4.1	601	3	US-09-949-016-60737	Sequence 60737, A
94	8	4.1	601	3	US-09-949-016-60738	Sequence 60738, A
95	8	4.1	601	3	US-09-949-016-60739	Sequence 60739, A
96	8	4.1	601	3	US-09-949-016-111391	Sequence 111391,
97	8	4.1	601	3	US-09-949-016-111392	Sequence 111392,
98	8	4.1	601	3	US-09-949-016-147156	Sequence 147156,
99	8	4.1	601	3	US-09-949-016-154644	Sequence 154644,
100	8	4.1	601	3	US-09-949-016-154645	Sequence 154645,
101	8	4.1	1380	3	US-09-134-000C-3234	Sequence 3234, Ap
102	8	4.1	1465	4	US-09-605-703B-525	Sequence 525, App
103	8	4.1	1570	4	US-09-605-703B-523	Sequence 523, App
104	8	4.1	1697	3	US-09-902-540-8882	Sequence 8882, Ap
105	8	4.1	2249	3	US-08-814-052-19	Sequence 19, Appl
106	8	4.1	2279	3	US-08-814-052-17	Sequence 17, Appl
107	8	4.1	2300	3	US-08-814-052-18	Sequence 18, Appl
108	8	4.1	2792	3	US-10-104-047-458	Sequence 458, App
109	8	4.1	2957	3	US-09-221-017B-775	Sequence 775, App
110	8	4.1	3098	3	US-10-104-047-401	Sequence 401, App
111	8	4.1	3183	2	US-08-939-218A-1	Sequence 1, Appli
112	8	4.1	3187	7	PCT-US95-06815-1	Sequence 1, Appli
113	8	4.1	3192	2	US-08-706-037-26	Sequence 26, Appl
114	8	4.1	3192	2	US-08-940-661A-1	Sequence 1, Appli
115	8	4.1	3192	2	US-09-083-485-1	Sequence 1, Appli
116	8	4.1	3192	2	US-09-005-397-26	Sequence 26, Appl
117	8	4.1	4447	3	US-09-949-016-15763	Sequence 15763, A
118	8	4.1	4623	3	US-09-949-016-15769	Sequence 15769, A
119	8	4.1	9704	3	US-09-814-951A-3	Sequence 3, Appli
120	8	4.1	9704	3	US-10-109-860B-3	Sequence 3, Appli
121	8	4.1	9905	3	US-09-949-016-16862	Sequence 16862, A
122	8	4.1	9937	3	US-09-902-540-946	Sequence 946, App
123	8	4.1	45086	3	US-09-949-016-14816	Sequence 14816, A
124	8	4.1	134890	3	US-09-949-016-15602	Sequence 15602, A
125	8	4.1	275110	3	US-09-949-016-12706	Sequence 12706, A
126	8	4.1	275110	3	US-09-949-016-16070	Sequence 16070, A
127	8	4.1	283538	3	US-09-949-016-13506	Sequence 13506, A
128	8	4.1	374159	3	US-09-949-016-15868	Sequence 15868, A
129	7	3.6	21	3	US-09-011-143-17	Sequence 17, Appl
130	7	3.6	21	3	US-09-011-143-18	Sequence 18, Appl
131	7	3.6	21	3	US-09-302-495-17	Sequence 17, Appl
132	7	3.6	21	3	US-09-302-495-18	Sequence 18, Appl
133	7	3.6	21	3	US-10-079-616-17	Sequence 17, Appl
134	7	3.6	21	3	US-10-079-616-18	Sequence 18, Appl
135	7	3.6	32	2	US-08-859-998-383	Sequence 383, App
136	7	3.6	32	3	US-09-225-928-383	Sequence 383, App
137	7	3.6	32	3	US-09-225-201B-383	Sequence 383, App
138	7	3.6	39	3	US-09-079-984A-16	Sequence 16, Appl
139	7	3.6	39	3	US-09-390-729-16	Sequence 16, Appl
140	7	3.6	146	3	US-09-513-999C-35664	Sequence 35664, A
141	7	3.6	153	3	US-08-651-136C-39	Sequence 39, Appl
142	7	3.6	153	3	US-09-229-911A-39	Sequence 39, Appl
143	7	3.6	153	3	US-10-007-521-39	Sequence 39, Appl
144	7	3.6	186	3	US-09-787-986A-8	Sequence 8, Appli
145	7	3.6	225	2	US-08-073-807A-7	Sequence 7, Appli
146	7	3.6	233	3	US-09-513-999C-35730	Sequence 35730, A
147	7	3.6	235	3	US-09-009-156-9	Sequence 9, Appli
148	7	3.6	235	3	US-09-372-154-9	Sequence 9, Appli
149	7	3.6	235	3	US-09-950-688-9	Sequence 9, Appli
150	7	3.6	270	3	US-09-248-796A-12538	Sequence 12538, A
151	7	3.6	271	3	US-09-313-294A-848	Sequence 848, App
152	7	3.6	277	3	US-09-313-294A-6859	Sequence 6859, Ap
153	7	3.6	299	3	US-09-313-294A-786	Sequence 786, App
154	7	3.6	299	4	US-09-297-648-564	Sequence 564, App
155	7	3.6	301	3	US-09-270-767-2250	Sequence 2250, Ap
156	7	3.6	301	3	US-09-270-767-17532	Sequence 17532, A
c 157	7	3.6	313	3	US-09-621-976-16883	Sequence 16883, A
158	7	3.6	314	3	US-09-513-999C-22788	Sequence 22788, A
159	7	3.6	323	3	US-09-009-156-8	Sequence 8, Appli
160	7	3.6	323	3	US-09-372-154-8	Sequence 8, Appli
161	7	3.6	323	3	US-09-392-184-25	Sequence 25, Appl
162	7	3.6	323	3	US-09-950-688-8	Sequence 8, Appli
163	7	3.6	326	3	US-09-673-395A-64	Sequence 64, Appl
c 164	7	3.6	332	3	US-09-513-999C-11474	Sequence 11474, A
c 165	7	3.6	375	3	US-09-601-198-91	Sequence 91, Appl
c 166	7	3.6	376	3	US-09-149-476-201	Sequence 201, App
167	7	3.6	409	3	US-09-640-211A-1395	Sequence 1395, Ap
168	7	3.6	419	3	US-09-799-451-705	Sequence 705, App
169	7	3.6	419	3	US-09-533-559-2175	Sequence 2175, Ap
170	7	3.6	435	3	US-09-328-352-1934	Sequence 1934, Ap
171	7	3.6	441	3	US-09-252-991A-14937	Sequence 14937, A
172	7	3.6	442	3	US-09-621-976-8885	Sequence 8885, Ap
173	7	3.6	458	3	US-09-621-976-583	Sequence 583, App
174	7	3.6	459	3	US-09-248-796A-3939	Sequence 3939, Ap
c 175	7	3.6	461	3	US-09-812-484-26	Sequence 26, Appl
c 176	7	3.6	469	3	US-09-621-976-16570	Sequence 16570, A
177	7	3.6	502	3	US-09-270-767-9437	Sequence 9437, Ap
178	7	3.6	502	3	US-09-270-767-24719	Sequence 24719, A
179	7	3.6	520	3	US-09-621-976-1422	Sequence 1422, Ap
180	7	3.6	523	3	US-09-270-767-5175	Sequence 5175, Ap
181	7	3.6	523	3	US-09-270-767-20457	Sequence 20457, A
c 182	7	3.6	524	3	US-09-621-976-3041	Sequence 3041, Ap
183	7	3.6	539	3	US-09-949-016-5422	Sequence 5422, Ap
c 184	7	3.6	550	3	US-09-149-476-19	Sequence 19, Appl
185	7	3.6	564	3	US-09-270-767-3283	Sequence 3283, Ap
186	7	3.6	564	3	US-09-270-767-18565	Sequence 18565, A
187	7	3.6	576	3	US-09-134-000C-3119	Sequence 3119, Ap
188	7	3.6	585	3	US-09-248-796A-4233	Sequence 4233, Ap
c 189	7	3.6	596	3	US-09-513-999C-8218	Sequence 8218, Ap
c 190	7	3.6	600	3	US-09-270-767-29877	Sequence 29877, A
191	7	3.6	601	3	US-09-949-016-18467	Sequence 18467, A
192	7	3.6	601	3	US-09-949-016-18612	Sequence 18612, A
c 193	7	3.6	601	3	US-09-949-016-22576	Sequence 22576, A
c 194	7	3.6	601	3	US-09-949-016-22577	Sequence 22577, A
c 195	7	3.6	601	3	US-09-949-016-31911	Sequence 31911, A
c 196	7	3.6	601	3	US-09-949-016-31912	Sequence 31912, A
c 197	7	3.6	601	3	US-09-949-016-31913	Sequence 31913, A
c 198	7	3.6	601	3	US-09-949-016-35016	Sequence 35016, A
199	7	3.6	601	3	US-09-949-016-35539	Sequence 35539, A
200	7	3.6	601	3	US-09-949-016-38687	Sequence 38687, A

ALIGNMENTS

```
RESULT 1
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
```

LOCATION: (1)..(591)
-09-917-265A-35

:gnment Scores:
:d. No.: 1.85e-196 Length: 591
:re: 197.00 Matches: 197
:cent Similarity: 100.0% Conservative: 0
:t Local Similarity: 100.0% Mismatches: 0
:ry Match: 100.0% Indels: 0
: 3 Gaps: 0

-10-821-670A-36 (1-197) x US-09-917-265A-35 (1-591)

```
          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

SULT 2
-09-917-265A-37/c
Sequence 37, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 37
LENGTH: 591
TYPE: DNA
ORGANISM: Felis catus

US-09-917-265A-37

Alignment Scores:
Pred. No.: 1.85e-196 Length: 591
Score: 197.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-36 (1-197) x US-09-917-265A-37 (1-591)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 3
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:

NAME/KEY: CDS
LOCATION: (1)..(666)
09-917-265A-32

gnment Scores:

d. No.:	2.08e-196	Length:	666
re:	197.00	Matches:	197
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	100.0%	Indels:	0
	3	Gaps:	0

10-821-670A-36 (1-197) x US-09-917-265A-32 (1-666)

```
          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
```

ULT 4
09-917-265A-34/c
equence 34, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 34
LENGTH: 666
TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-34

Alignment Scores:

Pred. No.:	2.08e-196	Length:	666
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-917-265A-34 (1-666)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 5
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus

FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
-09-917-265A-43

:gnment Scores:
ed. No.: 4.66e-196 Length: 1533
ore: 197.00 Matches: 197
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 100.0% Indels: 0
: 3 Gaps: 0

-10-821-670A-36 (1-197) x US-09-917-265A-43 (1-1533)

```
          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

SULT 6
-09-917-265A-45/c
Sequence 45, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 45
LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.: 4.66e-196 Length: 1533
Score: 197.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-36 (1-197) x US-09-917-265A-45 (1-1533)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 7
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA

```
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1599)
09-917-265A-38

gnment Scores:
d. No.:                4.85e-196      Length:          1599
re:                    197.00         Matches:         197
cent Similarity:       100.0%         Conservative:    0
t Local Similarity:    100.0%         Mismatches:      0
ry Match:              100.0%         Indels:          0
                       3              Gaps:            0

10-821-670A-36 (1-197) x US-09-917-265A-38 (1-1599)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

ULT 8
09-917-265A-40/c
equence 40, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE:  2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:             4.85e-196      Length:          1599
Score:                 197.00         Matches:         197
Percent Similarity:    100.0%         Conservative:    0
Best Local Similarity: 100.0%         Mismatches:      0
Query Match:           100.0%         Indels:          0
DB:                    3              Gaps:            0

US-10-821-670A-36 (1-197) x US-09-917-265A-40 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
```

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,143
FILING DATE: 04-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
09-011-143-9

gnment Scores:

ed. No.:	2.28e-194	Length:	591
ore:	195.00	Matches:	195
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	99.0%	Indels:	0
	3	Gaps:	0

10-821-670A-36 (1-197) x US-09-011-143-9 (1-591)

```
          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585
```

RESULT 10
US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/302,495
; FILING DATE: 30-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,143
; FILING DATE: 04-FEB-1998
; APPLICATION NUMBER: PCT/JP97/01824
; FILING DATE: 29-MAY-1997
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: IMAMURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

Alignment Scores:

Pred. No.:	2.28e-194	Length:	591
Score:	195.00	Matches:	195
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-302-495-9 (1-591)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585
```

```
;ULT 11
 10-079-616-9
;equence 9, Application US/10079616
'atent No. 6566097
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
            STREET: 419 Seventh Street, N.W., Suite 300
            CITY: Washington
            STATE: D.C.
            COUNTRY: USA
            ZIP: 20004
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/10/079,616
            FILING DATE: 22-Feb-2002
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 09/011,143
            FILING DATE: 04-FEB-1998
            APPLICATION NUMBER: PCT/JP97/01824
            FILING DATE: 29-MAY-1997
            APPLICATION NUMBER: JP 165249/1996
            FILING DATE: 04-JUN-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: BROWDY, Roger L.
;              REGISTRATION NUMBER: 25,618
;              REFERENCE/DOCKET NUMBER: IMAMURA=1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 202-628-5197
;              TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 9:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 591 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

Alignment Scores:
Pred. No.:              2.28e-194      Length:          591
Score:                  195.00         Matches:         195
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            99.0%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-36 (1-197) x US-10-079-616-9 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

RESULT 12
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
```

```
  APPLICANT:  MAEDA, Hiroaki
  APPLICANT:  FUJIYASU, Takeshi
  APPLICANT:  IMAGAWA, Yoshitaka
  APPLICANT:  TOKIYOSHI, Sachio
  TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
  NUMBER OF SEQUENCES:  26
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  BROWDY AND NEIMARK
    STREET:  419 Seventh Street, N.W., Suite 300
    CITY:  Washington
    STATE:  D.C.
    COUNTRY:  USA
    ZIP:  20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/011,143
    FILING DATE:  04-FEB-1998
    CLASSIFICATION:  536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/JP97/01824
    FILING DATE:  29-MAY-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  JP 165249/1996
    FILING DATE:  04-JUN-1996
  ATTORNEY/AGENT INFORMATION:
    NAME:  BROWDY, Roger L.
    REGISTRATION NUMBER:  25,618
    REFERENCE/DOCKET NUMBER:  IMAMURA=1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  202-628-5197
    TELEFAX:  202-737-3528
 INFORMATION FOR SEQ ID NO:  26:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  689 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
-09-011-143-26

:gnment Scores:
ed. No.:              2.64e-194      Length:        689
ore:                  195.00         Matches:       195
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            99.0%          Indels:        0
:                     3              Gaps:          0

-10-821-670A-36 (1-197) x US-09-011-143-26 (1-689)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy      101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy      121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy      141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy      161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy      181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
Db      622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

RESULT 13
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26
```

```
gnment Scores:
d. No.:                2.64e-194      Length:          689
re:                    195.00         Matches:         195
cent Similarity:       100.0%         Conservative:    0
t Local Similarity:    100.0%         Mismatches:      0
ry Match:              99.0%          Indels:          0
                       3              Gaps:            0

10-821-670A-36 (1-197) x US-09-302-495-26 (1-689)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

ULT 14
10-079-616-26
equence 26, Application US/10079616
atent No. 6566097
 GENERAL INFORMATION:
     APPLICANT: IMAMURA, Takayuki
                MAEDA, Hiroaki
                FUJIYASU, Takeshi
                IMAGAWA, Yoshitaka
                TOKIYOSHI, Sachio
     TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
     NUMBER OF SEQUENCES: 26
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: BROWDY AND NEIMARK
          STREET: 419 Seventh Street, N.W., Suite 300
          CITY: Washington
          STATE: D.C.
          COUNTRY: USA
          ZIP: 20004
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

Alignment Scores:
Pred. No.:             2.64e-194      Length:          689
Score:                 195.00         Matches:         195
Percent Similarity:    100.0%         Conservative:    0
Best Local Similarity: 100.0%         Mismatches:      0
Query Match:           99.0%          Indels:          0
DB:                    3              Gaps:            0

US-10-821-670A-36 (1-197) x US-10-079-616-26 (1-689)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

       181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
           ||||||||||||||||||||||||||||||||||||||||||||||
       622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

SULT 15
-09-011-143-8
Sequence 8, Application US/09011143
Patent No. 6472509
 GENERAL INFORMATION:
   APPLICANT:  IMAMURA, Takayuki
   APPLICANT:  MAEDA, Hiroaki
   APPLICANT:  FUJIYASU, Takeshi
   APPLICANT:  IMAGAWA, Yoshitaka
   APPLICANT:  TOKIYOSHI, Sachio
   TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
   NUMBER OF SEQUENCES:  26
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  BROWDY AND NEIMARK
     STREET:  419 Seventh Street, N.W., Suite 300
     CITY:  Washington
     STATE:  D.C.
     COUNTRY:  USA
     ZIP:  20004
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/011,143
     FILING DATE:  04-FEB-1998
     CLASSIFICATION:  536
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  PCT/JP97/01824
     FILING DATE:  29-MAY-1997
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  JP 165249/1996
     FILING DATE:  04-JUN-1996
   ATTORNEY/AGENT INFORMATION:
     NAME:  BROWDY, Roger L.
     REGISTRATION NUMBER:  25,618
     REFERENCE/DOCKET NUMBER:  IMAMURA=1
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  202-628-5197
     TELEFAX:  202-737-3528
 INFORMATION FOR SEQ ID NO:  8:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1441 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-09-011-143-8

ignment Scores:
ed. No.:              5.39e-194      Length:         1441
ore:                  195.00         Matches:        195
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            99.0%          Indels:         0
:                     3              Gaps:           0

-10-821-670A-36 (1-197) x US-09-011-143-8 (1-1441)

         1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

        21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy          41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy          61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy          81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy         101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy         121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy         141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy         161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy         181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
               ||||||||||||||||||||||||||||||||||||||||||||||
Db         758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

RESULT 16
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
```

```
           TELEPHONE: 202-628-5197
           TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 8:
       SEQUENCE CHARACTERISTICS:
           LENGTH: 1441 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
-09-302-495-8

.gnment Scores:
:d. No.:                5.39e-194       Length:         1441
:re:                    195.00          Matches:        195
'cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              99.0%           Indels:         0
                        3               Gaps:           0

10-821-670A-36 (1-197) x US-09-302-495-8 (1-1441)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

:ULT 17
10-079-616-8
:equence 8, Application US/10079616
'atent No. 6566097
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

Alignment Scores:
Pred. No.:              5.39e-194       Length:         1441
Score:                  195.00          Matches:        195
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            99.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-079-616-8 (1-1441)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

       121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

       141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

       161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

       181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
           |||||||||||||||||||||||||||||||||||||||||||||
       758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

SULT 18
-09-917-265A-101
Sequence 101, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 101
  LENGTH: 561
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(561)
-09-917-265A-101

gnment Scores:
ed. No.:              4.92e-186      Length:          561
ore:                  187.00         Matches:         187
rcent Similarity:     100.0%         Conservative:    0
st Local Similarity:  100.0%         Mismatches:      0
ery Match:            94.9%          Indels:          0
:                     3              Gaps:            0

-10-821-670A-36 (1-197) x US-09-917-265A-101 (1-561)

        11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

        31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

        51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

        71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

        91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy         111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy         131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy         151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy         171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy         191 MetSerTyrLeuAsnAlaSer 197
               |||||||||||||||||||||
Db         541 ATGAGCTATCTGAATGCTTCC 561

RESULT 19
US-09-917-265A-103/c
; Sequence 103, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-103

Alignment Scores:
Pred. No.:              4.92e-186      Length:          561
Score:                  187.00         Matches:         187
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            94.9%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-36 (1-197) x US-09-917-265A-103 (1-561)

Qy          11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy          31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy          51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy          71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy          91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy         111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
```

```
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

      131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

      151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

      171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

      191 MetSerTyrLeuAsnAlaSer 197
          ||||||||||||||||||||||
       21 ATGAGCTATCTGAATGCTTCC 1

;ULT 20
·09-917-265A-49
;equence 49, Application US/09917265A
'atent No. 6818444
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
;EQ ID NO 49
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(591)
·09-917-265A-49

.gnment Scores:
:d. No.:              5.31e-45       Length:        591
:re:                  52.00          Matches:       52
'cent Similarity:     100.0%         Conservative:  0
:t Local Similarity:  100.0%         Mismatches:    0
:ry Match:            26.4%          Indels:        0
                      3              Gaps:          0

 10-821-670A-36 (1-197) x US-09-917-265A-49 (1-591)

       40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

       60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

       80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
          ||||||||||||||||||||||||||||||||||||
      238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

;ULT 21
·09-917-265A-51/c
;equence 51, Application US/09917265A
'atent No. 6818444
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
;EQ ID NO 51
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Canis familiaris
US-09-917-265A-51

Alignment Scores:
Pred. No.:              5.31e-45       Length:        591
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.4%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-36 (1-197) x US-09-917-265A-51 (1-591)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               ||||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 22
US-09-917-265A-46
; Sequence 46, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-46

Alignment Scores:
Pred. No.:              5.96e-45       Length:        666
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.4%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-36 (1-197) x US-09-917-265A-46 (1-666)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 23
-09-917-265A-48/c
Sequence 48, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
  LENGTH: 666
  TYPE: DNA
  ORGANISM: Canis familiaris
-09-917-265A-48

ignment Scores:
ed. No.:                5.96e-45        Length:         666
ore:                    52.00           Matches:        52
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              26.4%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-917-265A-48 (1-666)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 24
-09-079-984A-2
Sequence 2, Application US/09079984A
Patent No. 6231850
 GENERAL INFORMATION:
   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
   APPLICANT:  Yamada, Katsushige
   TITLE OF INVENTION:  Canine interleukin 12, a production method
   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
   TITLE OF INVENTION:  method using it
   NUMBER OF SEQUENCES:  16
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Miller & Christenbury Intellectual Property
     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
     STREET:  1600 Market Street, 39th Floor
     CITY:  Philadelphia
     STATE:  PA
     COUNTRY:  USA
     ZIP:  19103
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy Disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  WordPerfect 5.1
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/079,984A
     FILING DATE:  15-MAY-1998
   ATTORNEY/AGENT INFORMATION:
     NAME:  Austin R. Miller
     REGISTRATION NUMBER:  16,602
     REFERENCE/DOCKET NUMBER:  1051-98
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (215) 563-1810
     TELEFAX:  (215) 568-6946
 INFORMATION FOR SEQ ID NO:  2:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  669 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA to mRNA
   ORIGINAL SOURCE:
     ORGANISM:  Canis familiaris
   FEATURE:
     NAME/KEY:  Canine IL12
     LOCATION:  1 to 666
     IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

Alignment Scores:
Pred. No.:              5.99e-45        Length:         669
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-079-984A-2 (1-669)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 25
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
```

```
    MEDIUM TYPE:  Floppy Disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  WordPerfect 5.1
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/079,984A
    FILING DATE:  15-MAY-1998
  ATTORNEY/AGENT INFORMATION:
    NAME:  Austin R. Miller
    REGISTRATION NUMBER:  16,602
    REFERENCE/DOCKET NUMBER:  1051-98
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (215) 563-1810
    TELEFAX:  (215) 568-6946
INFORMATION FOR SEQ ID NO:  12:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  669 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA to mRNA
  ORIGINAL SOURCE:
    ORGANISM:  Canis familiaris
  FEATURE:
    NAME/KEY:  Canine IL12
    LOCATION:  1 to 666
    IDENTIFICATION METHOD:  Similarity
09-079-984A-12

gnment Scores:
d. No.:                5.99e-45       Length:         669
re:                    52.00          Matches:        52
cent Similarity:       100.0%         Conservative:   0
t Local Similarity:    100.0%         Mismatches:     0
ry Match:              26.4%          Indels:         0
                       3              Gaps:           0

10-821-670A-36 (1-197) x US-09-079-984A-12 (1-669)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

ULT 26
09-390-729-2
equence 2, Application US/09390729
atent No. 6562334
GENERAL INFORMATION:
  APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
  APPLICANT:  Yamada, Katsushige
  TITLE OF INVENTION:  Canine interleukin 12, a production method
  TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
  TITLE OF INVENTION:  method using it
  NUMBER OF SEQUENCES:  16
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Miller & Christenbury Intellectual Property
    ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
    STREET:  1600 Market Street, 39th Floor
    CITY:  Philadelphia
    STATE:  PA
    COUNTRY:  USA
    ZIP:  19103
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy Disk
    COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/390,729
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  09/079,984
;     FILING DATE:  15-MAY-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Austin R. Miller
;     REGISTRATION NUMBER:  16,602
;     REFERENCE/DOCKET NUMBER:  1051-98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-1810
;     TELEFAX:  (215) 568-6946
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  669 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM:  Canis familiaris
;   FEATURE:
;     NAME/KEY:  Canine IL12
;     LOCATION:  1 to 666
;     IDENTIFICATION METHOD:  Similarity
US-09-390-729-2

Alignment Scores:
Pred. No.:                5.99e-45       Length:         669
Score:                    52.00          Matches:        52
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              26.4%          Indels:         0
DB:                       3              Gaps:           0

US-10-821-670A-36 (1-197) x US-09-390-729-2 (1-669)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 27
US-09-390-729-12
; Sequence 12, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/390,729
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/079,984
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 666
IDENTIFICATION METHOD: Similarity
09-390-729-12

gnment Scores:

ed. No.:	5.99e-45	Length:	669
ore:	52.00	Matches:	52
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.4%	Indels:	0
:	3	Gaps:	0

10-821-670A-36 (1-197) x US-09-390-729-12 (1-669)

```
Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              ||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

SULT 28
09-917-265A-104
Sequence 104, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 104
LENGTH: 1455
TYPE: DNA
ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(897)
US-09-917-265A-104

Alignment Scores:

Pred. No.:	1.27e-44	Length:	1455
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-917-265A-104 (1-1455)

```
Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              ||||||||||||||||||||||||||||||||||||
Db        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579
```

RESULT 29
US-09-917-265A-106/c
; Sequence 106, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265A-106

Alignment Scores:

Pred. No.:	1.27e-44	Length:	1455
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-917-265A-106 (1-1455)

```
Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              ||||||||||||||||||||||||||||||||||||
Db        912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877
```

RESULT 30
US-09-917-265A-66

```
Sequence 66, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 66
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1533)
09-917-265A-66

Alignment Scores:
Pred. No.:                1.34e-44        Length:         1533
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.4%           Indels:         0
                          3               Gaps:           0

10-821-670A-36 (1-197) x US-09-917-265A-66 (1-1533)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 31
09-917-265A-68/c
Sequence 68, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 68
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Canis familiaris
09-917-265A-68

Alignment Scores:
Pred. No.:                1.34e-44        Length:         1533
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.4%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265A-68 (1-1533)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 32
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

Alignment Scores:
Pred. No.:                1.39e-44        Length:         1599
Score:                    52.00           Matches:        52
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              26.4%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265A-61 (1-1599)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db       1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 33
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
```

```
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 63
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Canis familiaris
-09-917-265A-63

:gnment Scores:
ed. No.:                1.39e-44        Length:         1599
ore:                    52.00           Matches:        52
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              26.4%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-917-265A-63 (1-1599)

         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 34
-09-949-016-20385
Sequence 20385, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20385
  LENGTH: 601
  TYPE: DNA
  ORGANISM: Human
-09-949-016-20385

:gnment Scores:
ed. No.:                5.71e-21        Length:         601
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-949-016-20385 (1-601)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         91 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 150

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||
Db         151 GCTTTCAGAATTCGGGCAGTGACTATT 177

RESULT 35
US-09-949-016-87352
; Sequence 87352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87352
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87352

Alignment Scores:
Pred. No.:              5.71e-21        Length:         601
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-949-016-87352 (1-601)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          91 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 150

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||
Db         151 GCTTTCAGAATTCGGGCAGTGACTATT 177

RESULT 36
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
```

```
  ATTORNEY/AGENT INFORMATION:
    NAME:  McDaniels, Patricia A.
    REGISTRATION NUMBER:  33,194
    REFERENCE/DOCKET NUMBER:  GI 5225
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  617-498-8401
    TELEFAX:  617-876-5851
INFORMATION FOR SEQ ID NO:  3:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  660 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
  ORIGINAL SOURCE:
    ORGANISM:  Homo sapiens
    CELL TYPE:  Lymphoblast
    CELL LINE:  RPMI 8866
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  1..660
·08-186-529-3

.gnment Scores:
:d. No.:                6.25e-21        Length:         660
)re:                    29.00           Matches:        29
'cent Similarity:       100.0%          Conservative:   0
it Local Similarity:    100.0%          Mismatches:     0
:ry Match:              14.7%           Indels:         0
                        2               Gaps:           0

·10-821-670A-36 (1-197) x US-08-186-529-3 (1-660)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

;ULT 37
·08-640-386A-3
;equence 3, Application US/08640386A
'atent No. 5756085
 GENERAL INFORMATION:
   APPLICANT:  Sykes, Megan
   APPLICANT:  Wolf, Stanley F.
   TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
   TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
     STREET:  87 CambridgePark Drive
     CITY:  Cambridge
     STATE:  MA
     COUNTRY:  USA
     ZIP:  02140
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/640,386A
     FILING DATE:
     CLASSIFICATION:  424
   ATTORNEY/AGENT INFORMATION:
     NAME:  Brown, Scott A.
     REGISTRATION NUMBER:  32,724
     REFERENCE/DOCKET NUMBER:  GI 5225A
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

Alignment Scores:
Pred. No.:                6.25e-21        Length:         660
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              14.7%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-36 (1-197) x US-08-640-386A-3 (1-660)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 38
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
```

```
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-08-184-009-199

ignment Scores:
ed. No.:                6.81e-21        Length:         721
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-36 (1-197) x US-08-184-009-199 (1-721)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

SULT 39
-08-458-356-199
Sequence 199, Application US/08458356
Patent No. 5942235
 GENERAL INFORMATION:
   APPLICANT:  Paoletti, Enzo
   APPLICANT:  Tartaglia, James
   APPLICANT:  Cox, William I.
   TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
   NUMBER OF SEQUENCES:  217
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Curtis, Morris & Safford
     STREET:  530 Fifth Avenue
     CITY:  New York
     STATE:  NY
     COUNTRY:  USA
     ZIP:  10036
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/458,356
     FILING DATE:  02-JUN-1995
     CLASSIFICATION:  424
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  US 08/184,009
     FILING DATE:  19-JAN-1994
   ATTORNEY/AGENT INFORMATION:
     NAME:  Frommer, William S.
     REGISTRATION NUMBER:  25,506
     REFERENCE/DOCKET NUMBER:  454310-2530
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (212) 840-3333
     TELEFAX:  (212) 840-0712
     TELEX:  425066CURTMS
 INFORMATION FOR SEQ ID NO:  199:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  721 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-08-458-356-199

ignment Scores:
ed. No.:                6.81e-21        Length:         721
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x US-08-458-356-199 (1-721)

Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy      179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
Db      662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 40
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

Alignment Scores:
Pred. No.:              6.81e-21        Length:         721
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-08-460-736-199 (1-721)

Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661
```

```
       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       662 GCTTTCAGAATTCGGGCAGTGACTATT 688

;ULT 41
·09-535-370-199
;equence 199, Application US/09535370
'atent No. 6537594
 GENERAL INFORMATION:
      APPLICANT: Paoletti, Enzo
                 Tartaglia, James
                 Cox, William I.
      TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
      NUMBER OF SEQUENCES: 217
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Curtis, Morris & Safford
           STREET: 530 Fifth Avenue
           CITY: New York
           STATE: NY
           COUNTRY: USA
           ZIP: 10036
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/535,370
           FILING DATE: 24-Mar-2000
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/460,736
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Frommer, William S.
           REGISTRATION NUMBER: 25,506
           REFERENCE/DOCKET NUMBER: 454310-2530
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (212) 840-3333
           TELEFAX: (212) 840-0712
           TELEX: 425066CURTMS
  INFORMATION FOR SEQ ID NO: 199:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 721 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 199:
 09-535-370-199

·gnment Scores:
:d. No.:              6.81e-21      Length:        721
>re:                  29.00         Matches:       29
'cent Similarity:     100.0%        Conservative:  0
:t Local Similarity:  100.0%        Mismatches:    0
:ry Match:            14.7%         Indels:        0
                      3             Gaps:          0

·10-821-670A-36 (1-197) x US-09-535-370-199 (1-721)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       662 GCTTTCAGAATTCGGGCAGTGACTATT 688

;ULT 42
·09-663-667-199
;equence 199, Application US/09663667

; Patent No. 6780407
;  GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/663,667
;            FILING DATE: 15-Sep-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/184,009
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 840-3333
;            TELEFAX: (212) 840-0712
;            TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 721 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 199:
;
US-09-663-667-199

Alignment Scores:
Pred. No.:              6.81e-21      Length:        721
Score:                  29.00         Matches:       29
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            14.7%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-36 (1-197) x US-09-663-667-199 (1-721)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 43
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;       NUMBER OF SEQUENCES: 33
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;            STREET: 2421 N.W. 41st Street, Suite A-1
```

```
          CITY: Gainesville
          STATE: Florida
          COUNTRY: United States of America
          ZIP: 32606
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/08/848,760B
          FILING DATE: 25-Jan-2001
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 08/838,702
          FILING DATE: 09-APR-1997
     ATTORNEY/AGENT INFORMATION:
          NAME: PACE, DORAN R.
          REGISTRATION NUMBER: 38,261
          REFERENCE/DOCKET NUMBER: CNG-100C1
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (352) 375-8100
          TELEFAX: (352) 372-5800
  INFORMATION FOR SEQ ID NO: 21:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 762 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
     MOLECULE TYPE: other nucleic acid
          DESCRIPTION: /desc = "DNA"
     SEQUENCE DESCRIPTION: SEQ ID NO: 21:
-08-848-760B-21

:gnment Scores:
ed. No.:                7.18e-21        Length:         762
ore:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-08-848-760B-21 (1-762)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 44
-09-826-025-21
Sequence 21, Application US/09826025
Patent No. 6730512
  GENERAL INFORMATION:
     APPLICANT: Chang, Lung-Ji
     TITLE OF INVENTION: Combination Immunogene Therapy
     NUMBER OF SEQUENCES: 25
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Medlen & Carroll, LLP
          STREET: 220 Montgomery Street, Suite 2200
          CITY: San Francisco
          STATE: California
          COUNTRY: United States of America
          ZIP: 94104
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/826,025
          FILING DATE: 04-Apr-2001
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 08/838,702
          FILING DATE: <Unknown>
     ATTORNEY/AGENT INFORMATION:
          NAME: Ingolia, Diane E.
          REGISTRATION NUMBER: 40,027
          REFERENCE/DOCKET NUMBER: CHANG-02687
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (415) 705-8410
          TELEFAX: (415) 397-8338
  INFORMATION FOR SEQ ID NO: 21:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 762 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
     MOLECULE TYPE: other nucleic acid
          DESCRIPTION: /desc = "DNA"
     SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

Alignment Scores:
Pred. No.:              7.18e-21        Length:         762
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-826-025-21 (1-762)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 45
US-09-543-679A-2890
; Sequence 2890, Application US/09543679A
; Patent No. 7034007
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
```

```
          NAME: Amzel, Viviana
          REGISTRATION NUMBER: 30,930
          REFERENCE/DOCKET NUMBER: EPI-0067191b
       TELECOMMUNICATION INFORMATION:
          TELEPHONE: 609-409-3035
          TELEFAX: 413-254-9245
          TELEX: <Unknown>
  INFORMATION FOR SEQ ID NO: 2890:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 762 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
       SEQUENCE DESCRIPTION: SEQ ID NO: 2890:
09-543-679A-2890

gnment Scores:
d. No.:              7.18e-21       Length:        762
re:                  29.00          Matches:       29
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            14.7%          Indels:        0
                     5              Gaps:          0

10-821-670A-36 (1-197) x US-09-543-679A-2890 (1-762)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

ULT 46
09-949-016-2462
equence 2462, Application US/09949016
atent No. 6812339
ENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE:  2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 2462
 LENGTH: 1019
 TYPE: DNA
 ORGANISM: Human
09-949-016-2462

gnment Scores:
d. No.:              9.52e-21       Length:        1019
re:                  29.00          Matches:       29
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            14.7%          Indels:        0
                     3              Gaps:          0

10-821-670A-36 (1-197) x US-09-949-016-2462 (1-1019)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       703 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 762

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         763 GCTTTCAGAATTCGGGCAGTGACTATT 789

RESULT 47
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  170..826
US-08-751-767A-1

Alignment Scores:
Pred. No.:           9.58e-21       Length:        1026
Score:               29.00          Matches:       29
Percent Similarity:  100.0%         Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:         14.7%          Indels:        0
DB:                  2              Gaps:          0

US-10-821-670A-36 (1-197) x US-08-751-767A-1 (1-1026)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 48
US-09-023-655-1041
; Sequence 1041, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
```

```
   APPLICANT:  Susan G. Stuart
   APPLICANT:  Jeffrey J. Seilhamer
   TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
   TITLE OF INVENTION:  EXPRESSION
   NUMBER OF SEQUENCES:  1508
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
     STREET:  3174 PORTER DRIVE
     CITY:  PALO ALTO
     STATE:  CALIFORNIA
     COUNTRY:  USA
     ZIP:  94304
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/023,655
     FILING DATE:  HEREWITH
     CLASSIFICATION:
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:
     FILING DATE:
     CLASSIFICATION:
   ATTORNEY/AGENT INFORMATION:
     NAME:  Zeller, Karen J.
     REGISTRATION NUMBER:  37,071
     REFERENCE/DOCKET NUMBER:  PA-0001 US
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (650) 855-0555
     TELEFAX:  (650) 845-4166
 INFORMATION FOR SEQ ID NO:  1041:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1026 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   IMMEDIATE SOURCE:
     LIBRARY:  GENBANK
     CLONE:  g180623
-09-023-655-1041

:gnment Scores:
ed. No.:                9.58e-21        Length:         1026
ore:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-023-655-1041 (1-1026)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

SULT 49
-09-949-016-130
Sequence 130, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 130
   LENGTH: 1026
   TYPE: DNA
   ORGANISM: Human
US-09-949-016-130

Alignment Scores:
Pred. No.:              9.58e-21        Length:         1026
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-949-016-130 (1-1026)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 50
US-09-634-368-6
; Sequence 6, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-09-634-368-6

Alignment Scores:
Pred. No.:              1.19e-20        Length:         1287
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-634-368-6 (1-1287)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254
```

```
SULT 51
08-684-687-3
equence 3, Application US/08684687
atent No. 5830451
GENERAL INFORMATION:
  APPLICANT:  KIEFF, ELLIOTT D.
  APPLICANT:  DEVERGNE, ODILE
  TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
  TITLE OF INVENTION:  THEREFOR
  NUMBER OF SEQUENCES:  8
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
    STREET:  600 ATLANTIC AVENUE
    CITY:  BOSTON
    STATE:  MA
    COUNTRY:  USA
    ZIP:  02210
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/684,687
    FILING DATE:
    CLASSIFICATION:  514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  60/005,092
    FILING DATE:  11-OCT-1995
  ATTORNEY/AGENT INFORMATION:
    NAME:  GATES, EDWARD R.
    REGISTRATION NUMBER:  31,616
    REFERENCE/DOCKET NUMBER:  B0801/7051
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  617-720-3500
    TELEFAX:  617-720-2441
INFORMATION FOR SEQ ID NO:  3:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1316 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA to mRNA
  HYPOTHETICAL:  NO
  ANTI-SENSE:  NO
  ORIGINAL SOURCE:
    ORGANISM:  HOMO SAPIENS
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  102..863
08-684-687-3

gnment Scores:
d. No.:              1.22e-20      Length:        1316
re:                  29.00         Matches:       29
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            14.7%         Indels:        0
                     2             Gaps:          0

10-821-670A-36 (1-197) x US-08-684-687-3 (1-1316)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       804 GCTTTCAGAATTCGGGCAGTGACTATT 830

SULT 52
09-851-520-3
equence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

Alignment Scores:
Pred. No.:              1.22e-20      Length:        1316
Score:                  29.00         Matches:       29
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            14.7%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-36 (1-197) x US-09-851-520-3 (1-1316)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         804 GCTTTCAGAATTCGGGCAGTGACTATT 830

RESULT 53
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
```

```
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1364 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  unknown
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  101..859
-08-265-087-3

ignment Scores:
ed. No.:                1.26e-20        Length:         1364
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-36 (1-197) x US-08-265-087-3 (1-1364)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||
       803 GCTTTCAGAATTCGGGCAGTGACTATT 829

SULT 54
-08-621-493-3
Sequence 3, Application US/08621493
Patent No. 5723127
 GENERAL INFORMATION:
   APPLICANT:  Scott, Phillip
   APPLICANT:  Trinchieri, Giorgio
   TITLE OF INVENTION:  Compositions and Methods for Use of
   TITLE OF INVENTION:  IL-12 as an Adjuvant
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Howson and Howson
     STREET:  Spring House Corporate Center, PO Box 457
     CITY:  Spring House
     STATE:  Pennsylvania
     COUNTRY:  USA
     ZIP:  19477
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/621,493
     FILING DATE:  25-MAR-1996
     CLASSIFICATION:  424
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  08/265,087
     FILING DATE:  17-JUN-1994
     APPLICATION NUMBER:  US 08/229,282
     FILING DATE:  18-APR-1994
   ATTORNEY/AGENT INFORMATION:
     NAME:  Bak, Mary E.
     REGISTRATION NUMBER:  31,215
     REFERENCE/DOCKET NUMBER:  WST51AUSA
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  215-540-9206
     TELEFAX:  215-540-5818
 INFORMATION FOR SEQ ID NO:  3:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1364 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

Alignment Scores:
Pred. No.:              1.26e-20        Length:         1364
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x US-08-621-493-3 (1-1364)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||
Db         803 GCTTTCAGAATTCGGGCAGTGACTATT 829

RESULT 55
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
```

LOCATION: 101..859
08-965-688-3

gnment Scores:
d. No.: 1.26e-20 Length: 1364
re: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 14.7% Indels: 0
2 Gaps: 0

10-821-670A-36 (1-197) x US-08-965-688-3 (1-1364)

159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
||||||||||||||||||||||||||||||||||||||||||||||||||||||
743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

179 AlaPheArgIleArgAlaValThrIle 187
|||||||||||||||||||||||||
803 GCTTTCAGAATTCGGGCAGTGACTATT 829

ULT 56
09-260-173-3
equence 3, Application US/09260173
atent No. 6168923
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/260,173
FILING DATE: 01-Mar-1999
CLASSIFICATION: <Unknown>
17-JUN-1994
18-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,688
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 101..859

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

Alignment Scores:
Pred. No.: 1.26e-20 Length: 1364
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-36 (1-197) x US-09-260-173-3 (1-1364)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

Qy 179 AlaPheArgIleArgAlaValThrIle 187
|||||||||||||||||||||||||
Db 803 GCTTTCAGAATTCGGGCAGTGACTATT 829

RESULT 57
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
; APPLICANT: TRINCHIERI, GIORGIO
; APPLICANT: PERUSSIA, BICE
; APPLICANT: CLARK, STEVEN C.
; APPLICANT: WONG, GORDON G.
; APPLICANT: HEWICK, RODNEY
; APPLICANT: KOBAYASHI, MICHIKO
; TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
; FILE REFERENCE: 01142.0142.0100
; CURRENT APPLICATION NUMBER: US/09/924,703
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/325,958
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/858,000
; PRIOR FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: 08/403,013
; PRIOR FILING DATE: 1995-03-13
; PRIOR APPLICATION NUMBER: 07/584,941
; PRIOR FILING DATE: 1990-09-18
; PRIOR APPLICATION NUMBER: 07/307,817
; PRIOR FILING DATE: 1989-02-07
; PRIOR APPLICATION NUMBER: 07/269,945
; PRIOR FILING DATE: 1988-11-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
; NAME/KEY: CDS
; LOCATION: (114)..(872)
US-09-924-703-5

Alignment Scores:
Pred. No.: 1.29e-20 Length: 1395
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-36 (1-197) x US-09-924-703-5 (1-1395)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
       756 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 815

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||
       816 GCTTTCAGAATTCGGGCAGTGACTATT 842

SULT 58
-08-751-767A-11
Sequence 11, Application US/08751767A
Patent No. 5994104
 GENERAL INFORMATION:
   APPLICANT:  ANDERSON, ROBERT J.
   APPLICANT:  GRANT, HUGH
   APPLICANT:  MACDONALD, IAN D.
   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
   NUMBER OF SEQUENCES:  80
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  NIXON & VANDERHYE P.C.
     STREET:  1100 NORTH GLEBE ROAD
     CITY:  ARLINGTON
     STATE:  VA
     COUNTRY:  USA
     ZIP:  22201
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/751,767A
     FILING DATE:  08-NOV-1996
     CLASSIFICATION:  536
   ATTORNEY/AGENT INFORMATION:
     NAME:  SADOFF, B.J.
     REGISTRATION NUMBER:  36,663
     REFERENCE/DOCKET NUMBER:  117-221
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  7038164091
     TELEFAX:  7038164100
 INFORMATION FOR SEQ ID NO:  11:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1560 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  1..1557
-08-751-767A-11

:gnment Scores:
ed. No.:                1.44e-20        Length:         1560
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-36 (1-197) x US-08-751-767A-11 (1-1560)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1441 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1500

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||
       1501 GCTTTCAGAATTCGGGCAGTGACTATT 1527

SULT 59
-08-751-767A-9
Sequence 9, Application US/08751767A
Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

Alignment Scores:
Pred. No.:              1.49e-20        Length:         1623
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x US-08-751-767A-9 (1-1623)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1504 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1563

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||
Db       1564 GCTTTCAGAATTCGGGCAGTGACTATT 1590

RESULT 60
US-09-310-842-2
; Sequence 2, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
```

```
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 2
  LENGTH: 1645
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  NAME/KEY: gene
  LOCATION: (1)..(1645)
  OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
  OTHER INFORMATION: Dumbbell
  FEATURE:
  NAME/KEY: misc_binding
  LOCATION: (1)..(2)
  OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
  OTHER INFORMATION: position 1 to 2  can be modified with amino or caroxy
  OTHER INFORMATION: features
  FEATURE:
  NAME/KEY: misc_binding
  LOCATION: (1644)..(1645)
  OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1644
  OTHER INFORMATION: to 1645  can be modified with amino or caroxy features
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
  OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
-09-310-842-2

.gnment Scores:
:d. No.:                1.51e-20        Length:         1645
)re:                    29.00           Matches:        29
'cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              14.7%           Indels:         0
                        3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-310-842-2 (1-1645)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1275 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1334

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
      1335 GCTTTCAGAATTCGGGCAGTGACTATT 1361

;ULT 61
 09-543-679A-2893
;equence 2893, Application US/09543679A
'atent No. 7034007
 GENERAL INFORMATION:
      APPLICANT: NYCE, Jonathan W.
      TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
                          COMPOSITIONS, KIT & METHOD FOR TREATMENT
                          OF AIRWAY DISORDERS ASSOCIATED WITH
                          BRONCHOCONSTRICTION, LUNG INFLAMMATION,
      NUMBER OF SEQUENCES: 3111
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
           STREET: 7 Clarke Drive
           CITY: Cranbury
           STATE: NJ
           COUNTRY: USA
           ZIP: 08512
      COMPUTER READABLE FORM:
           MEDIUM TYPE: CD-R
           COMPUTER: IBM Compatible
           OPERATING SYSTEM: DOS
           SOFTWARE: N/A
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/543,679A
           FILING DATE: 13-Apr-2000
           CLASSIFICATION: UNKNOWN
      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 60/127,958
;          FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Amzel, Viviana
;          REGISTRATION NUMBER: 30,930
;          REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 609-409-3035
;          TELEFAX: 413-254-9245
;          TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 2893:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 4521 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2893:
US-09-543-679A-2893

Alignment Scores:
Pred. No.:              4.02e-20        Length:         4521
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-543-679A-2893 (1-4521)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 62
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
;   APPLICANT:  ANDERSON, ROBERT J.
;   APPLICANT:  GRANT, HUGH
;   APPLICANT:  MACDONALD, IAN D.
;   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;   NUMBER OF SEQUENCES:  80
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  NIXON & VANDERHYE P.C.
;     STREET:  1100 NORTH GLEBE ROAD
;     CITY:  ARLINGTON
;     STATE:  VA
;     COUNTRY:  USA
;     ZIP:  22201
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/751,767A
;     FILING DATE:  08-NOV-1996
;     CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  SADOFF, B.J.
;     REGISTRATION NUMBER:  36,663
;     REFERENCE/DOCKET NUMBER:  117-221
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  7038164091
;     TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  6139 base pairs
```

```
     TYPE:  nucleic acid
     STRANDEDNESS:  both
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  3222..4841
-08-751-767A-7

:gnment Scores:
ed. No.:                5.4e-20         Length:         6139
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-36 (1-197) x US-08-751-767A-7 (1-6139)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      4725 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 4784

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
      4785 GCTTTCAGAATTCGGGCAGTGACTATT 4811

SULT 63
-09-949-016-11872
Sequence 11872, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11872
  LENGTH: 10764
  TYPE: DNA
  ORGANISM: Human
-09-949-016-11872

:gnment Scores:
ed. No.:                9.29e-20        Length:         10764
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-949-016-11872 (1-10764)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      8448 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 8507

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
      8508 GCTTTCAGAATTCGGGCAGTGACTATT 8534

SULT 64
-09-949-016-14204
Sequence 14204, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14204
;   LENGTH: 10765
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14204

Alignment Scores:
Pred. No.:              9.3e-20         Length:         10765
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-949-016-14204 (1-10765)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8448 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 8507

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db        8508 GCTTTCAGAATTCGGGCAGTGACTATT 8534

RESULT 65
US-09-949-016-20381
; Sequence 20381, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20381
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-20381

Alignment Scores:
Pred. No.:              6.33e-20        Length:         601
Score:                  28.00           Matches:        28
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.2%           Indels:         0
DB:                     3               Gaps:           0
```

```
-10-821-670A-36 (1-197) x US-09-949-016-20381 (1-601)

        42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       135 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 194

        62 AlaCysLeuProLeuGluLeuThr 69
           |||||||||||||||||||||||
       195 GCCTGTTTACCATTGGAATTAACC 218

SULT 66
 09-949-016-87348
Sequence 87348, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 87348
  LENGTH: 601
  TYPE: DNA
  ORGANISM: Human
-09-949-016-87348

.gnment Scores:
d. No.:              6.33e-20       Length:         601
re:                  28.00          Matches:        28
cent Similarity:     100.0%         Conservative:   0
t Local Similarity:  100.0%         Mismatches:     0
ry Match:            14.2%          Indels:         0
                     3              Gaps:           0

-10-821-670A-36 (1-197) x US-09-949-016-87348 (1-601)

        42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       135 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 194

        62 AlaCysLeuProLeuGluLeuThr 69
           |||||||||||||||||||||||
       195 GCCTGTTTACCATTGGAATTAACC 218

SULT 67
 09-011-143-24
Sequence 24, Application US/09011143
Patent No. 6472509
 GENERAL INFORMATION:
   APPLICANT:  IMAMURA, Takayuki
   APPLICANT:  MAEDA, Hiroaki
   APPLICANT:  FUJIYASU, Takeshi
   APPLICANT:  IMAGAWA, Yoshitaka
   APPLICANT:  TOKIYOSHI, Sachio
   TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
   NUMBER OF SEQUENCES:  26
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  BROWDY AND NEIMARK
     STREET:  419 Seventh Street, N.W., Suite 300
     CITY:  Washington
     STATE:  D.C.
     COUNTRY:  USA
     ZIP:  20004
   COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-24

Alignment Scores:
Pred. No.:              1.09e-18       Length:         79
Score:                  26.00          Matches:        26
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            13.2%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-36 (1-197) x US-09-011-143-24 (1-79)

Qy         50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

Qy         70 MetAsnGluSerCysLeu 75
              |||||||||||||||||||
Db         62 ATGAATGAGAGTTGCCTG 79

RESULT 68
US-09-302-495-24
; Sequence 24, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
```

```
          APPLICATION NUMBER: US/09/302,495
          FILING DATE: 30-Apr-1999
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: US/09/011,143
          FILING DATE: 04-FEB-1998
          APPLICATION NUMBER: PCT/JP97/01824
          FILING DATE: 29-MAY-1997
          APPLICATION NUMBER: JP 165249/1996
          FILING DATE: 04-JUN-1996
     ATTORNEY/AGENT INFORMATION:
          NAME: BROWDY, Roger L.
          REGISTRATION NUMBER: 25,618
          REFERENCE/DOCKET NUMBER: IMAMURA=1
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 24:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 79 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: cDNA
     SEQUENCE DESCRIPTION: SEQ ID NO: 24:
-09-302-495-24

:gnment Scores:
ed. No.:                1.09e-18        Length:         79
ore:                    26.00           Matches:        26
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.2%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-302-495-24 (1-79)

        50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 69
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

        70 MetAsnGluSerCysLeu 75
           |||||||||||||||||||
        62 ATGAATGAGAGTTGCCTG 79

SULT 69
-10-079-616-24
Sequence 24, Application US/10079616
Patent No. 6566097
  GENERAL INFORMATION:
     APPLICANT: IMAMURA, Takayuki
                MAEDA, Hiroaki
                FUJIYASU, Takeshi
                IMAGAWA, Yoshitaka
                TOKIYOSHI, Sachio
     TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
     NUMBER OF SEQUENCES: 26
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: BROWDY AND NEIMARK
          STREET: 419 Seventh Street, N.W., Suite 300
          CITY: Washington
          STATE: D.C.
          COUNTRY: USA
          ZIP: 20004
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/10/079,616
          FILING DATE: 22-Feb-2002
          CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/011,143
;              FILING DATE: 04-FEB-1998
;              APPLICATION NUMBER: PCT/JP97/01824
;              FILING DATE: 29-MAY-1997
;              APPLICATION NUMBER: JP 165249/1996
;              FILING DATE: 04-JUN-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: BROWDY, Roger L.
;              REGISTRATION NUMBER: 25,618
;              REFERENCE/DOCKET NUMBER: IMAMURA=1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 202-628-5197
;              TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 24:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 79 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-079-616-24

Alignment Scores:
Pred. No.:              1.09e-18        Length:         79
Score:                  26.00           Matches:        26
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.2%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-079-616-24 (1-79)

Qy          50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

Qy          70 MetAsnGluSerCysLeu 75
               |||||||||||||||||||
Db          62 ATGAATGAGAGTTGCCTG 79

RESULT 70
US-09-011-143-25/c
; Sequence 25, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
```

```
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  JP 165249/1996
     FILING DATE:  04-JUN-1996
   ATTORNEY/AGENT INFORMATION:
     NAME:  BROWDY, Roger L.
     REGISTRATION NUMBER:  25,618
     REFERENCE/DOCKET NUMBER:  IMAMURA=1
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  202-628-5197
     TELEFAX:  202-737-3528
 INFORMATION FOR SEQ ID NO:  25:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  36 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
·09-011-143-25

.gnment Scores:
:d. No.:                0.000215        Length:         36
)re:                    12.00           Matches:        12
·cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              6.1%            Indels:         0
                        3               Gaps:           0

10-821-670A-36 (1-197) x US-09-011-143-25 (1-36)

       116 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 127
           ||||||||||||||||||||||||||||||||||||
        36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

;ULT 71
·09-302-495-25/c
;equence 25, Application US/09302495
)atent No. 6518045
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
            STREET: 419 Seventh Street, N.W., Suite 300
            CITY: Washington
            STATE: D.C.
            COUNTRY: USA
            ZIP: 20004
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/302,495
            FILING DATE: 30-Apr-1999
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: US/09/011,143
            FILING DATE: 04-FEB-1998
            APPLICATION NUMBER: PCT/JP97/01824
            FILING DATE: 29-MAY-1997
            APPLICATION NUMBER: JP 165249/1996
            FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
            NAME: BROWDY, Roger L.
            REGISTRATION NUMBER: 25,618
            REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 202-628-5197
            TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 25:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 36 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-302-495-25

Alignment Scores:
Pred. No.:              0.000215        Length:         36
Score:                  12.00           Matches:        12
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.1%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-302-495-25 (1-36)

Qy         116 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 127
               ||||||||||||||||||||||||||||||||||||
Db          36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

RESULT 72
US-10-079-616-25/c
; Sequence 25, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 36 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
```

```
          TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
-10-079-616-25

gnment Scores:
ed. No.:                0.000215        Length:         36
ore:                    12.00           Matches:        12
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              6.1%            Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-10-079-616-25 (1-36)

        116 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 127
            ||||||||||||||||||||||||||||||||||||
         36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

SULT 73
-09-917-265A-91
Sequence 91, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 91
  LENGTH: 39
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
-09-917-265A-91

gnment Scores:
ed. No.:                0.00257         Length:         39
ore:                    11.00           Matches:        11
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              5.6%            Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-917-265A-91 (1-39)

         10 ProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||
          7 CCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 39

SULT 74
-09-917-265A-83
Sequence 83, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-83

Alignment Scores:
Pred. No.:              0.0432          Length:         60
Score:                  10.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.1%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265A-83 (1-60)

Qy          1 ArgAsnLeuProThrProThrProSerPro 10
              ||||||||||||||||||||||||||||||
Db         29 AGAAACTTGCCAACCCCTACTCCATCCCCG 58

RESULT 75
US-09-917-265A-84/c
; Sequence 84, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-84

Alignment Scores:
Pred. No.:              0.0432          Length:         60
Score:                  10.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.1%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265A-84 (1-60)

Qy          1 ArgAsnLeuProThrProThrProSerPro 10
              ||||||||||||||||||||||||||||||
Db         32 AGAAACTTGCCAACCCCTACTCCATCCCCG 3

RESULT 76
US-09-634-368-1
; Sequence 1, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
```

NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 582
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine p35
OTHER INFORMATION: coding sequence for mature protein
09-634-368-1

gnment Scores:

d. No.:	0.388	Length:	582
re:	10.00	Matches:	10
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	5.1%	Indels:	0
	3	Gaps:	0

10-821-670A-36 (1-197) x US-09-634-368-1 (1-582)

```
Qy        104 SerIleTyrGluAspLeuLysMetTyrGln 113
              ||||||||||||||||||||||||||||
Db        298 AGCATCTATGAGGACTTGAAGATGTACCAG 327
```

ULT 77
08-385-335A-10
equence 10, Application US/08385335A
atent No. 5891680
GENERAL INFORMATION:
APPLICANT: Lieschke, Graham J.
APPLICANT: Mulligan, Richard C.
TITLE OF INVENTION: Bioactive Fusion Proteins
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,335A
FILING DATE: 08-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
08-385-335A-10

gnment Scores:

d. No.:	0.473	Length:	713
re:	10.00	Matches:	10
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	5.1%	Indels:	0
	2	Gaps:	0

US-10-821-670A-36 (1-197) x US-08-385-335A-10 (1-713)

```
Qy        104 SerIleTyrGluAspLeuLysMetTyrGln 113
              ||||||||||||||||||||||||||||
Db        410 AGCATCTATGAGGACTTGAAGATGTACCAG 439
```

RESULT 78
US-09-634-368-5
; Sequence 5, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/09/634,368
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: Fc-p35 fusion protein coding sequence
US-09-634-368-5

Alignment Scores:

Pred. No.:	0.831	Length:	1278
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.1%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-634-368-5 (1-1278)

```
Qy        104 SerIleTyrGluAspLeuLysMetTyrGln 113
              ||||||||||||||||||||||||||||
Db        994 AGCATCTATGAGGACTTGAAGATGTACCAG 1023
```

RESULT 79
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/09/634,368
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

Alignment Scores:

Pred. No.:	1.01	Length:	1569
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0

st Local Similarity: 100.0% Mismatches: 0
ery Match: 5.1% Indels: 0
: 3 Gaps: 0

-10-821-670A-36 (1-197) x US-09-634-368-12 (1-1569)

104 SerIleTyrGluAspLeuLysMetTyrGln 113
||||||||||||||||||||||||||||
298 AGCATCTATGAGGACTTGAAGATGTACCAG 327

SULT 80
-09-634-368-11
Sequence 11, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/09/634,368
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 2013
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
-09-634-368-11

gnment Scores:
ed. No.: 1.29 Length: 2013
ore: 10.00 Matches: 10
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 5.1% Indels: 0
: 3 Gaps: 0

-10-821-670A-36 (1-197) x US-09-634-368-11 (1-2013)

104 SerIleTyrGluAspLeuLysMetTyrGln 113
||||||||||||||||||||||||||||
298 AGCATCTATGAGGACTTGAAGATGTACCAG 327

SULT 81
-09-634-368-13
Sequence 13, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/09/634,368
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 2709
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
OTHER INFORMATION: sequence
-09-634-368-13

Alignment Scores:
Pred. No.: 1.72 Length: 2709
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-36 (1-197) x US-09-634-368-13 (1-2709)

Qy 104 SerIleTyrGluAspLeuLysMetTyrGln 113
||||||||||||||||||||||||||||
Db 994 AGCATCTATGAGGACTTGAAGATGTACCAG 1023

RESULT 82
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
; GENERAL INFORMATION:
; APPLICANT: Rakhmilevich, Alexander
; TITLE OF INVENTION: IL-12 Gene Therapy of Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,206A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 110229.91144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6295 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "plasmid pWRG3196"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(955..1260, 1334..1675)
; OTHER INFORMATION: /product= "p35 gene product"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2377..3384
; OTHER INFORMATION: /product= "p40 gene product"
US-08-659-206A-4

Alignment Scores:
Pred. No.: 3.88 Length: 6295
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-36 (1-197) x US-08-659-206A-4 (1-6295)

```
       104 SerIleTyrGluAspLeuLysMetTyrGln 113
           ||||||||||||||||||||||||||||
      1391 AGCATCTATGAGGACTTGAAGATGTACCAG 1420

SULT 83
08-659-206A-1
Sequence 1, Application US/08659206A
Patent No. 5922685
GENERAL INFORMATION:
  APPLICANT:  Rakhmilevich, Alexander
  TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
  NUMBER OF SEQUENCES:  6
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Quarles & Brady
    STREET:  1 South Pinckney Street
    CITY:  Madison
    STATE:  WI
    COUNTRY:  US
    ZIP:  53703
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/659,206A
    FILING DATE:
    CLASSIFICATION:  435
  ATTORNEY/AGENT INFORMATION:
    NAME:  Seay, Nicholas J
    REGISTRATION NUMBER:  27386
    REFERENCE/DOCKET NUMBER:  110229.91144
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  608-251-5000
    TELEFAX:  608-251-9166
INFORMATION FOR SEQ ID NO:  1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  7287 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  circular
  MOLECULE TYPE:  other nucleic acid
    DESCRIPTION:  /desc = "Plasmid DNA"
  IMMEDIATE SOURCE:
    CLONE:  pWRG3169
  FEATURE:
    NAME/KEY:  promoter
    LOCATION:  1..628
  FEATURE:
    NAME/KEY:  iDNA
    LOCATION:  629..810
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  join(953..1258, 1332..1673)
    OTHER INFORMATION:  /product= "p35 gene product"
  FEATURE:
    NAME/KEY:  polyA_site
    LOCATION:  1797..2024
  FEATURE:
    NAME/KEY:  promoter
    LOCATION:  2110..2737
  FEATURE:
    NAME/KEY:  iDNA
    LOCATION:  2738..2919
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  2983..3990
    OTHER INFORMATION:  /product= "p40 gene product"
  FEATURE:
    NAME/KEY:  polyA_site
    LOCATION:  4075..4306
08-659-206A-1

Alignment Scores:
Pred. No.:                4.47          Length:          7287
Score:                    10.00         Matches:         10
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              5.1%          Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-36 (1-197) x US-08-659-206A-1 (1-7287)

Qy        104 SerIleTyrGluAspLeuLysMetTyrGln 113
              ||||||||||||||||||||||||||||
Db       1389 AGCATCTATGAGGACTTGAAGATGTACCAG 1418

RESULT 84
US-09-917-265A-96/c
; Sequence 96, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-96

Alignment Scores:
Pred. No.:                0.409         Length:          51
Score:                    9.00          Matches:         9
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              4.6%          Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-36 (1-197) x US-09-917-265A-96 (1-51)

Qy        187 IleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||
Db         49 ATCAATAGAATGATGTCCTACTTGAAC 23

RESULT 85
US-08-464-700-53/c
; Sequence 53, Application US/08464700
; Patent No. 6232458
;  GENERAL INFORMATION:
;    APPLICANT:  WEISS, ANTHONY S
;    APPLICANT:  MARTIN, STEPHEN L
;    TITLE OF INVENTION:  SYNTHETIC POLYNUCLEOTIDES
;    NUMBER OF SEQUENCES:  54
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

```
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/464,700
     FILING DATE:  7-JUN-1995
     CLASSIFICATION:  435
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  AU PL6520
     FILING DATE:  22-DEC-1992
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  AU PL9661
     FILING DATE:  28-JUN-1993
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  PCT/AU93/00655
     FILING DATE:  16-DEC-1993
   ATTORNEY/AGENT INFORMATION:
     NAME:  Bak, Mary E.
     REGISTRATION NUMBER:  31,215
     REFERENCE/DOCKET NUMBER:  GHC3USA
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  215-540-9200
     TELEFAX:  215-540-5818
 INFORMATION FOR SEQ ID NO:  53:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  2210 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   HYPOTHETICAL:  NO
   ANTI-SENSE:  NO
-08-464-700-53

:gnment Scores:
ed. No.:                15.6          Length:          2210
ore:                    9.00          Matches:         9
:cent Similarity:       100.0%        Conservative:    0
st Local Similarity:    100.0%        Mismatches:      0
ery Match:              4.6%          Indels:          0
:                       3             Gaps:            0

-10-821-670A-36 (1-197) x US-08-464-700-53 (1-2210)

          4 ProThrProThrProSerProGlyMet 12
            |||||||||||||||||||||||||||
       1603 CCGACACCAACTCCAAGTCCAGGGATG 1577

SULT 86
-08-641-627A-37/c
Sequence 37, Application US/08641627A
Patent No. 5726040
 GENERAL INFORMATION:
   APPLICANT:  Ensley PhD, Burt D.
   APPLICANT:  Ludmer, Matthew
   TITLE OF INVENTION:  Cosmetic Compositions Including
   TITLE OF INVENTION:  Tropoelastin Isomorphs
   NUMBER OF SEQUENCES:  37
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Choate, Hall & Stewart
     STREET:  53 State Street
     CITY:  Boston
     STATE:  MA
     COUNTRY:  usa
     ZIP:  02109
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/641,627A
     FILING DATE:  02-MAY-1996
     CLASSIFICATION:  435
   ATTORNEY/AGENT INFORMATION:
     NAME:  Jarrell Ph.D., Brenda H.
;      REGISTRATION NUMBER:  39,223
;      REFERENCE/DOCKET NUMBER:  0062912-0001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-5000
;      TELEFAX:  (617) 248-4000
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2242 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      STRAIN:  tropoelastin cDNA (cHE-3)
US-08-641-627A-37

Alignment Scores:
Pred. No.:                15.9          Length:          2242
Score:                    9.00          Matches:         9
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              4.6%          Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-36 (1-197) x US-08-641-627A-37 (1-2242)

Qy          4 ProThrProThrProSerProGlyMet 12
              |||||||||||||||||||||||||||
Db       1740 CCGACACCAACTCCAAGTCCAGGGATG 1714

RESULT 87
US-08-678-039A-39/c
; Sequence 39, Application US/08678039A
; Patent No. 5858662
;  GENERAL INFORMATION:
;    APPLICANT:  Keating, Mark T.
;    APPLICANT:  Morris, Colleen A.
;    TITLE OF INVENTION:  Diagnosis of Williams Syndrome and
;    TITLE OF INVENTION:  Williams Syndrome Cognitive Profile by Analysis of the
;    TITLE OF INVENTION:  Presence or Absence of a LIM-Kinase Gene
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rothwell, Figg, Ernst & Kurz, P.C.
;      STREET:  555 Thirteenth Street, N.W., Suite 701 East
;      STREET:  Tower
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/678,039A
;      FILING DATE:  10-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Saxe, Stephen A.
;      REGISTRATION NUMBER:  38,609
;      REFERENCE/DOCKET NUMBER:  2323-120A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-624-1589
;      TELEFAX:  202-783-6031
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2427 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
```

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 49..2424
08-678-039A-39

gnment Scores:

d. No.:	17.1	Length:	2427
re:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.6%	Indels:	0
	2	Gaps:	0

10-821-670A-36 (1-197) x US-08-678-039A-39 (1-2427)

```
          4 ProThrProThrProSerProGlyMet 12
            |||||||||||||||||||||||||||
       1826 CCGACACCAACTCCAAGTCCAGGGATG 1800
```

ULT 88
10-104-047-945/c
equence 945, Application US/10104047
atent No. 6943241
ENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 945
LENGTH: 2845
TYPE: DNA
ORGANISM: Homo sapiens
10-104-047-945

gnment Scores:

d. No.:	20	Length:	2845
re:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.6%	Indels:	0
	3	Gaps:	0

10-821-670A-36 (1-197) x US-10-104-047-945 (1-2845)

```
          4 ProThrProThrProSerProGlyMet 12
            |||||||||||||||||||||||||||
       1420 CCGACACCAACTCCAAGTCCAGGGATG 1394
```

ULT 89
09-396-196G-121547
equence 121547, Application US/09396196G
atent No. 6821724
ENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 121547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-121547

Alignment Scores:

Pred. No.:	2.27	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-396-196G-121547 (1-25)

```
Qy        172 LysLeuCysIleLeuLeuHisAla 179
              ||||||||||||||||||||||||
Db          1 AAGCTCTGCATCCTGCTTCACGCC 24
```

RESULT 90
US-09-917-265A-90/c
; Sequence 90, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-917-265A-90

Alignment Scores:

Pred. No.:	2.45	Length:	27
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-917-265A-90 (1-27)

```
Qy        190 MetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||
Db         27 ATGATGAGCTATCTGAATGCTTCC 4
```

RESULT 91
US-09-917-265A-92/c
; Sequence 92, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111

```
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 92
  LENGTH: 41
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
-09-917-265A-92

:gnment Scores:
ed. No.:                3.67          Length:         41
ore:                    8.00          Matches:        8
:cent Similarity:       100.0%        Conservative:   0
st Local Similarity:    100.0%        Mismatches:     0
ery Match:              4.1%          Indels:         0
:                       3             Gaps:           0

-10-821-670A-36 (1-197) x US-09-917-265A-92 (1-41)

        190 MetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||
         41 ATGATGAGCTATCTGAATGCTTCC 18

SULT 92
-09-621-976-13237/c
Sequence 13237, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, J.B.
 APPLICANT:  Jobert, S.
 APPLICANT:  Giordano, J.Y.
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: GENSET.054PR2
 CURRENT APPLICATION NUMBER: US/09/621,976
 CURRENT FILING DATE:  2000-07-21
 NUMBER OF SEQ ID NOS: 19335
 SOFTWARE: Patent.pm
SEQ ID NO 13237
  LENGTH: 452
  TYPE: DNA
  ORGANISM: Homo sapiens
-09-621-976-13237

:gnment Scores:
ed. No.:                37.4          Length:         452
ore:                    8.00          Matches:        8
:cent Similarity:       100.0%        Conservative:   0
st Local Similarity:    100.0%        Mismatches:     0
ery Match:              4.1%          Indels:         0
:                       3             Gaps:           0

-10-821-670A-36 (1-197) x US-09-621-976-13237 (1-452)

          3 LeuProThrProThrProSerPro 10
            |||||||||||||||||||||||||
        148 CTCCCCACTCCTACCCCCTCACCA 125

SULT 93
-09-949-016-60737/c
Sequence 60737, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60737
  LENGTH: 601
  TYPE: DNA
  ORGANISM: Human
US-09-949-016-60737

Alignment Scores:
Pred. No.:              49.2          Length:         601
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.1%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-36 (1-197) x US-09-949-016-60737 (1-601)

Qy          82 LeuIleThrAsnGlySerCysLeu 89
               |||||||||||||||||||||||||
Db         408 TTAATAACAAATGGTTCATGTTTG 385

RESULT 94
US-09-949-016-60738/c
Sequence 60738, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60738
  LENGTH: 601
  TYPE: DNA
  ORGANISM: Human
US-09-949-016-60738

Alignment Scores:
Pred. No.:              49.2          Length:         601
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.1%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-36 (1-197) x US-09-949-016-60738 (1-601)

Qy          82 LeuIleThrAsnGlySerCysLeu 89
               |||||||||||||||||||||||||
Db          49 TTAATAACAAATGGTTCATGTTTG 26

RESULT 95
US-09-949-016-60739/c
Sequence 60739, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
```

```
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 60739
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
09-949-016-60739

gnment Scores:
d. No.:              49.2          Length:        601
re:                  8.00          Matches:       8
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            4.1%          Indels:        0
                     3             Gaps:          0

10-821-670A-36 (1-197) x US-09-949-016-60739 (1-601)

        82 LeuIleThrAsnGlySerCysLeu 89
           |||||||||||||||||||||||||
        48 TTAATAACAAATGGTTCATGTTTG 25

ULT 96
09-949-016-111391
equence 111391, Application US/09949016
atent No. 6812339
ENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE:  2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 111391
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
09-949-016-111391

gnment Scores:
d. No.:              49.2          Length:        601
re:                  8.00          Matches:       8
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            4.1%          Indels:        0
                     3             Gaps:          0

10-821-670A-36 (1-197) x US-09-949-016-111391 (1-601)

       168 LysThrLysIleLysLeuCysIle 175
           ||||||||||||||||||||||||
       505 AAAACCAAGATCAAACTTTGTATA 528

ULT 97
09-949-016-111392
equence 111392, Application US/09949016
atent No. 6812339
ENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111392
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-111392

Alignment Scores:
Pred. No.:           49.2          Length:        601
Score:               8.00          Matches:       8
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         4.1%          Indels:        0
DB:                  3             Gaps:          0

US-10-821-670A-36 (1-197) x US-09-949-016-111392 (1-601)

Qy         168 LysThrLysIleLysLeuCysIle 175
               ||||||||||||||||||||||||
Db         506 AAAACCAAGATCAAACTTTGTATA 529

RESULT 98
US-09-949-016-147156/c
; Sequence 147156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 147156
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-147156

Alignment Scores:
Pred. No.:           49.2          Length:        601
Score:               8.00          Matches:       8
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         4.1%          Indels:        0
DB:                  3             Gaps:          0

US-10-821-670A-36 (1-197) x US-09-949-016-147156 (1-601)

Qy           3 LeuProThrProThrProSerPro 10
               |||||||||||||||||||||||||
Db         224 CTCCCCACTCCCACGCCGTCTCCC 201

RESULT 99
```

-09-949-016-154644/c
Sequence 154644, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 154644
LENGTH: 601
TYPE: DNA
ORGANISM: Human
-09-949-016-154644

gnment Scores:

ed. No.:	49.2	Length:	601
ore:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	4.1%	Indels:	0
:	3	Gaps:	0

-10-821-670A-36 (1-197) x US-09-949-016-154644 (1-601)

```
        172 LysLeuCysIleLeuLeuHisAla 179
            ||||||||||||||||||||||||
        354 AAGCTGTGTATTTTATTGCATGCA 331
```

SULT 100
-09-949-016-154645/c
Sequence 154645, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 154645
LENGTH: 601
TYPE: DNA
ORGANISM: Human
-09-949-016-154645

gnment Scores:

ed. No.:	49.2	Length:	601
ore:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	4.1%	Indels:	0
:	3	Gaps:	0

-10-821-670A-36 (1-197) x US-09-949-016-154645 (1-601)

```
Qy      172 LysLeuCysIleLeuLeuHisAla 179
            ||||||||||||||||||||||||
Db      596 AAGCTGTGTATTTTATTGCATGCA 573
```

Search completed: June 10, 2006, 04:48:51
Job time : 138.303 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 11, 2006, 22:10:55 ; Search time 951.372 Seconds
(without alignments)
3816.589 Million cell updates/sec

le: US-10-821-670A-36
fect score: 197
quence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 18892170 seqs, 6143817638 residues

d size: 1

al number of hits satisfying chosen parameters: 37767822

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110503_27781/app_query.fasta_1
B=Published_Applications_NA_Main -QFMT=fastap
UFFIX=oligo.p2n.200scores.rnpbm -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
NITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
OCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
ORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
SER=US10821670_@CGN_1_1_4932_@runat_07062006_110503_27781 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	197	100.0	591	3	US-09-917-265-35	Sequence 35, Appl
c 2	197	100.0	591	3	US-09-917-265-37	Sequence 37, Appl
3	197	100.0	591	9	US-10-821-670-35	Sequence 35, Appl
c 4	197	100.0	591	9	US-10-821-670-37	Sequence 37, Appl
5	197	100.0	666	3	US-09-917-265-32	Sequence 32, Appl
c 6	197	100.0	666	3	US-09-917-265-34	Sequence 34, Appl
7	197	100.0	666	9	US-10-821-670-32	Sequence 32, Appl
c 8	197	100.0	666	9	US-10-821-670-34	Sequence 34, Appl
9	197	100.0	1533	3	US-09-917-265-43	Sequence 43, Appl
c 10	197	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
11	197	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
c 12	197	100.0	1533	9	US-10-821-670-45	Sequence 45, Appl
13	197	100.0	1599	3	US-09-917-265-38	Sequence 38, Appl
c 14	197	100.0	1599	3	US-09-917-265-40	Sequence 40, Appl
15	197	100.0	1599	9	US-10-821-670-38	Sequence 38, Appl
c 16	197	100.0	1599	9	US-10-821-670-40	Sequence 40, Appl
17	195	99.0	591	6	US-10-079-616-9	Sequence 9, Appli
18	195	99.0	689	6	US-10-079-616-26	Sequence 26, Appl
19	195	99.0	1441	6	US-10-079-616-8	Sequence 8, Appli
20	187	94.9	561	3	US-09-917-265-101	Sequence 101, App
c 21	187	94.9	561	3	US-09-917-265-103	Sequence 103, App
22	187	94.9	561	9	US-10-821-670-101	Sequence 101, App
c 23	187	94.9	561	9	US-10-821-670-103	Sequence 103, App
24	54	27.4	669	7	US-10-041-672C-2	Sequence 2, Appli
25	52	26.4	591	3	US-09-917-265-49	Sequence 49, Appl
c 26	52	26.4	591	3	US-09-917-265-51	Sequence 51, Appl
27	52	26.4	591	9	US-10-821-670-49	Sequence 49, Appl
c 28	52	26.4	591	9	US-10-821-670-51	Sequence 51, Appl
29	52	26.4	666	3	US-09-917-265-46	Sequence 46, Appl
c 30	52	26.4	666	3	US-09-917-265-48	Sequence 48, Appl
31	52	26.4	666	9	US-10-821-670-46	Sequence 46, Appl
c 32	52	26.4	666	9	US-10-821-670-48	Sequence 48, Appl
33	52	26.4	1455	3	US-09-917-265-104	Sequence 104, App
c 34	52	26.4	1455	3	US-09-917-265-106	Sequence 106, App
35	52	26.4	1455	9	US-10-821-670-104	Sequence 104, App
c 36	52	26.4	1455	9	US-10-821-670-106	Sequence 106, App
37	52	26.4	1533	3	US-09-917-265-66	Sequence 66, Appl
c 38	52	26.4	1533	3	US-09-917-265-68	Sequence 68, Appl
39	52	26.4	1533	9	US-10-821-670-66	Sequence 66, Appl
c 40	52	26.4	1533	9	US-10-821-670-68	Sequence 68, Appl
41	52	26.4	1599	3	US-09-917-265-61	Sequence 61, Appl
c 42	52	26.4	1599	3	US-09-917-265-63	Sequence 63, Appl
43	52	26.4	1599	9	US-10-821-670-61	Sequence 61, Appl
c 44	52	26.4	1599	9	US-10-821-670-63	Sequence 63, Appl
45	29	14.7	201	8	US-10-741-601-946	Sequence 946, App
46	29	14.7	201	8	US-10-741-601-947	Sequence 947, App
47	29	14.7	201	8	US-10-741-601-951	Sequence 951, App
48	29	14.7	201	8	US-10-741-601-955	Sequence 955, App
49	29	14.7	201	8	US-10-741-601-957	Sequence 957, App
50	29	14.7	201	8	US-10-741-601-960	Sequence 960, App
51	29	14.7	201	8	US-10-741-601-7417	Sequence 7417, Ap
52	29	14.7	201	8	US-10-741-601-7418	Sequence 7418, Ap
53	29	14.7	201	8	US-10-741-601-7431	Sequence 7431, Ap
c 54	29	14.7	201	8	US-10-741-601-11370	Sequence 11370, A
c 55	29	14.7	201	8	US-10-741-601-11372	Sequence 11372, A
c 56	29	14.7	201	8	US-10-741-601-11417	Sequence 11417, A
57	29	14.7	201	9	US-10-741-600-3487	Sequence 3487, Ap
58	29	14.7	201	9	US-10-741-600-3488	Sequence 3488, Ap
59	29	14.7	201	9	US-10-741-600-3492	Sequence 3492, Ap
60	29	14.7	201	9	US-10-741-600-3496	Sequence 3496, Ap
61	29	14.7	201	9	US-10-741-600-3498	Sequence 3498, Ap
62	29	14.7	201	9	US-10-741-600-3501	Sequence 3501, Ap
63	29	14.7	201	9	US-10-741-600-20963	Sequence 20963, A
64	29	14.7	201	9	US-10-741-600-20964	Sequence 20964, A
65	29	14.7	201	9	US-10-741-600-20992	Sequence 20992, A
c 66	29	14.7	201	9	US-10-741-600-28831	Sequence 28831, A
c 67	29	14.7	201	9	US-10-741-600-28833	Sequence 28833, A
c 68	29	14.7	201	9	US-10-741-600-28877	Sequence 28877, A
69	29	14.7	201	10	US-10-995-561-1976	Sequence 1976, Ap
70	29	14.7	201	10	US-10-995-561-1977	Sequence 1977, Ap
71	29	14.7	201	10	US-10-995-561-1981	Sequence 1981, Ap
72	29	14.7	201	10	US-10-995-561-1986	Sequence 1986, Ap
73	29	14.7	201	10	US-10-995-561-1988	Sequence 1988, Ap
74	29	14.7	201	10	US-10-995-561-1991	Sequence 1991, Ap

75	29	14.7	201	10	US-10-995-561-18302	Sequence 18302, A
76	29	14.7	201	10	US-10-995-561-18303	Sequence 18303, A
77	29	14.7	201	10	US-10-995-561-18335	Sequence 18335, A
78	29	14.7	201	10	US-10-995-561-26362	Sequence 26362, A
79	29	14.7	201	10	US-10-995-561-26545	Sequence 26545, A
80	29	14.7	201	10	US-10-995-561-26548	Sequence 26548, A
81	29	14.7	201	10	US-10-995-561-73346	Sequence 73346, A
82	29	14.7	201	10	US-10-995-561-73349	Sequence 73349, A
83	29	14.7	201	10	US-10-995-561-73383	Sequence 73383, A
84	29	14.7	660	3	US-09-754-014-6	Sequence 6, Appli
85	29	14.7	660	3	US-09-754-014-7	Sequence 7, Appli
86	29	14.7	660	3	US-09-754-014-8	Sequence 8, Appli
87	29	14.7	660	3	US-09-836-866-4	Sequence 4, Appli
88	29	14.7	721	7	US-10-267-384-199	Sequence 199, App
89	29	14.7	762	3	US-09-826-025-21	Sequence 21, Appl
90	29	14.7	762	9	US-10-785-577-21	Sequence 21, Appl
91	29	14.7	762	9	US-10-688-845-57	Sequence 57, Appl
92	29	14.7	811	7	US-10-373-456-19	Sequence 19, Appl
93	29	14.7	856	7	US-10-349-507-4	Sequence 4, Appli
94	29	14.7	856	7	US-10-267-565-4	Sequence 4, Appli
95	29	14.7	868	7	US-10-373-456-17	Sequence 17, Appl
96	29	14.7	1026	6	US-10-172-399-5	Sequence 5, Appli
97	29	14.7	1026	8	US-10-641-643-1041	Sequence 1041, Ap
98	29	14.7	1287	8	US-10-603-064-6	Sequence 6, Appli
99	29	14.7	1316	9	US-10-476-960-3	Sequence 3, Appli
100	29	14.7	1316	15	US-11-089-191-3	Sequence 3, Appli
101	29	14.7	1395	3	US-09-924-703-5	Sequence 5, Appli
102	29	14.7	1395	8	US-10-358-395-5	Sequence 5, Appli
103	29	14.7	1444	7	US-10-429-802-43	Sequence 43, Appl
104	29	14.7	1444	7	US-10-430-503-34	Sequence 34, Appl
105	29	14.7	1494	8	US-10-322-696-131	Sequence 131, App
106	29	14.7	1526	8	US-10-322-696-185	Sequence 185, App
107	29	14.7	1532	8	US-10-741-601-29	Sequence 29, Appl
108	29	14.7	1532	9	US-10-741-600-51	Sequence 51, Appl
109	29	14.7	1532	10	US-10-995-561-38	Sequence 38, Appl
110	29	14.7	1607	8	US-10-741-601-28	Sequence 28, Appl
111	29	14.7	1607	9	US-10-741-600-50	Sequence 50, Appl
112	29	14.7	1607	10	US-10-995-561-37	Sequence 37, Appl
113	29	14.7	1645	6	US-10-228-811-2	Sequence 2, Appli
114	29	14.7	1828	7	US-10-373-456-2	Sequence 2, Appli
115	29	14.7	2390	10	US-10-528-644A-53	Sequence 53, Appl
116	29	14.7	2466	7	US-10-373-456-1	Sequence 1, Appli
117	29	14.7	5686	7	US-10-136-837-1	Sequence 1, Appli
118	29	14.7	8578	3	US-09-828-825-1	Sequence 1, Appli
119	29	14.7	8578	3	US-09-828-825-3	Sequence 3, Appli
120	29	14.7	8608	3	US-09-828-825-7	Sequence 7, Appli
121	29	14.7	8623	3	US-09-828-825-5	Sequence 5, Appli
122	29	14.7	8629	3	US-09-828-825-15	Sequence 15, Appl
123	29	14.7	8638	3	US-09-828-825-9	Sequence 9, Appli
124	29	14.7	8644	3	US-09-828-825-13	Sequence 13, Appl
125	29	14.7	8659	3	US-09-828-825-11	Sequence 11, Appl
126	29	14.7	11453	10	US-10-511-237-3	Sequence 3, Appli
127	29	14.7	11569	10	US-10-511-237-1	Sequence 1, Appli
128	29	14.7	19277	8	US-10-741-601-5620	Sequence 5620, Ap
129	29	14.7	19277	9	US-10-741-600-17576	Sequence 17576, A
130	29	14.7	19277	10	US-10-995-561-13214	Sequence 13214, A
131	29	14.7	27277	8	US-10-322-696-130	Sequence 130, App
132	29	14.7	29618	8	US-10-741-601-5750	Sequence 5750, Ap
133	29	14.7	29618	9	US-10-741-600-17908	Sequence 17908, A
134	29	14.7	29618	10	US-10-995-561-13444	Sequence 13444, A
135	29	14.7	61916	8	US-10-741-601-5631	Sequence 5631, Ap
136	29	14.7	61916	9	US-10-741-600-17621	Sequence 17621, A
137	29	14.7	305312	10	US-10-995-561-13236	Sequence 13236, A
138	26	13.2	79	6	US-10-079-616-24	Sequence 24, Appl
139	23	11.7	71	7	US-10-041-672C-8	Sequence 8, Appli
140	20	10.2	201	8	US-10-741-601-943	Sequence 943, App
141	20	10.2	201	8	US-10-741-601-952	Sequence 952, App
142	20	10.2	201	8	US-10-741-601-7415	Sequence 7415, Ap
143	20	10.2	201	8	US-10-741-601-11410	Sequence 11410, A
144	20	10.2	201	9	US-10-741-600-3484	Sequence 3484, Ap
145	20	10.2	201	9	US-10-741-600-3493	Sequence 3493, Ap
146	20	10.2	201	9	US-10-741-600-20983	Sequence 20983, A
147	20	10.2	201	9	US-10-741-600-28870	Sequence 28870, A
148	20	10.2	201	10	US-10-995-561-1973	Sequence 1973, Ap
149	20	10.2	201	10	US-10-995-561-1983	Sequence 1983, Ap
150	20	10.2	201	10	US-10-995-561-18326	Sequence 18326, A
c 151	20	10.2	201	10	US-10-995-561-26586	Sequence 26586, A
c 152	20	10.2	201	10	US-10-995-561-73379	Sequence 73379, A
c 153	18	9.1	76	7	US-10-041-672C-6	Sequence 6, Appli
c 154	18	9.1	76	7	US-10-041-672C-9	Sequence 9, Appli
155	13	6.6	60	3	US-09-908-975-12410	Sequence 12410, A
156	13	6.6	201	10	US-10-995-561-1982	Sequence 1982, Ap
157	13	6.6	201	10	US-10-995-561-18376	Sequence 18376, A
c 158	13	6.6	201	10	US-10-995-561-26316	Sequence 26316, A
c 159	13	6.6	201	10	US-10-995-561-73335	Sequence 73335, A
c 160	12	6.1	36	6	US-10-079-616-25	Sequence 25, Appl
161	11	5.6	39	3	US-09-917-265-91	Sequence 91, Appl
162	11	5.6	39	9	US-10-821-670-91	Sequence 91, Appl
163	10	5.1	60	3	US-09-917-265-83	Sequence 83, Appl
c 164	10	5.1	60	3	US-09-917-265-84	Sequence 84, Appl
165	10	5.1	60	9	US-10-821-670-83	Sequence 83, Appl
c 166	10	5.1	60	9	US-10-821-670-84	Sequence 84, Appl
167	10	5.1	582	8	US-10-603-064-1	Sequence 1, Appli
168	10	5.1	600	16	US-11-136-527-4750	Sequence 4750, Ap
169	10	5.1	793	16	US-11-136-527-654	Sequence 654, App
170	10	5.1	1231	8	US-10-322-696-128	Sequence 128, App
171	10	5.1	1265	6	US-10-172-399-1	Sequence 1, Appli
172	10	5.1	1278	8	US-10-603-064-5	Sequence 5, Appli
173	10	5.1	1569	8	US-10-603-064-12	Sequence 12, Appl
174	10	5.1	2013	8	US-10-603-064-11	Sequence 11, Appl
175	10	5.1	2709	8	US-10-603-064-13	Sequence 13, Appl
176	10	5.1	5966	7	US-10-136-837-3	Sequence 3, Appli
177	10	5.1	11458	10	US-10-511-237-2	Sequence 2, Appli
178	10	5.1	27125	8	US-10-322-696-127	Sequence 127, App
c 179	9	4.6	51	3	US-09-917-265-96	Sequence 96, Appl
c 180	9	4.6	51	9	US-10-821-670-96	Sequence 96, Appl
c 181	9	4.6	190	10	US-10-287-436A-942	Sequence 942, App
182	9	4.6	201	8	US-10-741-601-7429	Sequence 7429, Ap
c 183	9	4.6	201	8	US-10-741-601-11308	Sequence 11308, A
c 184	9	4.6	201	9	US-10-741-600-5983	Sequence 5983, Ap
c 185	9	4.6	201	9	US-10-741-600-5985	Sequence 5985, Ap
c 186	9	4.6	201	9	US-10-741-600-5992	Sequence 5992, Ap
c 187	9	4.6	201	9	US-10-741-600-6000	Sequence 6000, Ap
c 188	9	4.6	201	9	US-10-741-600-6002	Sequence 6002, Ap
c 189	9	4.6	201	9	US-10-741-600-6009	Sequence 6009, Ap
190	9	4.6	201	9	US-10-741-600-20990	Sequence 20990, A
c 191	9	4.6	201	9	US-10-741-600-27751	Sequence 27751, A
c 192	9	4.6	201	9	US-10-741-600-27778	Sequence 27778, A
c 193	9	4.6	201	9	US-10-741-600-28770	Sequence 28770, A
c 194	9	4.6	201	10	US-10-995-561-3430	Sequence 3430, Ap
c 195	9	4.6	201	10	US-10-995-561-3435	Sequence 3435, Ap
c 196	9	4.6	201	10	US-10-995-561-3440	Sequence 3440, Ap
c 197	9	4.6	201	10	US-10-995-561-3451	Sequence 3451, Ap
c 198	9	4.6	201	10	US-10-995-561-3456	Sequence 3456, Ap
c 199	9	4.6	201	10	US-10-995-561-3461	Sequence 3461, Ap
200	9	4.6	201	10	US-10-995-561-18336	Sequence 18336, A

ALIGNMENTS

```
RESULT 1
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
```

```
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(591)
  OTHER INFORMATION:
-09-917-265-35

:gnment Scores:
ed. No.:                4.17e-196       Length:         591
ore:                    197.00          Matches:        197
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              100.0%          Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-917-265-35 (1-591)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

SULT 2
-09-917-265-37/c
Sequence 37, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109

;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-37

Alignment Scores:
Pred. No.:              4.17e-196       Length:         591
Score:                  197.00          Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-37 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 3
US-10-821-670-35
; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
```

```
SEQ ID NO 35
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(591)
10-821-670-35

gnment Scores:
d. No.:              4.17e-196      Length:        591
re:                  197.00         Matches:       197
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            100.0%         Indels:        0
                     9              Gaps:          0

10-821-670A-36 (1-197) x US-10-821-670-35 (1-591)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

SULT 4
10-821-670-37/c
Sequence 37, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-37

Alignment Scores:
Pred. No.:              4.17e-196      Length:        591
Score:                  197.00         Matches:       197
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-36 (1-197) x US-10-821-670-37 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
```

```
SEQ ID NO 32
  LENGTH: 666
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(666)
  OTHER INFORMATION:
-09-917-265-32

:gnment Scores:
ed. No.:                4.65e-196       Length:         666
ore:                    197.00          Matches:        197
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              100.0%          Indels:         0
:                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-917-265-32 (1-666)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

SULT 6
-09-917-265-34/c
Sequence 34, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

Alignment Scores:
Pred. No.:              4.65e-196       Length:         666
Score:                  197.00          Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-34 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 7
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
```

```
SOFTWARE: PatentIn version 3.2
EQ ID NO 32
  LENGTH: 666
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(666)
10-821-670-32

gnment Scores:
d. No.:              4.65e-196      Length:        666
re:                  197.00         Matches:       197
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            100.0%         Indels:        0
                     9              Gaps:          0

10-821-670A-36 (1-197) x US-10-821-670-32 (1-666)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

ULT 8
 10-821-670-34/c
equence 34, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

Alignment Scores:
Pred. No.:              4.65e-196      Length:        666
Score:                  197.00         Matches:       197
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-36 (1-197) x US-10-821-670-34 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
```

SOFTWARE: PatentIn version 3.1
SEQ ID NO 43
LENGTH: 1533
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
OTHER INFORMATION:
-09-917-265-43

:gnment Scores:

ed. No.:	1.01e-195	Length:	1533
ore:	197.00	Matches:	197
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	100.0%	Indels:	0
:	3	Gaps:	0

-10-821-670A-36 (1-197) x US-09-917-265-43 (1-1533)

```
          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

SULT 10
-09-917-265-45/c
Sequence 45, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-45

Alignment Scores:

Pred. No.:	1.01e-195	Length:	1533
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-917-265-45 (1-1533)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 11
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04

```
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 43
 LENGTH: 1533
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1533)
10-821-670-43

gnment Scores:
d. No.:              1.01e-195      Length:        1533
re:                  197.00         Matches:       197
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            100.0%         Indels:        0
                     9              Gaps:          0

10-821-670A-36 (1-197) x US-10-821-670-43 (1-1533)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

ULT 12
10-821-670-45/c
equence 45, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:
Pred. No.:              1.01e-195      Length:        1533
Score:                  197.00         Matches:       197
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-36 (1-197) x US-10-821-670-45 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 13
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
```

```
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 38
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1599)
  OTHER INFORMATION:
-09-917-265-38

:gnment Scores:
:d. No.:              1.05e-195      Length:         1599
:ore:                 197.00         Matches:        197
:cent Similarity:     100.0%         Conservative:   0
:st Local Similarity: 100.0%         Mismatches:     0
:ery Match:           100.0%         Indels:         0
:                     3              Gaps:           0

-10-821-670A-36 (1-197) x US-09-917-265-38 (1-1599)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

SULT 14
-09-917-265-40/c
Sequence 40, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:
Pred. No.:              1.05e-195      Length:         1599
Score:                  197.00         Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-40 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 15
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
```

```
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 38
 LENGTH: 1599
 TYPE: DNA
 ORGANISM: Felis catus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1599)
10-821-670-38

gnment Scores:
d. No.:              1.05e-195      Length:        1599
re:                  197.00         Matches:       197
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            100.0%         Indels:        0
                     9              Gaps:          0

10-821-670A-36 (1-197) x US-10-821-670-38 (1-1599)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

ULT 16
10-821-670-40/c
equence 40, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:
Pred. No.:              1.05e-195      Length:        1599
Score:                  197.00         Matches:       197
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-36 (1-197) x US-10-821-670-40 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 17
US-10-079-616-9
; Sequence 9, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
```

```
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: BROWDY AND NEIMARK
           STREET: 419 Seventh Street, N.W., Suite 300
           CITY: Washington
           STATE: D.C.
           COUNTRY: USA
           ZIP: 20004
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/10/079,616
           FILING DATE: 22-Feb-2002
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 09/011,143
           FILING DATE: 04-FEB-1998
           APPLICATION NUMBER: PCT/JP97/01824
           FILING DATE: 29-MAY-1997
           APPLICATION NUMBER: JP 165249/1996
           FILING DATE: 04-JUN-1996
      ATTORNEY/AGENT INFORMATION:
           NAME: BROWDY, Roger L.
           REGISTRATION NUMBER: 25,618
           REFERENCE/DOCKET NUMBER: IMAMURA=1
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: 202-628-5197
           TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 9:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 591 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 9:
-10-079-616-9

:gnment Scores:
ed. No.:              5.21e-194      Length:        591
ore:                  195.00         Matches:       195
:rcent Similarity:    100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            99.0%          Indels:        0
:                     6              Gaps:          0

-10-821-670A-36 (1-197) x US-10-079-616-9 (1-591)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy      121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy      141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy      161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy      181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
Db      541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

RESULT 18
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

Alignment Scores:
Pred. No.:            6e-194         Length:        689
Score:                195.00         Matches:       195
Percent Similarity:   100.0%         Conservative:  0
```

```
:t Local Similarity:  100.0%          Mismatches:    0
:ry Match:            99.0%           Indels:        0
                      6               Gaps:          0

10-821-670A-36 (1-197) x US-10-079-616-26 (1-689)

          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
            |||||||||||||||||||||||||||||||||||||||||||||
        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

;ULT 19
10-079-616-8
;equence 8, Application US/10079616
;ublication No. US20020107366A1
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
            STREET: 419 Seventh Street, N.W., Suite 300
            CITY: Washington
            STATE: D.C.
            COUNTRY: USA
            ZIP: 20004
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/10/079,616
            FILING DATE: 22-Feb-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1441 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

Alignment Scores:
Pred. No.:              1.19e-193       Length:         1441
Score:                  195.00          Matches:        195
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            99.0%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-079-616-8 (1-1441)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              |||||||||||||||||||||||||||||||||||||||||||||
```

```
       758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

SULT 20
-09-917-265-101
Sequence 101, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 101
  LENGTH: 561
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(561)
  OTHER INFORMATION:
-09-917-265-101

gnment Scores:
ed. No.:              1.21e-185      Length:         561
ore:                  187.00         Matches:        187
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            94.9%          Indels:         0
:                     3              Gaps:           0

-10-821-670A-36 (1-197) x US-09-917-265-101 (1-561)

         11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

         31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

         51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

         71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

         91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

        111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

        131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

        151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

        171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy      191 MetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||
Db      541 ATGAGCTATCTGAATGCTTCC 561

RESULT 21
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERI
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-103

Alignment Scores:
Pred. No.:              1.21e-185      Length:         561
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            94.9%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-103 (1-561)

Qy       11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy       31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy       51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy       71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy       91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy      111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy      131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy      151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy      171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy      191 MetSerTyrLeuAsnAlaSer 197
            |||||||||||||||||||||
```

```
        21 ATGAGCTATCTGAATGCTTCC 1

SULT 22
-10-821-670-101
Sequence 101, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 101
  LENGTH: 561
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(561)
10-821-670-101

gnment Scores:
d. No.:              1.21e-185      Length:        561
re:                  187.00         Matches:       187
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            94.9%          Indels:        0
                     9              Gaps:          0

-10-821-670A-36 (1-197) x US-10-821-670-101 (1-561)

        11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

        31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

        51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

        71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

        91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

       111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

       131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

       151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

       171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy         191 MetSerTyrLeuAsnAlaSer 197
               |||||||||||||||||||||
Db         541 ATGAGCTATCTGAATGCTTCC 561

RESULT 23
US-10-821-670-103/c
; Sequence 103, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-103

Alignment Scores:
Pred. No.:              1.21e-185      Length:        561
Score:                  187.00         Matches:       187
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            94.9%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-36 (1-197) x US-10-821-670-103 (1-561)

Qy          11 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 30
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy          31 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 50
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy          51 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy          71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy          91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy         111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy         131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy         151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy         171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy         191 MetSerTyrLeuAsnAlaSer 197
```

```
                    ||||||||||||||||||||
          21 ATGAGCTATCTGAATGCTTCC 1

SULT 24
-10-041-672C-2
Sequence 2, Application US/10041672C
Publication No. US20030157059A1
GENERAL INFORMATION:
 APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
 APPLICANT:  Universitat Zurich
 TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
 FILE REFERENCE: NHL-NP-36
 CURRENT APPLICATION NUMBER: US/10/041,672C
 CURRENT FILING DATE:  2002-01-08
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
  LENGTH: 669
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: feline IL-12 p35
-10-041-672C-2

ignment Scores:
ed. No.:                3.99e-46        Length:         669
ore:                    54.00           Matches:        54
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              27.4%           Indels:         0
:                       7               Gaps:           0

-10-821-670A-36 (1-197) x US-10-041-672C-2 (1-669)

          91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

         111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

         131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
             |||||||||||||||||||||||||||||||||||||||||||
         466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507

SULT 25
-09-917-265-49
Sequence 49, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(591)
  OTHER INFORMATION:
-09-917-265-49

ignment Scores:
ed. No.:                4.44e-44        Length:         591
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-49 (1-591)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 26
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

Alignment Scores:
Pred. No.:              4.44e-44        Length:         591
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            26.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-51 (1-591)

Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 27
US-10-821-670-49
; Sequence 49, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
```

```
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 49
 LENGTH: 591
 TYPE: DNA
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(591)
10-821-670-49

gnment Scores:
d. No.:              4.44e-44      Length:        591
re:                  52.00         Matches:       52
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            26.4%         Indels:        0
                     9             Gaps:          0

10-821-670A-36 (1-197) x US-10-821-670-49 (1-591)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

ULT 28
10-821-670-51/c
equence 51, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 51
 LENGTH: 591
 TYPE: DNA
 ORGANISM: Canis familiaris
10-821-670-51

gnment Scores:
d. No.:              4.44e-44      Length:        591
re:                  52.00         Matches:       52
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            26.4%         Indels:        0
                     9             Gaps:          0

10-821-670A-36 (1-197) x US-10-821-670-51 (1-591)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy      60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy      80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
Db     354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 29
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

Alignment Scores:
Pred. No.:              4.96e-44      Length:        666
Score:                  52.00         Matches:       52
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.4%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-36 (1-197) x US-09-917-265-46 (1-666)

Qy      40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy      60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy      80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
Db     313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 30
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
```

ORGANISM: Canis familiaris
-09-917-265-48

gnment Scores:

ed. No.:	4.96e-44	Length:	666
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.4%	Indels:	0
	3	Gaps:	0

-10-821-670A-36 (1-197) x US-09-917-265-48 (1-666)

```
         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319
```

SULT 31
-10-821-670-46
Sequence 46, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
LENGTH: 666
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(666)
-10-821-670-46

gnment Scores:

ed. No.:	4.96e-44	Length:	666
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.4%	Indels:	0
	9	Gaps:	0

-10-821-670A-36 (1-197) x US-10-821-670-46 (1-666)

```
         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

SULT 32

US-10-821-670-48/c
; Sequence 48, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-821-670-48

Alignment Scores:

Pred. No.:	4.96e-44	Length:	666
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	26.4%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-821-670-48 (1-666)

```
Qy          40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy          80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319
```

RESULT 33
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(897)
; OTHER INFORMATION:
US-09-917-265-104

Alignment Scores:

Pred. No.:	1.02e-43	Length:	1455
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0

```
ry Match:            26.4%          Indels:        0
                     3              Gaps:          0

10-821-670A-36 (1-197) x US-09-917-265-104 (1-1455)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

ULT 34
09-917-265-106/c
equence 106, Application US/09917265
atent No. US20020052030A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE:  2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
EQ ID NO 106
 LENGTH: 1455
 TYPE: DNA
 ORGANISM: Canis familiaris
09-917-265-106

gnment Scores:
d. No.:              1.02e-43       Length:        1455
re:                  52.00          Matches:       52
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            26.4%          Indels:        0
                     3              Gaps:          0

10-821-670A-36 (1-197) x US-09-917-265-106 (1-1455)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

ULT 35
10-821-670-104
equence 104, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-10-821-670-104

Alignment Scores:
Pred. No.:              1.02e-43       Length:        1455
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.4%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-36 (1-197) x US-10-821-670-104 (1-1455)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

RESULT 36
US-10-821-670-106/c
; Sequence 106, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-106

Alignment Scores:
Pred. No.:              1.02e-43       Length:        1455
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.4%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-36 (1-197) x US-10-821-670-106 (1-1455)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913
```

```
        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           ||||||||||||||||||||||||||||||||||||
       912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

SULT 37
-09-917-265-66
Sequence 66, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1533)
  OTHER INFORMATION:
-09-917-265-66

gnment Scores:
ed. No.:               1.07e-43      Length:          1533
ore:                   52.00         Matches:         52
cent Similarity:       100.0%        Conservative:    0
st Local Similarity:   100.0%        Mismatches:      0
ery Match:             26.4%         Indels:          0
:                      3             Gaps:            0

-10-821-670A-36 (1-197) x US-09-917-265-66 (1-1533)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
      1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

SULT 38
-09-917-265-68/c
Sequence 68, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Canis familiaris
-09-917-265-68

Alignment Scores:
Pred. No.:             1.07e-43      Length:          1533
Score:                 52.00         Matches:         52
Percent Similarity:    100.0%        Conservative:    0
Best Local Similarity: 100.0%        Mismatches:      0
Query Match:           26.4%         Indels:          0
DB:                    3             Gaps:            0

US-10-821-670A-36 (1-197) x US-09-917-265-68 (1-1533)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 39
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

Alignment Scores:
Pred. No.:             1.07e-43      Length:          1533
Score:                 52.00         Matches:         52
Percent Similarity:    100.0%        Conservative:    0
Best Local Similarity: 100.0%        Mismatches:      0
Query Match:           26.4%         Indels:          0
DB:                    9             Gaps:            0

US-10-821-670A-36 (1-197) x US-10-821-670-66 (1-1533)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 40
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
```

```
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
;EQ ID NO 68
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Canis familiaris
·10-821-670-68

.gnment Scores:
;d. No.:              1.07e-43      Length:        1533
;re:                  52.00         Matches:       52
:cent Similarity:     100.0%        Conservative:  0
;t Local Similarity:  100.0%        Mismatches:    0
;ry Match:            26.4%         Indels:        0
                      9             Gaps:          0

10-821-670A-36 (1-197) x US-10-821-670-68 (1-1533)

        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

;ULT 41
 09-917-265-61
;equence 61, Application US/09917265
 atent No. US20020052030A1
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
;EQ ID NO 61
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1599)
  OTHER INFORMATION:
·09-917-265-61

.gnment Scores:
;d. No.:              1.12e-43      Length:        1599
;re:                  52.00         Matches:       52
:cent Similarity:     100.0%        Conservative:  0
;t Local Similarity:  100.0%        Mismatches:    0
;ry Match:            26.4%         Indels:        0
                      3             Gaps:          0

US-10-821-670A-36 (1-197) x US-09-917-265-61 (1-1599)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db       1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 42
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

Alignment Scores:
Pred. No.:              1.12e-43      Length:        1599
Score:                  52.00         Matches:       52
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            26.4%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-36 (1-197) x US-09-917-265-63 (1-1599)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 43
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
```

SEQ ID NO 61
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
-10-821-670-61

:gnment Scores:

ed. No.:	1.12e-43	Length:	1599
ore:	52.00	Matches:	52
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.4%	Indels:	0
:	9	Gaps:	0

-10-821-670A-36 (1-197) x US-10-821-670-61 (1-1599)

```
        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
      1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281
```

SULT 44
-10-821-670-63/c
Sequence 63, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
-10-821-670-63

:gnment Scores:

ed. No.:	1.12e-43	Length:	1599
ore:	52.00	Matches:	52
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.4%	Indels:	0
:	9	Gaps:	0

-10-821-670A-36 (1-197) x US-10-821-670-63 (1-1599)

```
        40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        60 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        80 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 91
           |||||||||||||||||||||||||||||||||||
```

Db 354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 45
US-10-741-601-946
; Sequence 946, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 946
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-946

Alignment Scores:

Pred. No.:	2.14e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-741-601-946 (1-201)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90
```

RESULT 46
US-10-741-601-947
; Sequence 947, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 947
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-947

Alignment Scores:

Pred. No.:	2.14e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.7%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-741-601-947 (1-201)

```
Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        179 AlaPheArgIleArgAlaValThrIle 187
```

```
                    ||||||||||||||||||||||||||
        72 GCTTTCAGAATTCGGGCAGTGACTATT 98

SULT 47
10-741-601-951
Sequence 951, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE:  2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 951
 LENGTH: 201
 TYPE: DNA
 ORGANISM: Homo sapiens
10-741-601-951

gnment Scores:
d. No.:                2.14e-20        Length:         201
re:                    29.00           Matches:        29
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              14.7%           Indels:         0
                       8               Gaps:           0

10-821-670A-36 (1-197) x US-10-741-601-951 (1-201)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       173 GCTTTCAGAATTCGGGCAGTGACTATT 199

SULT 48
10-741-601-955
Sequence 955, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE:  2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 955
 LENGTH: 201
 TYPE: DNA
 ORGANISM: Homo sapiens
10-741-601-955

gnment Scores:
d. No.:                2.14e-20        Length:         201
re:                    29.00           Matches:        29
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              14.7%           Indels:         0
                       8               Gaps:           0

10-821-670A-36 (1-197) x US-10-741-601-955 (1-201)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db          64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 49
US-10-741-601-957
; Sequence 957, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 957
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-957

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     8               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-601-957 (1-201)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db          72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 50
US-10-741-601-960
; Sequence 960, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 960
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-960

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     8               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-601-960 (1-201)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172
```

```
       179 AlaPheArgIleArgAlaValThrIle 187
           ||||||||||||||||||||||||||||
       173 GCTTTCAGAATTCGGGCAGTGACTATT 199

SULT 51
-10-741-601-7417
Sequence 7417, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001500
 CURRENT APPLICATION NUMBER: US/10/741,601
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 26415
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7417
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-7417

:gnment Scores:
ed. No.:              2.14e-20       Length:         201
ore:                  29.00          Matches:        29
:cent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            14.7%          Indels:         0
:                     8              Gaps:           0

-10-821-670A-36 (1-197) x US-10-741-601-7417 (1-201)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

       179 AlaPheArgIleArgAlaValThrIle 187
           ||||||||||||||||||||||||||||
        64 GCTTTCAGAATTCGGGCAGTGACTATT 90

SULT 52
-10-741-601-7418
Sequence 7418, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001500
 CURRENT APPLICATION NUMBER: US/10/741,601
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 26415
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7418
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-7418

:gnment Scores:
ed. No.:              2.14e-20       Length:         201
ore:                  29.00          Matches:        29
:cent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            14.7%          Indels:         0
:                     8              Gaps:           0

-10-821-670A-36 (1-197) x US-10-741-601-7418 (1-201)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               ||||||||||||||||||||||||||||
Db          72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 53
US-10-741-601-7431
; Sequence 7431, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7431
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7431

Alignment Scores:
Pred. No.:              2.14e-20       Length:         201
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            14.7%          Indels:         0
DB:                     8              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-601-7431 (1-201)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               ||||||||||||||||||||||||||||
Db         173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 54
US-10-741-601-11370/c
; Sequence 11370, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11370
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11370

Alignment Scores:
Pred. No.:              2.14e-20       Length:         201
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            14.7%          Indels:         0
DB:                     8              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-601-11370 (1-201)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       138 GCTTTCAGAATTCGGGCAGTGACTATT 112
```

```
;ULT 55
 10-741-601-11372/c
;equence 11372, Application US/10741601
'ublication No. US20040166519A1
;ENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001500
 CURRENT APPLICATION NUMBER: US/10/741,601
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 26415
 SOFTWARE: FastSEQ for Windows Version 4.0
;EQ ID NO 11372
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-11372

.gnment Scores:
:d. No.:                2.14e-20        Length:         201
)re:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              14.7%           Indels:         0
                        8               Gaps:           0

-10-821-670A-36 (1-197) x US-10-741-601-11372 (1-201)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       130 GCTTTCAGAATTCGGGCAGTGACTATT 104
```

```
;ULT 56
 10-741-601-11417/c
;equence 11417, Application US/10741601
'ublication No. US20040166519A1
;ENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001500
 CURRENT APPLICATION NUMBER: US/10/741,601
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 26415
 SOFTWARE: FastSEQ for Windows Version 4.0
;EQ ID NO 11417
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-11417

.gnment Scores:
:d. No.:                2.14e-20        Length:         201
)re:                    29.00           Matches:        29
'cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              14.7%           Indels:         0
                        8               Gaps:           0

 10-821-670A-36 (1-197) x US-10-741-601-11417 (1-201)
```

```
Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db          29 GCTTTCAGAATTCGGGCAGTGACTATT 3
```

```
RESULT 57
US-10-741-600-3487
; Sequence 3487, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3487
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3487

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-600-3487 (1-201)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db          64 GCTTTCAGAATTCGGGCAGTGACTATT 90
```

```
RESULT 58
US-10-741-600-3488
; Sequence 3488, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3488
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3488

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-600-3488 (1-201)
```

```
        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

SULT 59
-10-741-600-3492
Sequence 3492, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3492
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-600-3492

:gnment Scores:
ed. No.:                2.14e-20        Length:         201
ore:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       9               Gaps:           0

-10-821-670A-36 (1-197) x US-10-741-600-3492 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

SULT 60
-10-741-600-3496
Sequence 3496, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3496
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-600-3496

:gnment Scores:
ed. No.:                2.14e-20        Length:         201
ore:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       9               Gaps:           0
```

```
US-10-821-670A-36 (1-197) x US-10-741-600-3496 (1-201)

Qy          159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy          179 AlaPheArgIleArgAlaValThrIle 187
                |||||||||||||||||||||||||||
Db           64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 61
US-10-741-600-3498
; Sequence 3498, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3498
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3498

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-600-3498 (1-201)

Qy          159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy          179 AlaPheArgIleArgAlaValThrIle 187
                |||||||||||||||||||||||||||
Db           72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 62
US-10-741-600-3501
; Sequence 3501, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3501
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3501

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     9               Gaps:           0
```

```
-10-821-670A-36 (1-197) x US-10-741-600-3501 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

;ULT 63
 10-741-600-20963
;equence 20963, Application US/10741600
'ublication No. US20050026169A1
;ENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
;EQ ID NO 20963
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
 10-741-600-20963

.gnment Scores:
;d. No.:                2.14e-20        Length:         201
)re:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
;t Local Similarity:    100.0%          Mismatches:     0
;ry Match:              14.7%           Indels:         0
                        9               Gaps:           0

-10-821-670A-36 (1-197) x US-10-741-600-20963 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

;ULT 64
-10-741-600-20964
;equence 20964, Application US/10741600
'ublication No. US20050026169A1
;ENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
;EQ ID NO 20964
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
 10-741-600-20964

.gnment Scores:
;d. No.:                2.14e-20        Length:         201
)re:                    29.00           Matches:        29
'cent Similarity:       100.0%          Conservative:   0
;t Local Similarity:    100.0%          Mismatches:     0
;ry Match:              14.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-600-20964 (1-201)

Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy      179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
Db       72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 65
US-10-741-600-20992
; Sequence 20992, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20992
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20992

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-741-600-20992 (1-201)

Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy      179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
Db      173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 66
US-10-741-600-28831/c
; Sequence 28831, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28831
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28831

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
```

```
ery Match:            14.7%          Indels:        0
:                     9              Gaps:          0

-10-821-670A-36 (1-197) x US-10-741-600-28831 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        138 GCTTTCAGAATTCGGGCAGTGACTATT 112

SULT 67
-10-741-600-28833/c
Sequence 28833, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28833
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-600-28833

:gnment Scores:
ed. No.:              2.14e-20       Length:        201
ore:                  29.00          Matches:       29
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            14.7%          Indels:        0
:                     9              Gaps:          0

-10-821-670A-36 (1-197) x US-10-741-600-28833 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        130 GCTTTCAGAATTCGGGCAGTGACTATT 104

SULT 68
-10-741-600-28877/c
Sequence 28877, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28877
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-600-28877

:gnment Scores:
ed. No.:              2.14e-20       Length:        201
ore:                  29.00          Matches:       29
rcent Similarity:     100.0%         Conservative:  0
```

```
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            14.7%        Indels:        0
DB:                     9            Gaps:          0

US-10-821-670A-36 (1-197) x US-10-741-600-28877 (1-201)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db         29 GCTTTCAGAATTCGGGCAGTGACTATT 3

RESULT 69
US-10-995-561-1976
; Sequence 1976, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1976
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1976

Alignment Scores:
Pred. No.:              2.14e-20     Length:        201
Score:                  29.00        Matches:       29
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            14.7%        Indels:        0
DB:                     10           Gaps:          0

US-10-821-670A-36 (1-197) x US-10-995-561-1976 (1-201)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 70
US-10-995-561-1977
; Sequence 1977, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1977
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1977

Alignment Scores:
```

```
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-1977 (1-201)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 71
US-10-995-561-1981
Sequence 1981, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1981
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-995-561-1981

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-1981 (1-201)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 72
US-10-995-561-1986
Sequence 1986, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1986
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-995-561-1986

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-1986 (1-201)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 73
US-10-995-561-1988
; Sequence 1988, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1988
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1988

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-1988 (1-201)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 74
US-10-995-561-1991
; Sequence 1991, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1991
```

```
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-1991

:gnment Scores:
ed. No.:                2.14e-20        Length:         201
ore:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       10              Gaps:           0

-10-821-670A-36 (1-197) x US-10-995-561-1991 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

SULT 75
-10-995-561-18302
Sequence 18302, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18302
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-18302

:gnment Scores:
ed. No.:                2.14e-20        Length:         201
ore:                    29.00           Matches:        29
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       10              Gaps:           0

-10-821-670A-36 (1-197) x US-10-995-561-18302 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

SULT 76
-10-995-561-18303
Sequence 18303, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18303
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-995-561-18303

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-18303 (1-201)

Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy      179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
Db       72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 77
US-10-995-561-18335
; Sequence 18335, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18335
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18335

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-18335 (1-201)

Qy      159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy      179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
Db      173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 78
US-10-995-561-26362/c
; Sequence 26362, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
```

```
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE:  2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26362
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-995-561-26362

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
                        10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-26362 (1-201)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
        29 GCTTTCAGAATTCGGGCAGTGACTATT 3

RESULT 79
US-10-995-561-26545/c
Sequence 26545, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION:  DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE:  2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26545
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-995-561-26545

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
                        10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-26545 (1-201)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       138 GCTTTCAGAATTCGGGCAGTGACTATT 112

RESULT 80
US-10-995-561-26548/c
Sequence 26548, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION:  DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE:  2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26548
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-995-561-26548

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-26548 (1-201)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         130 GCTTTCAGAATTCGGGCAGTGACTATT 104

RESULT 81
US-10-995-561-73346/c
Sequence 73346, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION:  DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE:  2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73346
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-995-561-73346

Alignment Scores:
Pred. No.:              2.14e-20        Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-36 (1-197) x US-10-995-561-73346 (1-201)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         138 GCTTTCAGAATTCGGGCAGTGACTATT 112

RESULT 82
US-10-995-561-73349/c
Sequence 73349, Application US/10995561
```

```
Publication No. US20050272054A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73349
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-73349

gnment Scores:
d. No.:                2.14e-20        Length:         201
re:                    29.00           Matches:        29
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              14.7%           Indels:         0
                       10              Gaps:           0

-10-821-670A-36 (1-197) x US-10-995-561-73349 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        130 GCTTTCAGAATTCGGGCAGTGACTATT 104

SULT 83
-10-995-561-73383/c
Sequence 73383, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73383
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-73383

gnment Scores:
d. No.:                2.14e-20        Length:         201
re:                    29.00           Matches:        29
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              14.7%           Indels:         0
                       10              Gaps:           0

-10-821-670A-36 (1-197) x US-10-995-561-73383 (1-201)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
         29 GCTTTCAGAATTCGGGCAGTGACTATT 3
```

```
RESULT 84
US-09-754-014-6
; Sequence 6, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 660 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-754-014-6

Alignment Scores:
Pred. No.:              6.41e-20        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-754-014-6 (1-660)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 85
US-09-754-014-7
; Sequence 7, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
```

```
                Bruce Freimark
                Deepa Deshpande
      TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                          AND USES
      NUMBER OF SEQUENCES: 12
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Lyon & Lyon
           STREET: 633 West Fifth Street
                   Suite 4700
           CITY: Los Angeles
           STATE: California
           COUNTRY: U.S.A.
           ZIP: 90071-2066
      COMPUTER READABLE FORM:
           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                        storage
           COMPUTER: IBM Compatible
           OPERATING SYSTEM: IBM P.C. DOS 5.0
           SOFTWARE: FastSEQ for Windows 2.0
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/754,014
           FILING DATE: 03-Jan-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/948,958
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Berkman, Charles S.
           REGISTRATION NUMBER: 38,077
           REFERENCE/DOCKET NUMBER: 226/284
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 7:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 660 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
09-754-014-7

gnment Scores:
d. No.:              6.41e-20        Length:         660
re:                  29.00           Matches:        29
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            14.7%           Indels:         0
                     3               Gaps:           0

10-821-670A-36 (1-197) x US-09-754-014-7 (1-660)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       601 GCCTTCCGCATCCGCGCCGTGACCATC 627

ULT 86
09-754-014-8
equence 8, Application US/09754014
atent No. US20020119940A1
  GENERAL INFORMATION:
      APPLICANT: Jeff No. US20020119940A1dstrom
                 Bruce Freimark
                 Deepa Deshpande
      TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                          AND USES
      NUMBER OF SEQUENCES: 12
      CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Lyon & Lyon
;           STREET: 633 West Fifth Street
;                   Suite 4700
;           CITY: Los Angeles
;           STATE: California
;           COUNTRY: U.S.A.
;           ZIP: 90071-2066
;      COMPUTER READABLE FORM:
;           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                        storage
;           COMPUTER: IBM Compatible
;           OPERATING SYSTEM: IBM P.C. DOS 5.0
;           SOFTWARE: FastSEQ for Windows 2.0
;      CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/754,014
;           FILING DATE: 03-Jan-2001
;           CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/948,958
;           FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;           NAME: Berkman, Charles S.
;           REGISTRATION NUMBER: 38,077
;           REFERENCE/DOCKET NUMBER: 226/284
;      TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (213) 489-1600
;           TELEFAX: (213) 955-0440
;           TELEX: 67-3510
;  INFORMATION FOR SEQ ID NO: 8:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 660 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-754-014-8

Alignment Scores:
Pred. No.:              6.41e-20        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-754-014-8 (1-660)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         601 GCCTTCCGCATCCGGGCCGTGACCATC 627

RESULT 87
US-09-836-866-4
; Sequence 4, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020123473A1dstrom, Jeff
;                   Freimark, Bruce
;                   Deshpande, Deepa
;        TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                            DELIVERY SYTEMS AND USES
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
```

```
        ZIP: 90071-2066
      COMPUTER READABLE FORM:
        MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                     storage
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: IBM P.C. DOS 5.0
        SOFTWARE: FastSEQ for Windows 2.0
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/836,866
        FILING DATE: 16-Apr-2001
        CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/949,160
        FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
        NAME: Warburg, Richard J.
        REGISTRATION NUMBER: 32,327
        REFERENCE/DOCKET NUMBER: 226/285
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (213) 489-1600
        TELEFAX: (213) 955-0440
        TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 4:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 660 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
-09-836-866-4

gnment Scores:
d. No.:                6.41e-20        Length:         660
re:                    29.00           Matches:        29
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              14.7%           Indels:         0
                       3               Gaps:           0

-10-821-670A-36 (1-197) x US-09-836-866-4 (1-660)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 88
-10-267-384-199
Sequence 199, Application US/10267384
Publication No. US20030198623A1
  GENERAL INFORMATION:
      APPLICANT: Paoletti, Enzo
                 Tartaglia, James
                 Cox, William I.
      TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
      NUMBER OF SEQUENCES: 217
      CORRESPONDENCE ADDRESS:
        ADDRESSEE: Curtis, Morris & Safford
        STREET: 530 Fifth Avenue
        CITY: New York
        STATE: NY
        COUNTRY: USA
        ZIP: 10036
      COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/10/267,384
;       FILING DATE: 09-Oct-2002
;       CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Frommer, William S.
;       REGISTRATION NUMBER: 25,506
;       REFERENCE/DOCKET NUMBER: 454310-2530
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 840-3333
;       TELEFAX: (212) 840-0712
;       TELEX: 425066CURTMS
;  INFORMATION FOR SEQ ID NO: 199:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 721 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-10-267-384-199

Alignment Scores:
Pred. No.:              6.96e-20        Length:         721
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-267-384-199 (1-721)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 89
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Medlen & Carroll, LLP
;         STREET: 220 Montgomery Street, Suite 2200
;         CITY: San Francisco
;         STATE: California
;         COUNTRY: United States of America
;         ZIP: 94104
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/09/826,025
;         FILING DATE: 04-Apr-2001
;         CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: 08/838,702
;         FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;         NAME: Ingolia, Diane E.
;         REGISTRATION NUMBER: 40,027
;         REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (415) 705-8410
;         TELEFAX: (415) 397-8338
;  INFORMATION FOR SEQ ID NO: 21:
```

```
      SEQUENCE CHARACTERISTICS:
           LENGTH: 762 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
           DESCRIPTION: /desc = "DNA"
      SEQUENCE DESCRIPTION: SEQ ID NO: 21:
09-826-025-21

gnment Scores:
d. No.:                7.32e-20        Length:         762
re:                    29.00           Matches:        29
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              14.7%           Indels:         0
                       3               Gaps:           0

10-821-670A-36 (1-197) x US-09-826-025-21 (1-762)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||||
       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

ULT 90
10-785-577-21
equence 21, Application US/10785577
ublication No. US20040237129A1
 GENERAL INFORMATION:
      APPLICANT: Chang, Lung-Ji
      TITLE OF INVENTION: Combination Immunogene Therapy
      NUMBER OF SEQUENCES: 25
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Medlen & Carroll, LLP
           STREET: 220 Montgomery Street, Suite 2200
           CITY: San Francisco
           STATE: California
           COUNTRY: United States of America
           ZIP: 94104
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/10/785,577
           FILING DATE: 23-Feb-2004
           CLASSIFICATION: 424
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: US/08/838,702
           FILING DATE: 9-Apr-1997
      ATTORNEY/AGENT INFORMATION:
           NAME: Ingolia, Diane E.
           REGISTRATION NUMBER: 40,027
           REFERENCE/DOCKET NUMBER: CHANG-02687
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (415) 705-8410
           TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 21:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 762 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
           DESCRIPTION: /desc = "DNA"
      SEQUENCE DESCRIPTION: SEQ ID NO: 21:
10-785-577-21

Alignment Scores:
Pred. No.:                7.32e-20        Length:         762
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              14.7%           Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-785-577-21 (1-762)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 91
US-10-688-845-57
; Sequence 57, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
;  APPLICANT: Lotze, Michael T
;  APPLICANT:  Tahara, Hideaki
;  TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
;  FILE REFERENCE: UPT-004
;  CURRENT APPLICATION NUMBER: US/10/688,845
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,865
;  PRIOR FILING DATE: 2002-10-15
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-688-845-57

Alignment Scores:
Pred. No.:                7.32e-20        Length:         762
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              14.7%           Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-688-845-57 (1-762)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||||
Db         703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 92
US-10-373-456-19
; Sequence 19, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 811
```

TYPE: DNA
ORGANISM: Homo sapiens
-10-373-456-19

:gnment Scores:
ed. No.: 7.76e-20 Length: 811
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 14.7% Indels: 0
: 7 Gaps: 0

-10-821-670A-36 (1-197) x US-10-373-456-19 (1-811)

159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
489 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 548

179 AlaPheArgIleArgAlaValThrIle 187
|||||||||||||||||||||||||||
549 GCTTTCAGAATTCGGGCAGTGACTATT 575

SULT 93
-10-349-507-4
Sequence 4, Application US/10349507
Publication No. US20030199002A1
GENERAL INFORMATION:
APPLICANT: Hekimi , Siegfried
APPLICANT: Jiang , Ning
APPLICANT: Benard, Claire
APPLICANT: Kebir , Hania
APPLICANT: McCright, Brenton
APPLICANT: Lakowski , Bernard
TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REFERENCE: 11202-006-999
CURRENT APPLICATION NUMBER: US/10/349,507
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 10/312,187
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: PCT/CA01/00913
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/213,174
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/254,932
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 856
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (170)...(826)
-10-349-507-4

:gnment Scores:
ed. No.: 8.15e-20 Length: 856
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 14.7% Indels: 0
: 7 Gaps: 0

-10-821-670A-36 (1-197) x US-10-349-507-4 (1-856)

159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

179 AlaPheArgIleArgAlaValThrIle 187
|||||||||||||||||||||||||||
770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 94
US-10-267-565-4
; Sequence 4, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
; APPLICANT: Gately, Maurice
; APPLICANT: Gubler, Ulrich
; APPLICANT: Hulmes, Jeffery
; APPLICANT: Podlaski, Frank
; APPLICANT: Stern, Alvin
; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
; TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THERETO
; FILE REFERENCE: 11126-005
; CURRENT APPLICATION NUMBER: US/10/267,565
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 09/401,839
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/459,151
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 08/205,011
; PRIOR FILING DATE: 1994-03-02
; PRIOR APPLICATION NUMBER: 07/857,023
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/572,284
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: 07/520,935
; PRIOR FILING DATE: 1990-05-09
; PRIOR APPLICATION NUMBER: 07/455,708
; PRIOR FILING DATE: 1989-12-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)...(826)
US-10-267-565-4

Alignment Scores:
Pred. No.: 8.15e-20 Length: 856
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.7% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-36 (1-197) x US-10-267-565-4 (1-856)

Qy 159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy 179 AlaPheArgIleArgAlaValThrIle 187
|||||||||||||||||||||||||||
Db 770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 95
US-10-373-456-17
; Sequence 17, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
; APPLICANT: Podhajcer, Osvaldo
; TITLE OF INVENTION: Anti-Tumor Vaccine and Method
; FILE REFERENCE: 1423P-US/101141-14
; CURRENT APPLICATION NUMBER: US/10/373,456
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,836
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 20

```
SOFTWARE: PatentIn version 3.1
EQ ID NO 17
 LENGTH: 868
 TYPE: DNA
 ORGANISM: Homo sapiens
10-373-456-17

gnment Scores:
d. No.:                8.26e-20        Length:         868
re:                    29.00           Matches:        29
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              14.7%           Indels:         0
                       7               Gaps:           0

10-821-670A-36 (1-197) x US-10-373-456-17 (1-868)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       552 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 611

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||
       612 GCTTTCAGAATTCGGGCAGTGACTATT 638

ULT 96
10-172-399-5
equence 5, Application US/10172399
ublication No. US20030045495A1
ENERAL INFORMATION:
APPLICANT: Li, Chuan-Yuan
APPLICANT:  Dewhirst, Mark
APPLICANT:  Huang, Qian
TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
FILE REFERENCE: 180-129
CURRENT APPLICATION NUMBER: US/10/172,399
CURRENT FILING DATE:  2002-06-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
EQ ID NO 5
 LENGTH: 1026
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (170)..(829)
10-172-399-5

gnment Scores:
d. No.:                9.64e-20        Length:         1026
re:                    29.00           Matches:        29
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              14.7%           Indels:         0
                       6               Gaps:           0

10-821-670A-36 (1-197) x US-10-172-399-5 (1-1026)

       159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

       179 AlaPheArgIleArgAlaValThrIle 187
           |||||||||||||||||||||||||
       770 GCTTTCAGAATTCGGGCAGTGACTATT 796

ULT 97
10-641-643-1041
equence 1041, Application US/10641643
ublication No. US20040077003A1
 GENERAL INFORMATION:
      APPLICANT: Cocks, Benjamin G.
                 Susan G. Stuart
;                Jeffrey J. Seilhamer
;       TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;                           GENE EXPRESSION
;       NUMBER OF SEQUENCES: 1508
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;            STREET: 3174 PORTER DRIVE
;            CITY: PALO ALTO
;            STATE: CALIFORNIA
;            COUNTRY: USA
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/641,643
;            FILING DATE: 14-Aug-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Zeller, Karen J.
;            REGISTRATION NUMBER: 37,071
;            REFERENCE/DOCKET NUMBER: PA-0001 US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (650) 855-0555
;            TELEFAX: (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1041:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1026 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       IMMEDIATE SOURCE:
;            LIBRARY: GENBANK
;            CLONE: g180623
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1041 :
US-10-641-643-1041

Alignment Scores:
Pred. No.:             9.64e-20        Length:         1026
Score:                 29.00           Matches:        29
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           14.7%           Indels:         0
DB:                    8               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-641-643-1041 (1-1026)

Qy         159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy         179 AlaPheArgIleArgAlaValThrIle 187
               |||||||||||||||||||||||||
Db         770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 98
US-10-603-064-6
; Sequence 6, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
```

```
 PRIOR APPLICATION NUMBER: 60/147,924
 PRIOR FILING DATE: 1999-08-09
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
  LENGTH: 1287
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
  OTHER INFORMATION: fusion protein coding sequence
-10-603-064-6

:gnment Scores:
ed. No.:                1.19e-19        Length:         1287
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       8               Gaps:           0

-10-821-670A-36 (1-197) x US-10-603-064-6 (1-1287)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254

SULT 99
-10-476-960-3
Sequence 3, Application US/10476960
Publication No. US20040248828A1
GENERAL INFORMATION:
 APPLICANT: Brenda F. Baker
 APPLICANT:  Susan M. Freier
 APPLICANT:  Isis Pharmaceuticals, Inc.
 TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
 FILE REFERENCE: RTSP-0392
 CURRENT APPLICATION NUMBER: US/10/476,960
 CURRENT FILING DATE:  2003-11-05
 PRIOR APPLICATION NUMBER: 09/851,520
 PRIOR FILING DATE: 2001-05-07
 NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
  LENGTH: 1316
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (102)...(863)
-10-476-960-3

:gnment Scores:
ed. No.:                1.21e-19        Length:         1316
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              14.7%           Indels:         0
:                       9               Gaps:           0

-10-821-670A-36 (1-197) x US-10-476-960-3 (1-1316)

        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

        179 AlaPheArgIleArgAlaValThrIle 187
            |||||||||||||||||||||||||||
        804 GCTTTCAGAATTCGGGCAGTGACTATT 830
```

```
RESULT 100
US-11-089-191-3
; Sequence 3, Application US/11089191
; Publication No. US20050261228A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Susan Gregory
;  APPLICANT:  Ronnie C. Hanecak
;  APPLICANT:  Kevin P. Anderson
;  APPLICANT:  Ming-Yi Chiang
;  APPLICANT:  Vickie Brown-Driver
;  APPLICANT:  David J. Ecker
;  APPLICANT:  Timothy Vickers
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Eric G. Marcusson
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Sanjay Bhanot
;  APPLICANT:  Elizabeth J. Ackermann
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: BNDL-0021US.P1
;  CURRENT APPLICATION NUMBER: US/11/089,191
;  CURRENT FILING DATE:  2005-03-23
;  PRIOR APPLICATION NUMBER: 10/476,960
;  PRIOR FILING DATE: 2003-11-07
;  PRIOR APPLICATION NUMBER: PCT/US02/13871
;  PRIOR FILING DATE: 2002-05-01
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  PRIOR APPLICATION NUMBER: 10/67,236
;  PRIOR FILING DATE: 2003-09-17
;  PRIOR APPLICATION NUMBER: 10/038,335
;  PRIOR FILING DATE: 2002-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
;  PRIOR APPLICATION NUMBER: 10/515,546
;  PRIOR FILING DATE: 2004-11-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;    LENGTH: 1316
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (102)...(863)
US-11-089-191-3

Alignment Scores:
Pred. No.:              1.21e-19        Length:         1316
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.7%           Indels:         0
DB:                     15              Gaps:           0

US-10-821-670A-36 (1-197) x US-11-089-191-3 (1-1316)

Qy        159 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

Qy        179 AlaPheArgIleArgAlaValThrIle 187
              |||||||||||||||||||||||||||
Db        804 GCTTTCAGAATTCGGGCAGTGACTATT 830
```

arch completed: June 12, 2006, 17:15:34
time : 957.372 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 02:09:37 ; Search time 13.4261 Seconds
(without alignments)
2793.504 Million cell updates/sec

le: US-10-821-670A-36
fect score: 197
quence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 253354 seqs, 63461778 residues

d size: 1

al number of hits satisfying chosen parameters: 506227

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
)DEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110508_27905/app_query.fasta_1
B=Published_Applications_NA_New -QFMT=fastap
UFFIX=oligo.p2n.200scores.rnpbn -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
NITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
)CALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
)RM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
SER=US10821670_@CGN_1_1_62_@runat_07062006_110508_27905 -NCPU=6 -ICPU=3
) MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	9	4.6	2984	7	US-11-293-697-34	Sequence 34, Appl
2	8	4.1	528	6	US-10-322-836-19	Sequence 19, Appl
3	8	4.1	879	6	US-10-322-836-17	Sequence 17, Appl
4	8	4.1	1017	6	US-10-322-836-15	Sequence 15, Appl
5	8	4.1	1248	6	US-10-322-836-27	Sequence 27, Appl
6	8	4.1	1293	6	US-10-322-836-5	Sequence 5, Appli
7	8	4.1	1317	6	US-10-322-836-41	Sequence 41, Appl
8	8	4.1	1455	6	US-10-322-836-39	Sequence 39, Appl
9	8	4.1	1599	6	US-10-322-836-25	Sequence 25, Appl
10	8	4.1	1644	6	US-10-322-836-3	Sequence 3, Appli
11	8	4.1	1737	6	US-10-322-836-23	Sequence 23, Appl
12	8	4.1	1782	6	US-10-322-836-1	Sequence 1, Appli
13	8	4.1	2021	6	US-10-953-349-4560	Sequence 4560, Ap
14	8	4.1	2037	6	US-10-322-836-45	Sequence 45, Appl
15	8	4.1	2082	6	US-10-322-836-33	Sequence 33, Appl
16	8	4.1	2175	6	US-10-322-836-43	Sequence 43, Appl
17	8	4.1	2220	6	US-10-322-836-31	Sequence 31, Appl
18	8	4.1	3791	6	US-10-530-792A-1	Sequence 1, Appli
19	8	4.1	6663	7	US-11-217-529-3234	Sequence 3234, Ap
20	7	3.6	331	6	US-10-488-619-837	Sequence 837, App
c 21	7	3.6	399	6	US-10-148-883-27	Sequence 27, Appl
c 22	7	3.6	582	6	US-10-953-349-25251	Sequence 25251, A
23	7	3.6	660	7	US-11-217-529-81369	Sequence 81369, A
c 24	7	3.6	704	6	US-10-488-619-2648	Sequence 2648, Ap
25	7	3.6	894	7	US-11-217-529-1263	Sequence 1263, Ap
26	7	3.6	903	7	US-11-264-737-102	Sequence 102, App
27	7	3.6	906	6	US-10-953-349-4834	Sequence 4834, Ap
28	7	3.6	921	7	US-11-217-529-5460	Sequence 5460, Ap
29	7	3.6	953	7	US-11-311-754-5	Sequence 5, Appli
30	7	3.6	979	6	US-10-953-349-12779	Sequence 12779, A
c 31	7	3.6	994	6	US-10-953-349-28356	Sequence 28356, A
c 32	7	3.6	997	6	US-10-560-723-79	Sequence 79, Appl
33	7	3.6	1056	6	US-10-953-349-26293	Sequence 26293, A
34	7	3.6	1062	6	US-10-953-349-39566	Sequence 39566, A
c 35	7	3.6	1202	6	US-10-953-349-17414	Sequence 17414, A
c 36	7	3.6	1236	7	US-11-217-529-1292	Sequence 1292, Ap
c 37	7	3.6	1313	6	US-10-953-349-24555	Sequence 24555, A
c 38	7	3.6	1454	6	US-10-953-349-35965	Sequence 35965, A
39	7	3.6	1483	6	US-10-953-349-36433	Sequence 36433, A
40	7	3.6	1504	6	US-10-953-349-33213	Sequence 33213, A
c 41	7	3.6	1538	6	US-10-953-349-17700	Sequence 17700, A
c 42	7	3.6	1660	6	US-10-953-349-24275	Sequence 24275, A
c 43	7	3.6	1716	7	US-11-313-556-3	Sequence 3, Appli
44	7	3.6	1750	6	US-10-953-349-34792	Sequence 34792, A
c 45	7	3.6	1761	7	US-11-217-529-174380	Sequence 174380,
c 46	7	3.6	1804	7	US-11-251-465-7	Sequence 7, Appli
47	7	3.6	1831	7	US-11-311-754-27	Sequence 27, Appl
48	7	3.6	1868	6	US-10-505-928-693	Sequence 693, App
c 49	7	3.6	1914	6	US-10-953-349-11252	Sequence 11252, A
50	7	3.6	1933	7	US-11-293-697-275	Sequence 275, App
c 51	7	3.6	2036	7	US-11-293-697-1094	Sequence 1094, Ap
c 52	7	3.6	2037	7	US-11-217-529-77609	Sequence 77609, A
53	7	3.6	2126	7	US-11-293-697-1972	Sequence 1972, Ap
54	7	3.6	2241	7	US-11-217-529-2489	Sequence 2489, Ap
55	7	3.6	2275	7	US-11-293-697-507	Sequence 507, App
c 56	7	3.6	2315	6	US-10-511-937-649	Sequence 649, App
57	7	3.6	2651	6	US-10-196-749-135	Sequence 135, App
58	7	3.6	2651	7	US-11-101-316-23	Sequence 23, Appl
59	7	3.6	2662	7	US-11-293-697-753	Sequence 753, App
60	7	3.6	2805	7	US-11-217-529-82539	Sequence 82539, A
c 61	7	3.6	2905	7	US-11-293-697-74	Sequence 74, Appl
62	7	3.6	3138	7	US-11-312-958-55	Sequence 55, Appl
63	7	3.6	3294	7	US-11-293-697-1397	Sequence 1397, Ap
c 64	7	3.6	3558	6	US-10-505-928-814	Sequence 814, App
c 65	7	3.6	7422	7	US-11-217-529-1506	Sequence 1506, Ap
c 66	7	3.6	7758	6	US-10-505-928-236	Sequence 236, App
c 67	7	3.6	10660	7	US-11-264-737-165	Sequence 165, App
68	6	3.0	22	7	US-11-266-409-9	Sequence 9, Appli
69	6	3.0	25	7	US-11-217-529-36402	Sequence 36402, A
c 70	6	3.0	25	7	US-11-217-529-47657	Sequence 47657, A
71	6	3.0	25	7	US-11-217-529-87245	Sequence 87245, A
c 72	6	3.0	25	7	US-11-217-529-88955	Sequence 88955, A
73	6	3.0	25	7	US-11-217-529-109690	Sequence 109690,
74	6	3.0	25	7	US-11-217-529-148883	Sequence 148883,
75	6	3.0	25	7	US-11-217-529-162336	Sequence 162336,
76	6	3.0	25	7	US-11-217-529-162342	Sequence 162342,
c 77	6	3.0	25	7	US-11-217-529-184372	Sequence 184372,
c 78	6	3.0	51	7	US-11-143-642-246	Sequence 246, App
c 79	6	3.0	69	7	US-11-296-092-22	Sequence 22, Appl
c 80	6	3.0	84	6	US-10-525-817-154	Sequence 154, App
c 81	6	3.0	84	6	US-10-525-817-155	Sequence 155, App
c 82	6	3.0	84	6	US-10-525-817-156	Sequence 156, App

83	6	3.0	84	6	US-10-525-817-157	Sequence 157, App
84	6	3.0	93	7	US-11-217-529-6033	Sequence 6033, Ap
85	6	3.0	114	6	US-10-471-571A-5635	Sequence 5635, Ap
86	6	3.0	162	7	US-11-217-529-81244	Sequence 81244, A
87	6	3.0	205	6	US-10-148-883-21	Sequence 21, Appl
88	6	3.0	213	6	US-10-471-571A-4689	Sequence 4689, Ap
89	6	3.0	231	7	US-11-217-529-174474	Sequence 174474,
90	6	3.0	276	7	US-11-217-529-166542	Sequence 166542,
91	6	3.0	303	7	US-11-217-529-5007	Sequence 5007, Ap
92	6	3.0	303	7	US-11-217-529-5166	Sequence 5166, Ap
93	6	3.0	303	7	US-11-217-529-80985	Sequence 80985, A
94	6	3.0	303	7	US-11-217-529-81183	Sequence 81183, A
95	6	3.0	303	7	US-11-217-529-174171	Sequence 174171,
96	6	3.0	310	7	US-11-301-554-610	Sequence 610, App
97	6	3.0	327	7	US-11-217-529-4461	Sequence 4461, Ap
98	6	3.0	336	7	US-11-254-679-18	Sequence 18, Appl
99	6	3.0	345	6	US-10-511-937-623	Sequence 623, App
100	6	3.0	351	7	US-11-254-679-20	Sequence 20, Appl
101	6	3.0	362	7	US-11-301-554-1167	Sequence 1167, Ap
102	6	3.0	389	6	US-10-953-349-18005	Sequence 18005, A
103	6	3.0	389	7	US-11-301-554-900	Sequence 900, App
104	6	3.0	390	6	US-10-488-619-2081	Sequence 2081, Ap
105	6	3.0	400	6	US-10-488-619-2364	Sequence 2364, Ap
106	6	3.0	416	6	US-10-488-619-91	Sequence 91, Appl
107	6	3.0	421	6	US-10-488-619-316	Sequence 316, App
108	6	3.0	423	7	US-11-301-554-573	Sequence 573, App
109	6	3.0	437	6	US-10-560-723-109	Sequence 109, App
110	6	3.0	438	6	US-10-488-619-826	Sequence 826, App
111	6	3.0	438	6	US-10-488-619-2365	Sequence 2365, Ap
112	6	3.0	443	6	US-10-953-349-13876	Sequence 13876, A
113	6	3.0	463	6	US-10-488-619-2614	Sequence 2614, Ap
114	6	3.0	470	6	US-10-488-619-338	Sequence 338, App
115	6	3.0	474	6	US-10-473-173-278	Sequence 278, App
116	6	3.0	474	7	US-11-217-529-3714	Sequence 3714, Ap
117	6	3.0	477	6	US-10-148-883-20	Sequence 20, Appl
118	6	3.0	480	7	US-11-301-554-1170	Sequence 1170, Ap
119	6	3.0	480	7	US-11-297-957-5	Sequence 5, Appli
120	6	3.0	500	7	US-11-136-524-87	Sequence 87, Appl
121	6	3.0	508	7	US-11-296-092-18	Sequence 18, Appl
122	6	3.0	508	7	US-11-296-092-19	Sequence 19, Appl
123	6	3.0	511	6	US-10-511-937-2900	Sequence 2900, Ap
124	6	3.0	511	6	US-10-953-349-38082	Sequence 38082, A
125	6	3.0	517	6	US-10-473-173-459	Sequence 459, App
126	6	3.0	520	6	US-10-953-349-29838	Sequence 29838, A
127	6	3.0	522	6	US-10-488-619-1461	Sequence 1461, Ap
128	6	3.0	534	7	US-11-217-529-78894	Sequence 78894, A
129	6	3.0	536	6	US-10-953-349-10529	Sequence 10529, A
130	6	3.0	536	6	US-10-953-349-13039	Sequence 13039, A
131	6	3.0	540	7	US-11-301-554-14	Sequence 14, Appl
132	6	3.0	540	7	US-11-217-529-76012	Sequence 76012, A
133	6	3.0	552	7	US-11-217-529-4706	Sequence 4706, Ap
134	6	3.0	557	6	US-10-953-349-5665	Sequence 5665, Ap
135	6	3.0	558	7	US-11-217-529-82089	Sequence 82089, A
136	6	3.0	561	7	US-11-301-554-72	Sequence 72, Appl
137	6	3.0	564	7	US-11-301-554-729	Sequence 729, App
138	6	3.0	564	7	US-11-217-529-174198	Sequence 174198,
139	6	3.0	565	6	US-10-953-349-9446	Sequence 9446, Ap
140	6	3.0	571	6	US-10-488-619-1362	Sequence 1362, Ap
141	6	3.0	579	6	US-10-560-723-169	Sequence 169, App
142	6	3.0	594	7	US-11-217-529-342	Sequence 342, App
143	6	3.0	599	7	US-11-301-554-1892	Sequence 1892, Ap
144	6	3.0	603	7	US-11-217-529-81147	Sequence 81147, A
145	6	3.0	609	6	US-10-953-349-17062	Sequence 17062, A
146	6	3.0	611	6	US-10-511-937-3111	Sequence 3111, Ap
147	6	3.0	612	6	US-10-471-571A-3357	Sequence 3357, Ap
148	6	3.0	615	6	US-10-953-349-18285	Sequence 18285, A
149	6	3.0	616	6	US-10-953-349-38776	Sequence 38776, A
150	6	3.0	616	6	US-10-148-883-6	Sequence 6, Appli
151	6	3.0	616	6	US-10-148-883-19	Sequence 19, Appl
152	6	3.0	617	6	US-10-953-349-31813	Sequence 31813, A
153	6	3.0	626	6	US-10-953-349-38454	Sequence 38454, A
154	6	3.0	631	6	US-10-953-349-27089	Sequence 27089, A
155	6	3.0	640	6	US-10-953-349-35681	Sequence 35681, A
156	6	3.0	642	7	US-11-217-529-78002	Sequence 78002, A
157	6	3.0	648	7	US-11-217-529-81312	Sequence 81312, A
c 158	6	3.0	666	7	US-11-217-529-77277	Sequence 77277, A
c 159	6	3.0	669	7	US-11-257-062-37	Sequence 37, Appl
c 160	6	3.0	669	7	US-11-217-529-174016	Sequence 174016,
161	6	3.0	677	7	US-11-136-524-20	Sequence 20, Appl
162	6	3.0	684	7	US-11-217-529-77983	Sequence 77983, A
163	6	3.0	696	6	US-10-953-349-5986	Sequence 5986, Ap
164	6	3.0	699	6	US-10-471-571A-4419	Sequence 4419, Ap
165	6	3.0	701	6	US-10-953-349-36866	Sequence 36866, A
c 166	6	3.0	702	6	US-10-953-349-40119	Sequence 40119, A
167	6	3.0	705	6	US-10-953-349-25288	Sequence 25288, A
c 168	6	3.0	717	6	US-10-953-349-27207	Sequence 27207, A
c 169	6	3.0	718	6	US-10-953-349-4712	Sequence 4712, Ap
c 170	6	3.0	728	6	US-10-953-349-7939	Sequence 7939, Ap
c 171	6	3.0	732	6	US-10-471-571A-1157	Sequence 1157, Ap
172	6	3.0	735	7	US-11-217-529-77210	Sequence 77210, A
173	6	3.0	735	7	US-11-217-529-80568	Sequence 80568, A
174	6	3.0	738	7	US-11-217-529-3017	Sequence 3017, Ap
175	6	3.0	740	6	US-10-953-349-37753	Sequence 37753, A
c 176	6	3.0	747	6	US-10-953-349-4053	Sequence 4053, Ap
c 177	6	3.0	766	6	US-10-953-349-9488	Sequence 9488, Ap
c 178	6	3.0	766	6	US-10-953-349-16518	Sequence 16518, A
c 179	6	3.0	776	6	US-10-953-349-10625	Sequence 10625, A
180	6	3.0	789	6	US-10-471-571A-2447	Sequence 2447, Ap
181	6	3.0	789	7	US-11-217-529-76157	Sequence 76157, A
c 182	6	3.0	798	7	US-11-217-529-1769	Sequence 1769, Ap
183	6	3.0	798	7	US-11-217-529-173454	Sequence 173454,
184	6	3.0	802	6	US-10-953-349-16472	Sequence 16472, A
c 185	6	3.0	806	6	US-10-953-349-19195	Sequence 19195, A
186	6	3.0	810	7	US-11-217-529-3877	Sequence 3877, Ap
187	6	3.0	816	6	US-10-953-349-36509	Sequence 36509, A
188	6	3.0	822	6	US-10-953-349-37373	Sequence 37373, A
189	6	3.0	824	6	US-10-488-619-1821	Sequence 1821, Ap
c 190	6	3.0	829	6	US-10-953-349-37645	Sequence 37645, A
c 191	6	3.0	830	6	US-10-953-349-39705	Sequence 39705, A
c 192	6	3.0	831	6	US-10-471-571A-789	Sequence 789, App
193	6	3.0	835	6	US-10-953-349-13657	Sequence 13657, A
194	6	3.0	841	6	US-10-953-349-34781	Sequence 34781, A
195	6	3.0	849	7	US-11-217-529-80730	Sequence 80730, A
c 196	6	3.0	855	7	US-11-217-529-2895	Sequence 2895, Ap
c 197	6	3.0	861	6	US-10-471-571A-4551	Sequence 4551, Ap
198	6	3.0	867	6	US-10-953-349-30927	Sequence 30927, A
199	6	3.0	874	6	US-10-505-928-248	Sequence 248, App
200	6	3.0	878	6	US-10-953-349-6367	Sequence 6367, Ap

ALIGNMENTS

```
RESULT 1
US-11-293-697-34/c
; Sequence 34, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 2984
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-34

Alignment Scores:
Pred. No.:                4.83          Length:          2984
Score:                    9.00          Matches:         9
Percent Similarity:       100.0%        Conservative:    0
```

st Local Similarity: 100.0% Mismatches: 0
ery Match: 4.6% Indels: 0
: 7 Gaps: 0

-10-821-670A-36 (1-197) x US-11-293-697-34 (1-2984)

4 ProThrProThrProSerProGlyMet 12
1505 CCGACACCAACTCCAAGTCCAGGGATG 1479

SULT 2
-10-322-836-19
Sequence 19, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(525)
-10-322-836-19

gnment Scores:
ed. No.: 9.99 Length: 528
ore: 8.00 Matches: 8
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 4.1% Indels: 0
: 6 Gaps: 0

-10-821-670A-36 (1-197) x US-10-322-836-19 (1-528)

31 GlnLysAlaArgGlnThrLeuGlu 38
61 CAAAAAGCCAGGCAGACCCTGGAG 84

SULT 3
-10-322-836-17
Sequence 17, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(876)
US-10-322-836-17

Alignment Scores:
Pred. No.: 16.2 Length: 879
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.1% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-36 (1-197) x US-10-322-836-17 (1-879)

Qy 31 GlnLysAlaArgGlnThrLeuGlu 38
Db 61 CAAAAAGCCAGGCAGACCCTGGAG 84

RESULT 4
US-10-322-836-15
; Sequence 15, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1014)
US-10-322-836-15

Alignment Scores:
Pred. No.: 18.5 Length: 1017
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.1% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-36 (1-197) x US-10-322-836-15 (1-1017)

Qy 31 GlnLysAlaArgGlnThrLeuGlu 38
Db 61 CAAAAAGCCAGGCAGACCCTGGAG 84

RESULT 5
US-10-322-836-27
; Sequence 27, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
EQ ID NO 27
LENGTH: 1248
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1245)
10-322-836-27

gnment Scores:

d. No.:	22.5	Length:	1248
re:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.1%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-322-836-27 (1-1248)

```
        31 GlnLysAlaArgGlnThrLeuGlu 38
           ||||||||||||||||||||||||
       781 CAAAAAGCCAGGCAGACCCTGGAG 804
```

ULT 6
10-322-836-5
equence 5, Application US/10322836
ublication No. US20060090212A1
ENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
EQ ID NO 5
LENGTH: 1293
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1290)
10-322-836-5

gnment Scores:

d. No.:	23.2	Length:	1293
re:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.1%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-322-836-5 (1-1293)

```
        31 GlnLysAlaArgGlnThrLeuGlu 38
           ||||||||||||||||||||||||
       826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

RESULT 7
US-10-322-836-41
; Sequence 41, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1314)
US-10-322-836-41

Alignment Scores:

Pred. No.:	23.6	Length:	1317
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-322-836-41 (1-1317)

```
Qy         31 GlnLysAlaArgGlnThrLeuGlu 38
              ||||||||||||||||||||||||
Db         61 CAAAAAGCCAGGCAGACCCTGGAG 84
```

RESULT 8
US-10-322-836-39
; Sequence 39, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1452)
US-10-322-836-39

Alignment Scores:

Pred. No.:	26	Length:	1455

```
ore:                 8.00          Matches:       8
cent Similarity:     100.0%        Conservative:  0
st Local Similarity: 100.0%        Mismatches:    0
ery Match:           4.1%          Indels:        0
:                    6             Gaps:          0

-10-821-670A-36 (1-197) x US-10-322-836-39 (1-1455)

        31 GlnLysAlaArgGlnThrLeuGlu 38
           ||||||||||||||||||||||||
        61 CAAAAAGCCAGGCAGACCCTGGAG 84

SULT 9
-10-322-836-25
Sequence 25, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
 APPLICANT: Turner, Alexander C., Jr.
 APPLICANT:  Zambrowicz, Brian
 APPLICANT:  Nehls, Michael
 APPLICANT:  Freidrich, Glenn A.
 APPLICANT:  Sands, Arthur T.
 TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
 TITLE OF INVENTION:  ENCODED THEREBY
 FILE REFERENCE: 8535-0037-999
 CURRENT APPLICATION NUMBER: US/10/322,836
 CURRENT FILING DATE:  2002-12-18
 PRIOR APPLICATION NUMBER: US/09/579,114
 PRIOR FILING DATE: 2000-05-25
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 3.0
EQ ID NO 25
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Homo sapien
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)...(1596)
-10-322-836-25

gnment Scores:
d. No.:              28.4          Length:        1599
ore:                 8.00          Matches:       8
cent Similarity:     100.0%        Conservative:  0
st Local Similarity: 100.0%        Mismatches:    0
ery Match:           4.1%          Indels:        0
:                    6             Gaps:          0

-10-821-670A-36 (1-197) x US-10-322-836-25 (1-1599)

        31 GlnLysAlaArgGlnThrLeuGlu 38
           ||||||||||||||||||||||||
       781 CAAAAAGCCAGGCAGACCCTGGAG 804

SULT 10
-10-322-836-3
Sequence 3, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
 APPLICANT: Turner, Alexander C., Jr.
 APPLICANT:  Zambrowicz, Brian
 APPLICANT:  Nehls, Michael
 APPLICANT:  Freidrich, Glenn A.
 APPLICANT:  Sands, Arthur T.
 TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
 TITLE OF INVENTION:  ENCODED THEREBY
 FILE REFERENCE: 8535-0037-999
 CURRENT APPLICATION NUMBER: US/10/322,836
 CURRENT FILING DATE:  2002-12-18
 PRIOR APPLICATION NUMBER: US/09/579,114
 PRIOR FILING DATE: 2000-05-25
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 1644
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1641)
US-10-322-836-3

Alignment Scores:
Pred. No.:           29.1          Length:        1644
Score:               8.00          Matches:       8
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         4.1%          Indels:        0
DB:                  6             Gaps:          0

US-10-821-670A-36 (1-197) x US-10-322-836-3 (1-1644)

Qy         31 GlnLysAlaArgGlnThrLeuGlu 38
              ||||||||||||||||||||||||
Db        826 CAAAAAGCCAGGCAGACCCTGGAG 849

RESULT 11
US-10-322-836-23
; Sequence 23, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 1737
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1734)
US-10-322-836-23

Alignment Scores:
Pred. No.:           30.7          Length:        1737
Score:               8.00          Matches:       8
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         4.1%          Indels:        0
DB:                  6             Gaps:          0

US-10-821-670A-36 (1-197) x US-10-322-836-23 (1-1737)

Qy         31 GlnLysAlaArgGlnThrLeuGlu 38
              ||||||||||||||||||||||||
Db        781 CAAAAAGCCAGGCAGACCCTGGAG 804

RESULT 12
US-10-322-836-1
; Sequence 1, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
```

APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
EQ ID NO 1
LENGTH: 1782
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1779)
10-322-836-1

gnment Scores:

d. No.:	31.4	Length:	1782
re:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.1%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-322-836-1 (1-1782)

```
        31 GlnLysAlaArgGlnThrLeuGlu 38
           ||||||||||||||||||||||||
       826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

ULT 13
10-953-349-4560
equence 4560, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 4560
LENGTH: 2021
TYPE: DNA
ORGANISM: Arabidopsis thaliana
10-953-349-4560

gnment Scores:

d. No.:	35.4	Length:	2021
re:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.1%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-953-349-4560 (1-2021)

```
        99 ThrLeuCysLeuSerSerIleTyr 106
           ||||||||||||||||||||||||
     1004 ACCTTGTGTTTGTCTTCTATCTAT 1027
```

ULT 14
10-322-836-45
equence 45, Application US/10322836
ublication No. US20060090212A1
ENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2034)
US-10-322-836-45

Alignment Scores:

Pred. No.:	35.6	Length:	2037
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-322-836-45 (1-2037)

```
Qy         31 GlnLysAlaArgGlnThrLeuGlu 38
              ||||||||||||||||||||||||
Db        781 CAAAAAGCCAGGCAGACCCTGGAG 804
```

RESULT 15
US-10-322-836-33
; Sequence 33, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2079)
US-10-322-836-33

Alignment Scores:

Pred. No.:	36.4	Length:	2082
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-322-836-33 (1-2082)

```
        31 GlnLysAlaArgGlnThrLeuGlu 38
           ||||||||||||||||||||||||
       826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

SULT 16
-10-322-836-43
Sequence 43, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 2175
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2172)
-10-322-836-43

gnment Scores:

d. No.:	37.9	Length:	2175
re:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.1%	Indels:	0
	6	Gaps:	0

-10-821-670A-36 (1-197) x US-10-322-836-43 (1-2175)

```
        31 GlnLysAlaArgGlnThrLeuGlu 38
           ||||||||||||||||||||||||
       781 CAAAAAGCCAGGCAGACCCTGGAG 804
```

SULT 17
-10-322-836-31
Sequence 31, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 2220
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2217)

US-10-322-836-31

Alignment Scores:

Pred. No.:	38.7	Length:	2220
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-322-836-31 (1-2220)

```
Qy         31 GlnLysAlaArgGlnThrLeuGlu 38
              ||||||||||||||||||||||||
Db        826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

RESULT 18
US-10-530-792A-1
; Sequence 1, Application US/10530792A
; Publication No. US20060105340A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-008
; CURRENT APPLICATION NUMBER: US/10/530,792A
; CURRENT FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-530-792A-1

Alignment Scores:

Pred. No.:	64	Length:	3791
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-530-792A-1 (1-3791)

```
Qy         86 GlySerCysLeuAlaSerArgLys 93
              |||||||||||||||||||||||
Db        231 GGGTCATGCCTGGCCAGCAGAAAG 254
```

RESULT 19
US-11-217-529-3234
; Sequence 3234, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3

```
SEQ ID NO 3234
  LENGTH: 6663
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
11-217-529-3234

gnment Scores:
d. No.:                109          Length:        6663
re:                    8.00         Matches:       8
cent Similarity:       100.0%       Conservative:  0
t Local Similarity:    100.0%       Mismatches:    0
ry Match:              4.1%         Indels:        0
                       7            Gaps:          0

10-821-670A-36 (1-197) x US-11-217-529-3234 (1-6663)

       139 ThrAlaIleAspGluLeuLeuGln 146
           ||||||||||||||||||||||||
      1729 ACTGCCATTGATGAACTATTACAA 1752

ULT 20
10-488-619-837
equence 837, Application US/10488619
ublication No. US20060099578A1
ENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
FILE REFERENCE: 98-01 WO
CURRENT APPLICATION NUMBER: US/10/488,619
CURRENT FILING DATE:  2004-03-01
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: PatentIn version 3.1
EQ ID NO 837
  LENGTH: 331
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: misc_feature
  LOCATION: (1)..(331)
  OTHER INFORMATION: n is g, c, a or t
10-488-619-837

gnment Scores:
d. No.:                68.1         Length:        331
re:                    7.00         Matches:       7
cent Similarity:       100.0%       Conservative:  0
t Local Similarity:    100.0%       Mismatches:    0
ry Match:              3.6%         Indels:        0
                       6            Gaps:          0

10-821-670A-36 (1-197) x US-10-488-619-837 (1-331)

        86 GlySerCysLeuAlaSerArg 92
           ||||||||||||||||||||
       108 GGCTCCTGCCTGGCCTCTAGG 128

ULT 21
10-148-883-27/c
equence 27, Application US/10148883
ublication No. US20060115811A1
ENERAL INFORMATION:
APPLICANT: Jay White et al.
TITLE OF INVENTION: Cytochrome P450RA1-2 and Related Proteins
FILE REFERENCE: 11812-49
CURRENT APPLICATION NUMBER: US/10/148,883
CURRENT FILING DATE:  2003-02-13
PRIOR APPLICATION NUMBER: US 60/171,110
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: US 60/178,314
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.3

; SEQ ID NO 27
;   LENGTH: 399
;   TYPE: DNA
;   ORGANISM: Rattus rattus
US-10-148-883-27

Alignment Scores:
Pred. No.:                81.2         Length:        399
Score:                    7.00         Matches:       7
Percent Similarity:       100.0%       Conservative:  0
Best Local Similarity:    100.0%       Mismatches:    0
Query Match:              3.6%         Indels:        0
DB:                       6            Gaps:          0

US-10-821-670A-36 (1-197) x US-10-148-883-27 (1-399)

Qy           4 ProThrProThrProSerPro 10
               ||||||||||||||||||||||
Db          42 CCGACACCAACTCCAAGCCCT 22

RESULT 22
US-10-953-349-25251/c
; Sequence 25251, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25251
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-25251

Alignment Scores:
Pred. No.:                116          Length:        582
Score:                    7.00         Matches:       7
Percent Similarity:       100.0%       Conservative:  0
Best Local Similarity:    100.0%       Mismatches:    0
Query Match:              3.6%         Indels:        0
DB:                       6            Gaps:          0

US-10-821-670A-36 (1-197) x US-10-953-349-25251 (1-582)

Qy         139 ThrAlaIleAspGluLeuLeu 145
               ||||||||||||||||||||
Db          88 ACGGCCATAGATGAGTTGCTG 68

RESULT 23
US-11-217-529-81369
; Sequence 81369, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81369
```

LENGTH: 660
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-81369

:gnment Scores:

ed. No.:	130	Length:	660
ore:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
	7	Gaps:	0

-10-821-670A-36 (1-197) x US-11-217-529-81369 (1-660)

```
        106 TyrGluAspLeuLysMetTyr 112
            ||||||||||||||||||||
        124 TATGAAGACCTGAAGATGTAT 144
```

SULT 24
-10-488-619-2648/c
Sequence 2648, Application US/10488619
Publication No. US20060099578A1
GENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
FILE REFERENCE: 98-01 WO
CURRENT APPLICATION NUMBER: US/10/488,619
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2648
LENGTH: 704
TYPE: DNA
ORGANISM: Mus musculus
-10-488-619-2648

:gnment Scores:

ed. No.:	139	Length:	704
ore:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
	6	Gaps:	0

-10-821-670A-36 (1-197) x US-10-488-619-2648 (1-704)

```
        144 LeuLeuGlnAlaLeuAsnVal 150
            ||||||||||||||||||||
        154 CTTCTCCAAGCTCTGAATGTC 134
```

SULT 25
-11-217-529-1263
Sequence 1263, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1263
LENGTH: 894
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1263

Alignment Scores:

Pred. No.:	174	Length:	894
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x US-11-217-529-1263 (1-894)

```
Qy          4 ProThrProThrProSerPro 10
              ||||||||||||||||||||
Db        766 CCAACTCCAACTCCGTCGCCA 786
```

RESULT 26
US-11-264-737-102
; Sequence 102, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Pictaggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn Qun
; TITLE OF INVENTION: DOCOSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 102
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Ostreococcus tauri
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: synthetic C20/22 fatty acid elongase (codon-optimized)
US-11-264-737-102

Alignment Scores:

Pred. No.:	175	Length:	903
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x US-11-264-737-102 (1-903)

```
Qy          3 LeuProThrProThrProSer 9
              ||||||||||||||||||||
Db         56 CTACCTACGCCTACGCCTTCG 76
```

RESULT 27
US-10-953-349-4834
; Sequence 4834, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

```
CURRENT FILING DATE:  2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 4834
 LENGTH: 906
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
10-953-349-4834

gnment Scores:
d. No.:                176            Length:        906
re:                    7.00           Matches:       7
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              3.6%           Indels:        0
                       6              Gaps:          0

10-821-670A-36 (1-197) x US-10-953-349-4834 (1-906)

        75 LeuAlaSerArgGluIleSer 81
           |||||||||||||||||||
       681 TTGGCTAGCAGAGAAATCAGT 701

ULT 28
11-217-529-5460
equence 5460, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 5460
 LENGTH: 921
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-5460

gnment Scores:
d. No.:                179            Length:        921
re:                    7.00           Matches:       7
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              3.6%           Indels:        0
                       7              Gaps:          0

10-821-670A-36 (1-197) x US-11-217-529-5460 (1-921)

       180 PheArgIleArgAlaValThr 186
           |||||||||||||||||||
       867 TTTCGAATTCGAGCGGTTACC 887

ULT 29
11-311-754-5
equence 5, Application US/11311754
ublication No. US20060099635A1
ENERAL INFORMATION:
APPLICANT: Vincent Ling
APPLICANT:  Kyriaki Dunussi-Joannopoulos
TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
FILE REFERENCE: GNN-007
CURRENT APPLICATION NUMBER: US/11/311,754
CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: US/09/667,135
;  PRIOR FILING DATE: 2000-09-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 953
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (24)..(950)
US-11-311-754-5

Alignment Scores:
Pred. No.:             184            Length:        953
Score:                 7.00           Matches:       7
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           3.6%           Indels:        0
DB:                    7              Gaps:          0

US-10-821-670A-36 (1-197) x US-11-311-754-5 (1-953)

Qy         156 ProGlnAsnSerSerLeuGlu 162
               |||||||||||||||||||
Db         225 CCACAGAACAGCTCCTTGGAA 245

RESULT 30
US-10-953-349-12779
; Sequence 12779, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12779
;   LENGTH: 979
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-12779

Alignment Scores:
Pred. No.:             189            Length:        979
Score:                 7.00           Matches:       7
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           3.6%           Indels:        0
DB:                    6              Gaps:          0

US-10-821-670A-36 (1-197) x US-10-953-349-12779 (1-979)

Qy           5 ThrProThrProSerProGly 11
               |||||||||||||||||||
Db         412 ACACCAACACCGTCGCCGGGG 432

RESULT 31
US-10-953-349-28356/c
; Sequence 28356, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
```

SEQ ID NO 28356
LENGTH: 994
TYPE: DNA
ORGANISM: Triticum aestivum
10-953-349-28356

gnment Scores:

d. No.:	192	Length:	994
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.6%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-953-349-28356 (1-994)

```
         92 ArgLysThrSerPheMetThr 98
            ||||||||||||||||||||
        340 AGGAAGACCAGCTTCATGACG 320
```

SULT 32
10-560-723-79/c
Sequence 79, Application US/10560723
Publication No. US20060115821A1
GENERAL INFORMATION:
APPLICANT: EXONHIT THERAPEUTICALS
TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
FILE REFERENCE: B0213WO
CURRENT APPLICATION NUMBER: US/10/560,723
CURRENT FILING DATE: 2005-12-15
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PatentIn version 3.1
SEQ ID NO 79
LENGTH: 997
TYPE: DNA
ORGANISM: Homo sapiens
10-560-723-79

gnment Scores:

d. No.:	192	Length:	997
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.6%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-560-723-79 (1-997)

```
         86 GlySerCysLeuAlaSerArg 92
            ||||||||||||||||||||
        839 GGCTCCTGCCTGGCCTCTAGG 819
```

SULT 33
10-953-349-26293
Sequence 26293, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 26293
LENGTH: 1056
TYPE: DNA
ORGANISM: Triticum aestivum
10-953-349-26293

gnment Scores:

Pred. No.:	203	Length:	1056
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-953-349-26293 (1-1056)

```
Qy          4 ProThrProThrProSerPro 10
              ||||||||||||||||||||
Db        432 CCGACTCCGACTCCGTCACCT 452
```

RESULT 34
US-10-953-349-39566
; Sequence 39566, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39566
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39566

Alignment Scores:

Pred. No.:	204	Length:	1062
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-953-349-39566 (1-1062)

```
Qy          98 ThrThrLeuCysLeuSerSer 104
               ||||||||||||||||||||
Db         188 ACTACGTTGTGTCTGAGTTCA 208
```

RESULT 35
US-10-953-349-17414/c
; Sequence 17414, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17414
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17414

Alignment Scores:

Pred. No.:	229	Length:	1202
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-953-349-17414 (1-1202)

```
       171 IleLysLeuCysIleLeuLeu 177
           ||||||||||||||||||||
       882 ATTAAACTCTGTATTTTACTT 862
```

ULT 36
11-217-529-1292/c
equence 1292, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 1292
LENGTH: 1236
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-1292

gnment Scores:

d. No.:	236	Length:	1236
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.6%	Indels:	0
	7	Gaps:	0

10-821-670A-36 (1-197) x US-11-217-529-1292 (1-1236)

```
         5 ThrProThrProSerProGly 11
           ||||||||||||||||||||
       328 ACACCAACTCCTTCTCCAGGG 308
```

ULT 37
10-953-349-24555/c
equence 24555, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 24555
LENGTH: 1313
TYPE: DNA
ORGANISM: Glycine max
10-953-349-24555

gnment Scores:

d. No.:	249	Length:	1313
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.6%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-953-349-24555 (1-1313)

```
Qy         152 SerValThrValProGlnAsn 158
               ||||||||||||||||||||
Db         199 AGTGTTACTGTTCCCCAAAAC 179
```

RESULT 38
US-10-953-349-35965/c
; Sequence 35965, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35965
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-35965

Alignment Scores:

Pred. No.:	275	Length:	1454
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-953-349-35965 (1-1454)

```
Qy         172 LysLeuCysIleLeuLeuHis 178
               ||||||||||||||||||||
Db         575 AAGCTCTGTATTCTGCTACAT 555
```

RESULT 39
US-10-953-349-36433
; Sequence 36433, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36433
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-36433

Alignment Scores:

Pred. No.:	280	Length:	1483
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-953-349-36433 (1-1483)

```
Qy          21 ThrLeuLeuArgAlaIleSer 27
               ||||||||||||||||||||
Db        1092 ACACTCTTGCGAGCCATCTCT 1112
```

RESULT 40
US-10-953-349-33213

```
Sequence 33213, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 33213
  LENGTH: 1504
  TYPE: DNA
  ORGANISM: Zea mays subsp. mays
US-10-953-349-33213

Alignment Scores:
Pred. No.:                283           Length:          1504
Score:                    7.00          Matches:         7
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              3.6%          Indels:          0
                          6             Gaps:            0

US-10-821-670A-36 (1-197) x US-10-953-349-33213 (1-1504)

          3 LeuProThrProThrProSer 9
            |||||||||||||||||||||
         40 CTCCCAACCCCAACCCCGTCC 60

RESULT 41
US-10-953-349-17700/c
Sequence 17700, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 17700
  LENGTH: 1538
  TYPE: DNA
  ORGANISM: Glycine max
US-10-953-349-17700

Alignment Scores:
Pred. No.:                289           Length:          1538
Score:                    7.00          Matches:         7
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              3.6%          Indels:          0
                          6             Gaps:            0

US-10-821-670A-36 (1-197) x US-10-953-349-17700 (1-1538)

        159 SerSerLeuGluGluProAsp 165
            ||||||||||||||||||||
        368 TCTTCACTTGAAGAACCCGAT 348

RESULT 42
US-10-953-349-24275/c
Sequence 24275, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 24275
  LENGTH: 1660
  TYPE: DNA
  ORGANISM: Glycine max
US-10-953-349-24275

Alignment Scores:
Pred. No.:                311           Length:          1660
Score:                    7.00          Matches:         7
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              3.6%          Indels:          0
DB:                       6             Gaps:            0

US-10-821-670A-36 (1-197) x US-10-953-349-24275 (1-1660)

Qy        172 LysLeuCysIleLeuLeuHis 178
              ||||||||||||||||||||
Db        965 AAGTTGTGTATTCTGTTGCAC 945

RESULT 43
US-11-313-556-3/c
Sequence 3, Application US/11313556
Publication No. US20060099195A1
  GENERAL INFORMATION:
       APPLICANT: Ostrand-Rosenberg, Suzanne
                  Baskar, Sivasubramanian
                  Glimcher, Laurie H.
                  Freeman, Gordon J.
                  Nadler, Lee M.
       TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
       NUMBER OF SEQUENCES: 4
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: LAHIVE & COCKFIELD
            STREET: 60 State Street, Suite 510
            CITY: Boston
            STATE: Massachusetts
            COUNTRY: USA
            ZIP: 02109
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.25
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/11/313,556
            FILING DATE: 20-Dec-2005
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: US/09/966,148
            FILING DATE: 27-Sep-2001
            APPLICATION NUMBER: 08/147,772
            FILING DATE: <Unknown>
       ATTORNEY/AGENT INFORMATION:
            NAME: Mandragouras, Amy E.
            REGISTRATION NUMBER: 36,207
            REFERENCE/DOCKET NUMBER: RPI-003
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: (617) 227-7400
            TELEFAX: (617) 227-5941
  INFORMATION FOR SEQ ID NO: 3:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 1716 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: double
            TOPOLOGY: linear
       MOLECULE TYPE: cDNA to mRNA
       HYPOTHETICAL: no
       ORIGINAL SOURCE:
```

```
          ORGANISM: Mus musculus
          DEVELOPMENTAL STAGE: germ line
          TISSUE TYPE: lymphoid
          CELL TYPE: B lymphocyte
          CELL LINE: 70Z and A20
      IMMEDIATE SOURCE:
          LIBRARY: cDNA in pCDM8 vector
          CLONE: B7 #'s 1 and 29
      FEATURE:
          NAME/KEY:  translated region
          LOCATION:  249 to 1166 bp
          IDENTIFICATION METHOD:  similarity to other pattern
      FEATURE:
          NAME/KEY:  Alternate ATG initiation codons
          LOCATION:  225 to 227 and 270 to 272
          IDENTIFICATION METHOD:  similarity to other pattern
      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
11-313-556-3

gnment Scores:
d. No.:              321          Length:        1716
re:                  7.00         Matches:       7
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            3.6%         Indels:        0
                     7            Gaps:          0

10-821-670A-36 (1-197) x US-11-313-556-3 (1-1716)

         4 ProThrProThrProSerPro 10
           ||||||||||||||||||||
      1631 CCCACCCCCACCCCGTCCCCC 1611

ULT 44
10-953-349-34792
equence 34792, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION:  ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE:  2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 34792
 LENGTH: 1750
 TYPE: DNA
 ORGANISM: Zea mays subsp. mays
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (63)..(63)
 OTHER INFORMATION: n is a, c, g, or t
10-953-349-34792

gnment Scores:
d. No.:              327          Length:        1750
re:                  7.00         Matches:       7
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            3.6%         Indels:        0
                     6            Gaps:          0

10-821-670A-36 (1-197) x US-10-953-349-34792 (1-1750)

         3 LeuProThrProThrProSer 9
           |||||||||||||||||||||
        90 CTCCCAACCCCAACCCCGTCC 110

ULT 45
11-217-529-174380/c
equence 174380, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174380
;   LENGTH: 1761
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174380

Alignment Scores:
Pred. No.:           329          Length:        1761
Score:               7.00         Matches:       7
Percent Similarity:  100.0%       Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:         3.6%         Indels:        0
DB:                  7            Gaps:          0

US-10-821-670A-36 (1-197) x US-11-217-529-174380 (1-1761)

Qy          22 LeuLeuArgAlaIleSerAsn 28
               ||||||||||||||||||||
Db         307 TTATTACGGGCGATATCAAAT 287

RESULT 46
US-11-251-465-7/c
; Sequence 7, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
;  APPLICANT: Brys, Reginald
;  APPLICANT:  Vandeghinste, Nick
;  APPLICANT:  Tomme, Peter
;  APPLICANT:  Klaassen, Hubertus
;  TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
;  TITLE OF INVENTION:  Same, Useful In The Treatment Of Joint Degenerative And
;  TITLE OF INVENTION:  Inflammatory Diseases
;  FILE REFERENCE: P30,172-A USA
;  CURRENT APPLICATION NUMBER: US/11/251,465
;  CURRENT FILING DATE:  2005-10-14
;  PRIOR APPLICATION NUMBER: 60/619,384
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 880
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
;   LENGTH: 1804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-251-465-7

Alignment Scores:
Pred. No.:           336          Length:        1804
Score:               7.00         Matches:       7
Percent Similarity:  100.0%       Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:         3.6%         Indels:        0
DB:                  7            Gaps:          0

US-10-821-670A-36 (1-197) x US-11-251-465-7 (1-1804)

Qy         144 LeuLeuGlnAlaLeuAsnVal 150
               ||||||||||||||||||||
```

1109 CTCCTGCAGGCTCTCAACGTG 1089

ULT 47
11-311-754-27
equence 27, Application US/11311754
ublication No. US20060099635A1
ENERAL INFORMATION:
APPLICANT: Vincent Ling
APPLICANT: Kyriaki Dunussi-Joannopoulos
TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
FILE REFERENCE: GNN-007
CURRENT APPLICATION NUMBER: US/11/311,754
CURRENT FILING DATE: 2005-12-19
PRIOR APPLICATION NUMBER: US/09/667,135
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 27
LENGTH: 1831
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hGL50-mIgG2am nucleotide sequence
11-311-754-27

gnment Scores:

d. No.:	341	Length:	1831
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.6%	Indels:	0
	7	Gaps:	0

10-821-670A-36 (1-197) x US-11-311-754-27 (1-1831)

```
Qy        156 ProGlnAsnSerSerLeuGlu 162
              ||||||||||||||||||||
Db        237 CCACAGAACAGCTCCTTGGAA 257
```

ULT 48
10-505-928-693
equence 693, Application US/10505928
ublication No. US20060088532A1
ENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
EQ ID NO 693
LENGTH: 1868
TYPE: DNA
ORGANISM: Homo sapiens
10-505-928-693

gnment Scores:

d. No.:	348	Length:	1868
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.6%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-505-928-693 (1-1868)

```
Qy         54 LysAspLysThrSerThrVal 60
              ||||||||||||||||||||
Db        708 AAAGACAAAACTTCAACAGTG 728
```

RESULT 49
US-10-953-349-11252/c
; Sequence 11252, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11252
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11252

Alignment Scores:

Pred. No.:	356	Length:	1914
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-953-349-11252 (1-1914)

```
Qy         61 GluAlaCysLeuProLeuGlu 67
              ||||||||||||||||||||
Db        932 GAAGCCTGTCTTCCTCTGGAA 912
```

RESULT 50
US-11-293-697-275
; Sequence 275, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 275
; LENGTH: 1933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-275

Alignment Scores:

Pred. No.:	359	Length:	1933
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x US-11-293-697-275 (1-1933)

```
Qy          3 LeuProThrProThrProSer 9
              ||||||||||||||||||||
Db       1778 CTCCCCACCCCCACACCATCT 1798
```

RESULT 51
US-11-293-697-1094/c
; Sequence 1094, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE

```
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE:  2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 1094
 LENGTH: 2036
 TYPE: DNA
 ORGANISM: Homo sapiens
11-293-697-1094

gnment Scores:
d. No.:                377            Length:        2036
re:                    7.00           Matches:       7
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              3.6%           Indels:        0
                       7              Gaps:          0

10-821-670A-36 (1-197) x US-11-293-697-1094 (1-2036)

        60 ValGluAlaCysLeuProLeu 66
           ||||||||||||||||||||
       582 GTTGAAGCTTGTCTCCCACTT 562

ULT 52
11-217-529-77609/c
equence 77609, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 77609
 LENGTH: 2037
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-77609

gnment Scores:
d. No.:                377            Length:        2037
re:                    7.00           Matches:       7
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              3.6%           Indels:        0
                       7              Gaps:          0

10-821-670A-36 (1-197) x US-11-217-529-77609 (1-2037)

        91 SerArgLysThrSerPheMet 97
           |||||||||||||||||||||
       314 TCTCGCAAAACTAGCTTTATG 294

ULT 53
11-293-697-1972
equence 1972, Application US/11293697
ublication No. US20060105376A1
ENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
```

```
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE:  2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1972
;   LENGTH: 2126
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1972

Alignment Scores:
Pred. No.:                393            Length:        2126
Score:                    7.00           Matches:       7
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              3.6%           Indels:        0
DB:                       7              Gaps:          0

US-10-821-670A-36 (1-197) x US-11-293-697-1972 (1-2126)

Qy           5 ThrProThrProSerProGly 11
               ||||||||||||||||||||
Db        1992 ACCCCTACCCCATCTCCAGGC 2012

RESULT 54
US-11-217-529-2489
; Sequence 2489, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2489
;   LENGTH: 2241
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-2489

Alignment Scores:
Pred. No.:                413            Length:        2241
Score:                    7.00           Matches:       7
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              3.6%           Indels:        0
DB:                       7              Gaps:          0

US-10-821-670A-36 (1-197) x US-11-217-529-2489 (1-2241)

Qy         106 TyrGluAspLeuLysMetTyr 112
               ||||||||||||||||||||
Db        1705 TATGAAGACTTGAAGATGTAC 1725

RESULT 55
US-11-293-697-507
; Sequence 507, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
```

TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 507
LENGTH: 2275
TYPE: DNA
ORGANISM: Homo sapiens
11-293-697-507

gnment Scores:

d. No.:	419	Length:	2275
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.6%	Indels:	0
	7	Gaps:	0

10-821-670A-36 (1-197) x US-11-293-697-507 (1-2275)

```
        72 GluSerCysLeuAlaSerArg 78
           ||||||||||||||||||||
      1307 GAGAGCTGCTTGGCTTCAAGG 1327
```

ULT 56
10-511-937-649/c
equence 649, Application US/10511937
ublication No. US20060088836A1
ENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
EQ ID NO 649
LENGTH: 2315
TYPE: DNA
ORGANISM: Homo sapiens
10-511-937-649

gnment Scores:

d. No.:	425	Length:	2315
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.6%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-511-937-649 (1-2315)

```
       157 GlnAsnSerSerLeuGluGlu 163
           ||||||||||||||||||||
      1460 CAGAATTCTTCATTAGAGGAA 1440
```

RESULT 57
US-10-196-749-135
; Sequence 135, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 135
; LENGTH: 2651
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-135

Alignment Scores:

Pred. No.:	483	Length:	2651
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-196-749-135 (1-2651)

```
Qy          4 ProThrProThrProSerPro 10
              ||||||||||||||||||||
Db        370 CCAACTCCAACTCCTTCTCCC 390
```

RESULT 58
US-11-101-316-23
; Sequence 23, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.

```
APPLICANT:  Wood,William I.
TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
TITLE OF INVENTION:  UNDEREXPRESSED IN MELANOMA
FILE REFERENCE: P3230R1C17C1
CURRENT APPLICATION NUMBER: US/11/101,316
CURRENT FILING DATE:  2005-04-06
PRIOR APPLICATION NUMBER: 10/063526
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 170
EQ ID NO 23
 LENGTH: 2651
 TYPE: DNA
 ORGANISM: Homo Sapien
11-101-316-23

gnment Scores:
d. No.:                 483             Length:         2651
re:                     7.00            Matches:        7
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.6%            Indels:         0
                        7               Gaps:           0

10-821-670A-36 (1-197) x US-11-101-316-23 (1-2651)

         4 ProThrProThrProSerPro 10
           ||||||||||||||||||||
       370 CCAACTCCAACTCCTTCTCCC 390

ULT 59
11-293-697-753
equence 753, Application US/11293697
ublication No. US20060105376A1
ENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE:  2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 753
 LENGTH: 2662
 TYPE: DNA
 ORGANISM: Homo sapiens
11-293-697-753

gnment Scores:
d. No.:                 485             Length:         2662
re:                     7.00            Matches:        7
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.6%            Indels:         0
                        7               Gaps:           0

10-821-670A-36 (1-197) x US-11-293-697-753 (1-2662)

       149 AsnValAsnSerValThrVal 155
           ||||||||||||||||||||
      1505 AATGTGAATTCAGTAACTGTG 1525

RESULT 60
US-11-217-529-82539
; Sequence 82539, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82539
;   LENGTH: 2805
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-82539

Alignment Scores:
Pred. No.:              510             Length:         2805
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.6%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-36 (1-197) x US-11-217-529-82539 (1-2805)

Qy         140 AlaIleAspGluLeuLeuGln 146
               ||||||||||||||||||||
Db        1738 GCCATTGATGAATTATTACAA 1758

RESULT 61
US-11-293-697-74/c
; Sequence 74, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
;   LENGTH: 2905
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-74

Alignment Scores:
Pred. No.:              527             Length:         2905
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.6%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-36 (1-197) x US-11-293-697-74 (1-2905)

Qy         156 ProGlnAsnSerSerLeuGlu 162
               ||||||||||||||||||||
Db         246 CCGCAAAACTCTTCGCTGGAG 226
```

```
ULT 62
-11-312-958-55
equence 55, Application US/11312958
ublication No. US20060100152A1
ENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT:  Rosenfeld, Julie Beth
APPLICANT:  Silos-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION:  PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION:  12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION:  27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION:  95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
TITLE OF INVENTION:  13424 MOLECULES
FILE REFERENCE: MPI02-027P1RNOMNIM
CURRENT APPLICATION NUMBER: US/11/312,958
CURRENT FILING DATE:  2005-12-20
PRIOR APPLICATION NUMBER: US/10/369,022
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 55
  LENGTH: 3138
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (161)...(3022)
-11-312-958-55

gnment Scores:
d. No.:                 567             Length:         3138
re:                     7.00            Matches:        7
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.6%            Indels:         0
                        7               Gaps:           0

-10-821-670A-36 (1-197) x US-11-312-958-55 (1-3138)

          4 ProThrProThrProSerPro 10
            ||||||||||||||||||||
       2504 CCCACACCCACGCCCTCGCCC 2524

ULT 63
-11-293-697-1397
equence 1397, Application US/11293697
ublication No. US20060105376A1
ENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1397
;   LENGTH: 3294
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1397

Alignment Scores:
Pred. No.:              593             Length:         3294
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.6%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-36 (1-197) x US-11-293-697-1397 (1-3294)

Qy          73 SerCysLeuAlaSerArgGlu 79
               |||||||||||||||||||||
Db        1271 AGTTGCTTAGCAAGCAGGGAA 1291

RESULT 64
US-10-505-928-814/c
; Sequence 814, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 814
;   LENGTH: 3558
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-814

Alignment Scores:
Pred. No.:              638             Length:         3558
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.6%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-505-928-814 (1-3558)

Qy          89 LeuAlaSerArgLysThrSer 95
               ||||||||||||||||||||
Db        460 CTTGCAAGCCGTAAAACTTCT 440

RESULT 65
US-11-217-529-1506/c
; Sequence 1506, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
```

```
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 1506
 LENGTH: 7422
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-1506

gnment Scores:
d. No.:                1.27e+03        Length:         7422
re:                    7.00            Matches:        7
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              3.6%            Indels:         0
                       7               Gaps:           0

10-821-670A-36 (1-197) x US-11-217-529-1506 (1-7422)

        63 CysLeuProLeuGluLeuThr 69
           |||||||||||||||||||
       685 TGTCTGCCGTTAGAGTTAACC 665

ULT 66
10-505-928-236/c
equence 236, Application US/10505928
ublication No. US20060088532A1
ENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE:  2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
EQ ID NO 236
 LENGTH: 7758
 TYPE: DNA
 ORGANISM: Homo sapiens
10-505-928-236

gnment Scores:
d. No.:                1.33e+03        Length:         7758
re:                    7.00            Matches:        7
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              3.6%            Indels:         0
                       6               Gaps:           0

10-821-670A-36 (1-197) x US-10-505-928-236 (1-7758)

         4 ProThrProThrProSerPro 10
           ||||||||||||||||||||
      6809 CCCACCCCCACCCCCAGCCCC 6789

ULT 67
11-264-737-165/c
equence 165, Application US/11264737
ublication No. US20060110806A1
ENERAL INFORMATION:
APPLICANT: E.I. duPont de Nemours & Co., Inc.
APPLICANT:  Damude, Howard Glenn
APPLICANT:  Gillies, Peter J.
APPLICANT:  Macool, Daniel Joseph
APPLICANT:  Pictaggio, Stephen K.
APPLICANT:  Ragghianti, James John
APPLICANT:  Seip, John E.
APPLICANT:  Xue, Zhixiong
APPLICANT:  Yadav, Narendra S.
APPLICANT:  Zhang, Hongxiang
;  APPLICANT:  Zhu, Quinn Qun
;  TITLE OF INVENTION: DOCOSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
;  FILE REFERENCE: CL3160 US NA
;  CURRENT APPLICATION NUMBER: US/11/264,737
;  CURRENT FILING DATE:  2005-11-01
;  NUMBER OF SEQ ID NOS: 467
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 165
;   LENGTH: 10660
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Plasmid pZP2FOEN4
US-11-264-737-165

Alignment Scores:
Pred. No.:             1.79e+03        Length:         10660
Score:                 7.00            Matches:        7
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           3.6%            Indels:         0
DB:                    7               Gaps:           0

US-10-821-670A-36 (1-197) x US-11-264-737-165 (1-10660)

Qy           3 LeuProThrProThrProSer 9
               |||||||||||||||||||||
Db        9542 CTACCTACGCCTACGCCTTCG 9522

RESULT 68
US-11-266-409-9
; Sequence 9, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
;  APPLICANT: SUZUMURA, AKIO
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
;  FILE REFERENCE: 279847US40
;  CURRENT APPLICATION NUMBER: US/11/266,409
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: US 60/624,851
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-11-266-409-9

Alignment Scores:
Pred. No.:             56.1            Length:         22
Score:                 6.00            Matches:        6
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           3.0%            Indels:         0
DB:                    7               Gaps:           0

US-10-821-670A-36 (1-197) x US-11-266-409-9 (1-22)

Qy         108 AspLeuLysMetTyrGln 113
               |||||||||||||||||
Db           1 GACTTGAAGATGTACCAG 18

RESULT 69
US-11-217-529-36402
; Sequence 36402, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
```

APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 36402
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-36402

gnment Scores:

d. No.:	63.2	Length:	25
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.0%	Indels:	0
	7	Gaps:	0

10-821-670A-36 (1-197) x US-11-217-529-36402 (1-25)

```
        56 LysThrSerThrValGlu 61
           |||||||||||||||||||
         3 AAAACCTCCACCGTAGAG 20
```

ULT 70
11-217-529-47657/c
equence 47657, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 47657
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-47657

gnment Scores:

d. No.:	63.2	Length:	25
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.0%	Indels:	0
	7	Gaps:	0

10-821-670A-36 (1-197) x US-11-217-529-47657 (1-25)

```
         1 ArgAsnLeuProThrPro 6
           ||||||||||||||||||||
        21 CGTAATTTACCCACGCCA 4
```

ULT 71
11-217-529-87245
equence 87245, Application US/11217529

; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87245
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-87245

Alignment Scores:

Pred. No.:	63.2	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x US-11-217-529-87245 (1-25)

```
Qy         57 ThrSerThrValGluAla 62
              |||||||||||||||||||
Db          3 ACCTCTACTGTGGAGGCA 20
```

RESULT 72
US-11-217-529-88955/c
; Sequence 88955, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88955
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-88955

Alignment Scores:

Pred. No.:	63.2	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x US-11-217-529-88955 (1-25)

```
Qy         90 AlaSerArgLysThrSer 95
              |||||||||||||||||||
```

```
        23 GCTTCAAGAAAGACATCC 6

ULT 73
11-217-529-109690
equence 109690, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 109690
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-109690

gnment Scores:
d. No.:                63.2          Length:         25
re:                    6.00          Matches:        6
cent Similarity:       100.0%        Conservative:   0
t Local Similarity:    100.0%        Mismatches:     0
ry Match:              3.0%          Indels:         0
                       7             Gaps:           0

10-821-670A-36 (1-197) x US-11-217-529-109690 (1-25)

       161 LeuGluGluProAspPhe 166
           |||||||||||||||||||
         5 CTTGAGGAACCCGATTTT 22

ULT 74
11-217-529-148883
equence 148883, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 148883
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-148883

gnment Scores:
d. No.:                63.2          Length:         25
re:                    6.00          Matches:        6
cent Similarity:       100.0%        Conservative:   0
t Local Similarity:    100.0%        Mismatches:     0
ry Match:              3.0%          Indels:         0
                       7             Gaps:           0

US-10-821-670A-36 (1-197) x US-11-217-529-148883 (1-25)

Qy         101 CysLeuSerSerIleTyr 106
               ||||||||||||||||||
Db           4 TGCCTTTCCTCTATTTAT 21

RESULT 75
US-11-217-529-162336
; Sequence 162336, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162336
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-162336

Alignment Scores:
Pred. No.:                63.2          Length:         25
Score:                    6.00          Matches:        6
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              3.0%          Indels:         0
DB:                       7             Gaps:           0

US-10-821-670A-36 (1-197) x US-11-217-529-162336 (1-25)

Qy          97 MetThrThrLeuCysLeu 102
               |||||||||||||||||||
Db           4 ATGACCACCCTTTGCCTC 21

RESULT 76
US-11-217-529-162342
; Sequence 162342, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162342
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-162342

Alignment Scores:
Pred. No.:                63.2          Length:         25
```

›re:	6.00	Matches:	6
:cent Similarity:	100.0%	Conservative:	0
:t Local Similarity:	100.0%	Mismatches:	0
›ry Match:	3.0%	Indels:	0
	7	Gaps:	0

·10-821-670A-36 (1-197) x US-11-217-529-162342 (1-25)

```
        97 MetThrThrLeuCysLeu 102
           |||||||||||||||||
         3 ATGACCACCCTTTGCCTC 20
```

:ULT 77
·11-217-529-184372/c
:equence 184372, Application US/11217529
:ublication No. US20060099612A1
:ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
:EQ ID NO 184372
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
·11-217-529-184372

:gnment Scores:			
:d. No.:	63.2	Length:	25
›re:	6.00	Matches:	6
:cent Similarity:	100.0%	Conservative:	0
:t Local Similarity:	100.0%	Mismatches:	0
›ry Match:	3.0%	Indels:	0
	7	Gaps:	0

·10-821-670A-36 (1-197) x US-11-217-529-184372 (1-25)

```
        20 GlnThrLeuLeuArgAla 25
           |||||||||||||||||
        21 CAGACTCTTCTGAGAGCC 4
```

:ULT 78
·11-143-642-246/c
:equence 246, Application US/11143642
:ublication No. US20060099610A1
:ENERAL INFORMATION:
APPLICANT: Jukka T. SALONEN et al.
TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF ACUTE MYOCARDIAL INFARCTIC
FILE REFERENCE: 0933-0245PUS1
CURRENT APPLICATION NUMBER: US/11/143,642
CURRENT FILING DATE: 2005-06-03
NUMBER OF SEQ ID NOS: 2039
SOFTWARE: PatentIn version 3.3
:EQ ID NO 246
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
·11-143-642-246

:gnment Scores:			
:d. No.:	124	Length:	51
›re:	6.00	Matches:	6
:cent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x US-11-143-642-246 (1-51)

```
Qy         89 LeuAlaSerArgLysThr 94
              |||||||||||||||||
Db         49 TTAGCAAGCAGGAAAACT 32
```

RESULT 79
US-11-296-092-22/c
; Sequence 22, Application US/11296092
; Publication No. US20060105427A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,092
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 22
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-11-296-092-22

Alignment Scores:			
Pred. No.:	165	Length:	69
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	7	Gaps:	0

10-821-670A-36 (1-197) x US-11-296-092-22 (1-69)

```
       102 LeuSerSerIleTyrGlu 107
           ||||||||||||||||||
        27 CTTTCGTCCATCTATGAG 10
```

ULT 80
10-525-817-154/c
equence 154, Application US/10525817
ublication No. US20060099592A1
ENERAL INFORMATION:
APPLICANT: Nuevolution A/S
ITLE OF INVENTION: Enzymatic encoding
FILE REFERENCE: P912PC00
CURRENT APPLICATION NUMBER: US/10/525,817
CURRENT FILING DATE: 2005-02-25
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.1
EQ ID NO 154
LENGTH: 84
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially produced
10-525-817-154

gnment Scores:

d. No.:	198	Length:	84
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.0%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-525-817-154 (1-84)

```
       90 AlaSerArgLysThrSer 95
          |||||||||||||||||||
       35 GCTTCTAGGAAGACTTCC 18
```

ULT 81
10-525-817-155/c
equence 155, Application US/10525817
ublication No. US20060099592A1
ENERAL INFORMATION:
APPLICANT: Nuevolution A/S
TITLE OF INVENTION: Enzymatic encoding
FILE REFERENCE: P912PC00
CURRENT APPLICATION NUMBER: US/10/525,817
CURRENT FILING DATE: 2005-02-25
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.1
EQ ID NO 155
LENGTH: 84
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially produced
10-525-817-155

gnment Scores:

d. No.:	198	Length:	84
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.0%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-525-817-155 (1-84)

```
       90 AlaSerArgLysThrSer 95
          |||||||||||||||||||
```

```
Db         35 GCTTCTAGGAAGACTTCC 18
```

RESULT 82
US-10-525-817-156/c
; Sequence 156, Application US/10525817
; Publication No. US20060099592A1
; GENERAL INFORMATION:
; APPLICANT: Nuevolution A/S
; TITLE OF INVENTION: Enzymatic encoding
; FILE REFERENCE: P912PC00
; CURRENT APPLICATION NUMBER: US/10/525,817
; CURRENT FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced
US-10-525-817-156

Alignment Scores:

Pred. No.:	198	Length:	84
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-525-817-156 (1-84)

```
Qy         90 AlaSerArgLysThrSer 95
              |||||||||||||||||||
Db         35 GCTTCTAGGAAGACTTCC 18
```

RESULT 83
US-10-525-817-157/c
; Sequence 157, Application US/10525817
; Publication No. US20060099592A1
; GENERAL INFORMATION:
; APPLICANT: Nuevolution A/S
; TITLE OF INVENTION: Enzymatic encoding
; FILE REFERENCE: P912PC00
; CURRENT APPLICATION NUMBER: US/10/525,817
; CURRENT FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced
US-10-525-817-157

Alignment Scores:

Pred. No.:	198	Length:	84
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-525-817-157 (1-84)

```
Qy         90 AlaSerArgLysThrSer 95
              |||||||||||||||||||
Db         35 GCTTCTAGGAAGACTTCC 18
```

RESULT 84
US-11-217-529-6033/c
; Sequence 6033, Application US/11217529

```
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6033
  LENGTH: 93
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
11-217-529-6033

gnment Scores:
d. No.:                 218             Length:         93
re:                     6.00            Matches:        6
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.0%            Indels:         0
                        7               Gaps:           0

10-821-670A-36 (1-197) x US-11-217-529-6033 (1-93)

       152 SerValThrValProGln 157
           ||||||||||||||||||
        45 TCTGTGACCGTCCCCCAA 28

ULT 85
10-471-571A-5635
equence 5635, Application US/10471571A
ublication No. US20060115490A1
ENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE:  2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
EQ ID NO 5635
  LENGTH: 114
  TYPE: DNA
  ORGANISM: Staphylococcus aureus
10-471-571A-5635

gnment Scores:
d. No.:                 264             Length:         114
re:                     6.00            Matches:        6
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.0%            Indels:         0
                        6               Gaps:           0

10-821-670A-36 (1-197) x US-10-471-571A-5635 (1-114)

        70 MetAsnGluSerCysLeu 75
           |||||||||||||||||||
        79 ATGAATGAAAGTTGCCTT 96

ULT 86
11-217-529-81244
equence 81244, Application US/11217529
```

```
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81244
;   LENGTH: 162
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81244

Alignment Scores:
Pred. No.:              368             Length:         162
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.0%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-36 (1-197) x US-11-217-529-81244 (1-162)

Qy         101 CysLeuSerSerIleTyr 106
               ||||||||||||||||||
Db          78 TGCCTTTCCTCTATTTAT 95

RESULT 87
US-10-148-883-21/c
; Sequence 21, Application US/10148883
; Publication No. US20060115811A1
; GENERAL INFORMATION:
;  APPLICANT: Jay White et al.
;  TITLE OF INVENTION: Cytochrome P450RA1-2 and Related Proteins
;  FILE REFERENCE: 11812-49
;  CURRENT APPLICATION NUMBER: US/10/148,883
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US 60/171,110
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: US 60/178,314
;  PRIOR FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
;   LENGTH: 205
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-148-883-21

Alignment Scores:
Pred. No.:              459             Length:         205
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.0%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-148-883-21 (1-205)

Qy           4 ProThrProThrProSer 9
               ||||||||||||||||||
Db          31 CCGACACCAACTCCAAGC 14

RESULT 88
```

```
10-471-571A-4689/c
equence 4689, Application US/10471571A
ublication No. US20060115490A1
ENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE:  2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
EQ ID NO 4689
 LENGTH: 213
 TYPE: DNA
 ORGANISM: Staphylococcus aureus
10-471-571A-4689

gnment Scores:
d. No.:                476             Length:         213
re:                    6.00            Matches:        6
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              3.0%            Indels:         0
                       6               Gaps:           0

10-821-670A-36 (1-197) x US-10-471-571A-4689 (1-213)

       130 GlnIlePheLeuAspGln 135
           ||||||||||||||||||
        31 CAAATTTTTCTGGATCAA 14

ULT 89
11-217-529-174474/c
equence 174474, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 174474
 LENGTH: 231
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-174474

gnment Scores:
d. No.:                514             Length:         231
re:                    6.00            Matches:        6
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              3.0%            Indels:         0
                       7               Gaps:           0

10-821-670A-36 (1-197) x US-11-217-529-174474 (1-231)

        79 GluIleSerLeuIleThr 84
           |||||||||||||||||
       141 GAGATTTCCCTCATCACC 124

ULT 90
```

```
US-11-217-529-166542
; Sequence 166542, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166542
;   LENGTH: 276
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-166542

Alignment Scores:
Pred. No.:                607             Length:         276
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.0%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-36 (1-197) x US-11-217-529-166542 (1-276)

Qy          37 LeuGluPheTyrSerCys 42
               ||||||||||||||||||
Db          11 TTGGAGTTTTATAGTTGT 28

RESULT 91
US-11-217-529-5007/c
; Sequence 5007, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5007
;   LENGTH: 303
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-5007

Alignment Scores:
Pred. No.:                663             Length:         303
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              3.0%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-36 (1-197) x US-11-217-529-5007 (1-303)
```

```
          2 AsnLeuProThrProThr 7
            ||||||||||||||||||
         95 AATTTACCAACACCGACT 78

ULT 92
11-217-529-5166/c
equence 5166, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
EQ ID NO 5166
  LENGTH: 303
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
11-217-529-5166

gnment Scores:
d. No.:                663            Length:          303
re:                    6.00           Matches:         6
cent Similarity:       100.0%         Conservative:    0
t Local Similarity:    100.0%         Mismatches:      0
ry Match:              3.0%           Indels:          0
                       7              Gaps:            0

10-821-670A-36 (1-197) x US-11-217-529-5166 (1-303)

          2 AsnLeuProThrProThr 7
            ||||||||||||||||||
         95 AATTTACCAACACCGACT 78

ULT 93
11-217-529-80985/c
equence 80985, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
EQ ID NO 80985
  LENGTH: 303
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
11-217-529-80985

gnment Scores:
d. No.:                663            Length:          303
re:                    6.00           Matches:         6
cent Similarity:       100.0%         Conservative:    0
t Local Similarity:    100.0%         Mismatches:      0
Query Match:           3.0%           Indels:          0
DB:                    7              Gaps:            0

US-10-821-670A-36 (1-197) x US-11-217-529-80985 (1-303)

Qy          2 AsnLeuProThrProThr 7
              ||||||||||||||||||
Db         95 AACTTACCAACACCGACT 78

RESULT 94
US-11-217-529-81183/c
; Sequence 81183, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81183
;   LENGTH: 303
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81183

Alignment Scores:
Pred. No.:             663            Length:          303
Score:                 6.00           Matches:         6
Percent Similarity:    100.0%         Conservative:    0
Best Local Similarity: 100.0%         Mismatches:      0
Query Match:           3.0%           Indels:          0
DB:                    7              Gaps:            0

US-10-821-670A-36 (1-197) x US-11-217-529-81183 (1-303)

Qy          2 AsnLeuProThrProThr 7
              ||||||||||||||||||
Db         95 AATTTACCAACACCAACT 78

RESULT 95
US-11-217-529-174171/c
; Sequence 174171, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174171
;   LENGTH: 303
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174171
```

gnment Scores:
d. No.: 663 Length: 303
re: 6.00 Matches: 6
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 3.0% Indels: 0
7 Gaps: 0

10-821-670A-36 (1-197) x US-11-217-529-174171 (1-303)

101 CysLeuSerSerIleTyr 106
||||||||||||||||||
234 TGTCTGAGCAGTATTTAT 217

ULT 96
11-301-554-610/c
equence 610, Application US/11301554
ublication No. US20060088527A1
ENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C21
CURRENT APPLICATION NUMBER: US/11/301,554
CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US 10/113,872
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 10/017,754
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/849,626
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 09/736,457
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 09/702,705
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US 09/677,419
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 09/671,325
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/658,824
PRIOR FILING DATE: 2000-09-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 610
LENGTH: 310
TYPE: DNA
ORGANISM: Homo sapiens
11-301-554-610

gnment Scores:
d. No.: 678 Length: 310
re: 6.00 Matches: 6
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 3.0% Indels: 0
7 Gaps: 0

US-10-821-670A-36 (1-197) x US-11-301-554-610 (1-310)

Qy 35 GlnThrLeuGluPheTyr 40
||||||||||||||||||
Db 106 CAAACTCTGGAGTTCTAT 89

RESULT 97
US-11-217-529-4461
; Sequence 4461, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4461
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4461

Alignment Scores:
Pred. No.: 712 Length: 327
Score: 6.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 3.0% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-36 (1-197) x US-11-217-529-4461 (1-327)

Qy 84 ThrAsnGlySerCysLeu 89
||||||||||||||||||
Db 93 ACTAATGGAAGTTGTTTA 110

RESULT 98
US-11-254-679-18/c
; Sequence 18, Application US/11254679
; Publication No. US20060099207A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Kiener, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyle, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMGB1 and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103

SOFTWARE: PatentIn version 3.3
EQ ID NO 18
LENGTH: 336
TYPE: DNA
ORGANISM: Homo sapiens
11-254-679-18

gnment Scores:

d. No.:	731	Length:	336
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.0%	Indels:	0
	7	Gaps:	0

10-821-670A-36 (1-197) x US-11-254-679-18 (1-336)

```
        57 ThrSerThrValGluAla 62
           |||||||||||||||||
       307 ACGTCCACTGTGGAGGCC 290
```

ULT 99
10-511-937-623
equence 623, Application US/10511937
ublication No. US20060088836A1
ENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
EQ ID NO 623
LENGTH: 345
TYPE: DNA
ORGANISM: Homo sapiens
10-511-937-623

gnment Scores:

d. No.:	749	Length:	345
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.0%	Indels:	0
	6	Gaps:	0

10-821-670A-36 (1-197) x US-10-511-937-623 (1-345)

```
        36 ThrLeuGluPheTyrSer 41
           |||||||||||||||||
       124 ACTCTTGAGTTCTATTCT 141
```

ULT 100
11-254-679-20
equence 20, Application US/11254679
ublication No. US20060099207A1
ENERAL INFORMATION:
APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Kiener, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyle, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMGB1 and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-254-679-20

Alignment Scores:

Pred. No.:	762	Length:	351
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x US-11-254-679-20 (1-351)

```
Qy        154 ThrValProGlnAsnSer 159
              |||||||||||||||||
Db        284 ACTGTACCACAGAATTCT 301
```

Search completed: June 10, 2006, 02:12:58
Job time : 41.4261 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

M protein - nucleic search, using frame_plus_p2n model

un on: June 10, 2006, 01:33:29 ; Search time 5057.64 Seconds
(without alignments)
4210.361 Million cell updates/sec

tle: US-10-821-670A-33
rfect score: 222
equence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Pgapext 7.0
Delop 60.0 , Delext 60.0

arched: 6366136 seqs, 31973710525 residues

ord size: 1

tal number of hits satisfying chosen parameters: 12722138

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110449_27523/app_query.fasta_1
B=GenEmbl -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rge -MINMATCH=0.1
OOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
RANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
LIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
AXLEN=2000000000 -HOST=abss08
SER=US10821670_@CGN_1_1_6646_@runat_07062006_110449_27523 -NCPU=6 -ICPU=3
NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	222	100.0	666	2	AR595952	AR595952 Sequence
2	222	100.0	666	2	AR595953	AR595953 Sequence
3	222	100.0	669	14	FCIL12P35	Y07761 Felis catus
4	220	99.1	689	2	AR242451	AR242451 Sequence
5	220	99.1	689	2	AR280219	AR280219 Sequence
6	220	99.1	689	2	AR322434	AR322434 Sequence
7	220	99.1	1441	2	AR242438	AR242438 Sequence
8	220	99.1	1441	2	AR280206	AR280206 Sequence
9	220	99.1	1441	2	AR322421	AR322421 Sequence
10	197	88.7	591	2	AR595954	AR595954 Sequence
c 11	197	88.7	591	2	AR595955	AR595955 Sequence
12	197	88.7	1533	2	AR595959	AR595959 Sequence
c 13	197	88.7	1533	2	AR595960	AR595960 Sequence
14	197	88.7	1599	2	AR595956	AR595956 Sequence
c 15	197	88.7	1599	2	AR595957	AR595957 Sequence
16	195	87.8	591	2	AR242439	AR242439 Sequence
17	195	87.8	591	2	AR280207	AR280207 Sequence
18	195	87.8	591	2	AR322422	AR322422 Sequence
19	187	84.2	561	2	AR596007	AR596007 Sequence
c 20	187	84.2	561	2	AR596008	AR596008 Sequence
21	154	69.4	669	14	FCU83185	U83185 Felis catus
22	84	37.8	285	14	AF054605	AF054605 Felis cat
23	65	29.3	669	2	AX076201	AX076201 Sequence
24	65	29.3	669	2	AX076483	AX076483 Sequence
25	65	29.3	4201	2	AX076477	AX076477 Sequence
26	59	26.6	660	2	AX154615	AX154615 Sequence
27	59	26.6	660	2	AX154619	AX154619 Sequence
28	59	26.6	660	2	AX154620	AX154620 Sequence
29	56	25.2	660	2	AX154616	AX154616 Sequence
30	52	23.4	591	2	BD171284	BD171284 Novel can
31	52	23.4	591	2	AR595963	AR595963 Sequence
c 32	52	23.4	591	2	AR595964	AR595964 Sequence
33	52	23.4	666	2	AR595961	AR595961 Sequence
c 34	52	23.4	666	2	AR595962	AR595962 Sequence
35	52	23.4	669	2	AR151062	AR151062 Sequence
36	52	23.4	669	2	AR151072	AR151072 Sequence
37	52	23.4	669	2	BD014654	BD014654 Process f
38	52	23.4	669	2	BD014664	BD014664 Process f
39	52	23.4	669	2	E15018	E15018 Canine mRNA
40	52	23.4	669	2	AR316461	AR316461 Sequence
41	52	23.4	669	2	AR316471	AR316471 Sequence
42	52	23.4	1282	2	BD171283	BD171283 Novel can
43	52	23.4	1455	2	AR596009	AR596009 Sequence
c 44	52	23.4	1455	2	AR596010	AR596010 Sequence
45	52	23.4	1533	2	AR595973	AR595973 Sequence
c 46	52	23.4	1533	2	AR595974	AR595974 Sequence
47	52	23.4	1599	2	AR595971	AR595971 Sequence
c 48	52	23.4	1599	2	AR595972	AR595972 Sequence
49	50	22.5	669	14	CFU49085	U49085 Canis famil
50	43	19.4	666	2	AX154613	AX154613 Sequence
51	42	18.9	618	14	AY603407	AY603407 Capra hir
52	42	18.9	666	14	AF173557	AF173557 Ovis arie
53	42	18.9	666	14	AY232819	AY232819 Bubalus b
54	42	18.9	690	14	AB246272	AB246272 Bubalus c
55	42	18.9	690	14	AB246352	AB246352 Bubalus b
56	42	18.9	690	14	AB246359	AB246359 Bubalus b
57	42	18.9	690	14	AF003542	AF003542 Capra hir
58	42	18.9	690	14	BTU14416	U14416 Bos taurus
59	40	18.0	666	14	CEU57751	U57751 Cervus elap
60	40	18.0	669	14	AB107653	AB107653 Lama glam
61	40	18.0	669	14	AB246672	AB246672 Camelus b
62	40	18.0	703	2	E35793	E35793 Process for
63	39	17.6	657	8	AY191828	AY191828 Synthetic
64	39	17.6	660	2	AX154614	AX154614 Sequence
65	39	17.6	660	2	AX154617	AX154617 Sequence
66	39	17.6	660	2	AX154621	AX154621 Sequence
67	37	16.7	660	2	AX154618	AX154618 Sequence
68	34	15.3	1426	14	PIGIL12PSU	L35765 Sus scrofa
69	31	14.0	666	2	AX154612	AX154612 Sequence
70	30	13.5	669	14	ECIL12P35	Y11130 Equus cabal
71	30	13.5	1626	8	AF401989	AF401989 Synthetic
72	29	13.1	660	2	AR008951	AR008951 Sequence
73	29	13.1	660	2	BD007071	BD007071 IL-12 gen
74	29	13.1	660	2	BD007079	BD007079 Gene expr
75	29	13.1	660	2	BD007080	BD007080 Gene expr

76	29	13.1	660	2	BD007081	BD007081 Gene expr
77	29	13.1	660	2	BD136037	BD136037 Interfero
78	29	13.1	660	2	BD136038	BD136038 Interfero
79	29	13.1	660	2	BD136039	BD136039 Interfero
80	29	13.1	660	2	I28592	I28592 Sequence 3
81	29	13.1	660	2	AX154634	AX154634 Sequence
82	29	13.1	702	2	CQ829447	CQ829447 Sequence
83	29	13.1	721	2	AR052862	AR052862 Sequence
84	29	13.1	721	2	AR288174	AR288174 Sequence
85	29	13.1	721	2	AR567161	AR567161 Sequence
86	29	13.1	762	2	BD105971	BD105971 Animal mo
87	29	13.1	762	2	CQ803343	CQ803343 Sequence
88	29	13.1	762	2	AR533401	AR533401 Sequence
89	29	13.1	762	5	AF101062	AF101062 Homo sapi
90	29	13.1	780	5	MMU19842	U19842 Macaca mula
91	29	13.1	823	5	AF180562	AF180562 Homo sapi
92	29	13.1	856	2	BD165801	BD165801 Antibody
93	29	13.1	1020	2	CQ716168	CQ716168 Sequence
94	29	13.1	1021	5	BC104982	BC104982 Homo sapi
95	29	13.1	1021	5	BC104984	BC104984 Homo sapi
96	29	13.1	1026	2	AR091390	AR091390 Sequence
97	29	13.1	1026	2	AR380496	AR380496 Sequence
98	29	13.1	1026	5	HUMCLMF35	M65271 Human cytot
99	29	13.1	1287	2	AR393790	AR393790 Sequence
100	29	13.1	1287	2	AX084108	AX084108 Sequence
101	29	13.1	1316	2	AR050785	AR050785 Sequence
102	29	13.1	1316	2	AR212036	AR212036 Sequence
103	29	13.1	1316	5	HUMNKSFP35	M65291 Human natur
104	29	13.1	1364	2	AR082685	AR082685 Sequence
105	29	13.1	1364	2	AR122961	AR122961 Sequence
106	29	13.1	1364	2	I28326	I28326 Sequence 3
107	29	13.1	1364	2	I89771	I89771 Sequence 3
108	29	13.1	1395	2	AR309637	AR309637 Sequence
109	29	13.1	1444	2	CS032085	CS032085 Sequence
110	29	13.1	1444	2	CS041037	CS041037 Sequence
111	29	13.1	1444	2	CS143811	CS143811 Sequence
112	29	13.1	1560	2	AR091395	AR091395 Sequence
113	29	13.1	1623	2	AR091394	AR091394 Sequence
114	29	13.1	1645	2	A92078	A92078 Sequence 2
115	29	13.1	1645	2	AR230689	AR230689 Sequence
116	29	13.1	3205	2	CS131489	CS131489 Sequence
117	29	13.1	5686	2	BD136048	BD136048 Interfero
118	29	13.1	6139	2	AR091393	AR091393 Sequence
119	29	13.1	11792	5	AF404773	AF404773 Homo sapi
120	29	13.1	157079	5	AC010370	AC010370 Homo sapi
121	29	13.1	176108	5	AC026118	AC026118 Homo sapi
122	29	13.1	300140	12	AC129109	AC129109 Homo sapi
123	27	12.2	785	5	AY234219	AY234219 Papio anu
124	27	12.2	786	5	CTU19835	U19835 Cercocebus
125	26	11.7	79	2	AR242449	AR242449 Sequence
126	26	11.7	79	2	AR280217	AR280217 Sequence
127	26	11.7	79	2	AR322432	AR322432 Sequence
128	26	11.7	817	14	AY686642	AY686642 Equus cab
129	23	10.4	71	2	AX076207	AX076207 Sequence
130	23	10.4	95	2	AR242447	AR242447 Sequence
131	23	10.4	95	2	AR280215	AR280215 Sequence
132	23	10.4	95	2	AR322430	AR322430 Sequence
133	21	9.5	711	14	BTA271034	AJ271034 Bos tauru
134	21	9.5	714	14	OAR271035	AJ271035 Ovis arie
135	18	8.1	76	2	AX076205	AX076205 Sequence
136	18	8.1	76	2	AX076208	AX076208 Sequence
137	16	7.2	666	6	AB025723	AB025723 Cavia por
138	15	6.8	827	6	AF421396	AF421396 Sigmodon
139	14	6.3	559	7	BV429425	BV429425 S237P6482
140	14	6.3	1239	6	AB085791	AB085791 Mesocrice
141	13	5.9	60	2	CQ542775	CQ542775 Sequence
142	13	5.9	660	2	BD136054	BD136054 Interfero
143	12	5.4	36	2	AR242450	AR242450 Sequence
144	12	5.4	36	2	AR280218	AR280218 Sequence
145	12	5.4	36	2	AR322433	AR322433 Sequence
146	12	5.4	144	14	AY388980S3	AY388982 Sus scrof
147	12	5.4	1119	6	AF288849	AF288849 Meriones
148	11	5.0	39	2	AR595997	AR595997 Sequence
149	11	5.0	672	6	AF288520	AF288520 Marmota m
150	11	5.0	672	6	MMIL12P35	X97018 M.monax mRN
151	10	4.5	39	2	AR151075	AR151075 Sequence
152	10	4.5	39	2	BD014667	BD014667 Process f
153	10	4.5	39	2	E15029	E15029 PCR primer
154	10	4.5	39	2	AR316474	AR316474 Sequence
155	10	4.5	60	2	AR595989	AR595989 Sequence
c 156	10	4.5	60	2	AR595990	AR595990 Sequence
157	10	4.5	146	14	AY575615	AY575615 Ovis arie
158	10	4.5	146	14	AY575616	AY575616 Ovis arie
c 159	10	4.5	322	7	BV094414	BV094414 RPAMMSEQ0
c 160	10	4.5	483	7	BV300932	BV300932 S239P60FH
161	10	4.5	582	2	AR393785	AR393785 Sequence
162	10	4.5	582	2	AX084103	AX084103 Sequence
163	10	4.5	660	2	E26662	E26662 Improved me
164	10	4.5	700	6	S82412S4	S82418 interleukin
165	10	4.5	713	2	AR069652	AR069652 Sequence
166	10	4.5	713	6	AF128212	AF128212 Mus muscu
167	10	4.5	713	6	AF128213	AF128213 Mus muscu
168	10	4.5	786	6	AF128210	AF128210 Mus muscu
169	10	4.5	786	6	AF128211	AF128211 Mus muscu
170	10	4.5	793	6	AF177031	AF177031 Rattus no
171	10	4.5	1265	6	MUSIL35A	M86672 Mus musculu
172	10	4.5	1278	2	AR393789	AR393789 Sequence
173	10	4.5	1278	2	AX084107	AX084107 Sequence
174	10	4.5	1569	2	AR393796	AR393796 Sequence
175	10	4.5	1569	2	AX084114	AX084114 Sequence
176	10	4.5	1669	8	AF411293	AF411293 Synthetic
177	10	4.5	2013	2	AR393795	AR393795 Sequence
178	10	4.5	2013	2	AX084113	AX084113 Sequence
179	10	4.5	2438	2	CQ812173	CQ812173 Sequence
180	10	4.5	2709	2	AR393797	AR393797 Sequence
181	10	4.5	2709	2	AX084115	AX084115 Sequence
182	10	4.5	5252	2	CQ803341	CQ803341 Sequence
183	10	4.5	5966	2	BD136050	BD136050 Interfero
184	10	4.5	9049	2	CQ803350	CQ803350 Sequence
185	10	4.5	10633	2	CQ803349	CQ803349 Sequence
186	10	4.5	11746	2	CQ803348	CQ803348 Sequence
187	10	4.5	38246	2	CQ803351	CQ803351 Sequence
c 188	10	4.5	176759	6	AC151973	AC151973 Mus muscu
c 189	10	4.5	195059	6	AC121306	AC121306 Mus muscu
190	10	4.5	206660	6	AC122356	AC122356 Mus muscu
c 191	10	4.5	215198	6	AC113180	AC113180 Mus muscu
192	10	4.5	218029	12	AC108606	AC108606 Rattus no
c 193	10	4.5	223879	12	AC111877	AC111877 Rattus no
194	10	4.5	248528	12	AC095666	AC095666 Rattus no
c 195	10	4.5	256720	6	AC110241	AC110241 Mus muscu
196	9	4.1	29	2	BD014609	BD014609 Process f
197	9	4.1	29	2	BD174649	BD174649 Process f
c 198	9	4.1	51	2	AR596002	AR596002 Sequence
c 199	9	4.1	190	5	HUMEL10	M17273 Human elast
200	9	4.1	282	2	AX308844	AX308844 Sequence

ALIGNMENTS

```
RESULT 1
AR595952
LOCUS       AR595952                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 32 from patent US 6818444.
ACCESSION   AR595952
VERSION     AR595952.1  GI:56646933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 32 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
```

```
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.17e-223       Length:         666
Score:                  222.00          Matches:        222
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR595952 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

            121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              ||||||
Db        661 GCTTCC 666

RESULT 2
AR595953/c
LOCUS       AR595953                666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.17e-223       Length:         666
Score:                  222.00          Matches:        222
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR595953 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
              ||||||
Db          6 GCTTCC 1

RESULT 3
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
```

```
RSION     Y07761.1  GI:2102662
YWORDS    interleukin-12 subunit p35.
URCE      Felis catus (cat)
ORGANISM  Felis catus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
          Felinae; Felis.
FERENCE   1
AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
TITLE     Molecular cloning of cat interleukin-12
JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
 PUBMED   9089110
FERENCE   2  (bases 1 to 669)
AUTHORS   Schijns,V.E.C.J.
TITLE     Direct Submission
JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
          Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
          Utrecht, NETHERLANDS
ATURES              Location/Qualifiers
   source           1. .669
                    /organism="Felis catus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9685"
                    /cell_type="lymphocyte"
                    /tissue_type="peripheral blood"
   gene             1. .669
                    /gene="IL-12.p35"
   CDS              1. .669
                    /gene="IL-12.p35"
                    /function="heterodimer with IL-12 p40 chain"
                    /codon_start=1
                    /product="interleukin-12 p35 chain"
                    /protein_id="CAA69067.1"
                    /db_xref="GI:2102663"
                    /db_xref="GOA:O02743"
                    /db_xref="InterPro:IPR004281"
                    /db_xref="InterPro:IPR009079"
                    /db_xref="UniProtKB/Swiss-Prot:O02743"
                    /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                    QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                    REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                    NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                    LNAS"
IGIN

ignment Scores:
ed. No.:              1.18e-223      Length:        669
ore:                  222.00         Matches:       222
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            100.0%         Indels:        0
:                     14             Gaps:          0

-10-821-670A-33 (1-222) x FCIL12P35 (1-669)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy       101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy       121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy       141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy       161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy       181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy       201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy       221 AlaSer 222
             ||||||
Db       661 GCTTCC 666

RESULT 4
AR242451
LOCUS       AR242451                689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.54e-221      Length:        689
Score:                  220.00         Matches:       220
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            99.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AR242451 (1-689)

Qy         1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy        21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy        41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp  80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

RESULT 5
AR280219
LOCUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6518045.
ACCESSION   AR280219
VERSION     AR280219.1  GI:29715609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.54e-221      Length:         689
Score:                  220.00         Matches:        220
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.1%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AR280219 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp  80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

RESULT 6
AR322434
LOCUS       AR322434                689 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 26 from patent US 6566097.
ACCESSION   AR322434
VERSION     AR322434.1  GI:33708187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 26 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.54e-221      Length:         689
Score:                  220.00         Matches:        220
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.1%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AR322434 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

SULT 7
242438
CUS       AR242438               1441 bp    mRNA    linear   PAT 20-DEC-2002
FINITION  Sequence 8 from patent US 6472509.
CESSION   AR242438
RSION     AR242438.1  GI:27288855
YWORDS    .
JRCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1441)
AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
ITLE      Feline cytokine protein
JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
          Juridical Foundation: The Chemo-Seso-Therapeutic Research
          Institute; Kumamoto;
          EPX;
ATURES             Location/Qualifiers
    source         1. .1441
                   /organism="unknown"
                   /mol_type="mRNA"
IGIN

ignment Scores:
ed. No.:              3e-221          Length:         1441
ore:                  220.00          Matches:        220
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            99.1%           Indels:         0
:                     2               Gaps:           0
```

```
US-10-821-670A-33 (1-222) x AR242438 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

RESULT 8
AR280206
LOCUS       AR280206               1441 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518045.
ACCESSION   AR280206
VERSION     AR280206.1  GI:29715596
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 8 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              3e-221          Length:         1441
Score:                  220.00          Matches:        220
Percent Similarity:     100.0%          Conservative:   0
```

```
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            99.1%         Indels:        0
::                    2             Gaps:          0

-10-821-670A-33 (1-222) x AR280206 (1-1441)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

SULT 9
322421
CUS       AR322421              1441 bp    mRNA    linear   PAT 17-AUG-2003
FINITION  Sequence 8 from patent US 6566097.
CCESSION  AR322421
RSION     AR322421.1  GI:33708174
YWORDS    .
URCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
FERENCE   1  (bases 1 to 1441)
 AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
 TITLE     Feline cytokine protein
 JOURNAL   Patent: US 6566097-A 8 20-MAY-2003;
           Juridical Foundation The Chemo-Sero-Therapeutic Research
           Institute;;
           EPX;
ATURES             Location/Qualifiers
     source        1. .1441
                   /organism="unknown"
                   /mol_type="mRNA"

IGIN
```

```
Alignment Scores:
Pred. No.:              3e-221        Length:          1441
Score:                  220.00        Matches:         220
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            99.1%         Indels:          0
DB:                     2             Gaps:            0

US-10-821-670A-33 (1-222) x AR322421 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

RESULT 10
AR595954
LOCUS       AR595954                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 35 from patent US 6818444.
ACCESSION   AR595954
VERSION     AR595954.1  GI:56646935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 35 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .591
                      /organism="unknown"
                      /mol_type="genomic DNA"
```

```
IGIN

lignment Scores:
ed. No.:                2.2e-197        Length:         591
ore:                    197.00          Matches:        197
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              88.7%           Indels:         0
:                       2               Gaps:           0

3-10-821-670A-33 (1-222) x AR595954 (1-591)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

SULT 11
595955/c
CUS        AR595955                 591 bp    DNA     linear   PAT 15-DEC-2004
FINITION   Sequence 37 from patent US 6818444.
CESSION    AR595955
RSION      AR595955.1  GI:56646936
YWORDS     .
URCE       Unknown.
ORGANISM   Unknown.
           Unclassified.
FERENCE    1  (bases 1 to 591)
AUTHORS    Wonderling,R.S. and Boroughs,K.L.
TITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL    Patent: US 6818444-A 37 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
ATURES              Location/Qualifiers
   source           1. .591
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN
```

```
Alignment Scores:
Pred. No.:              2.2e-197        Length:         591
Score:                  197.00          Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            88.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR595955 (1-591)

Qy          26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy          46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy          66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy          86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy         126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy         146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy         166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy         186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy         206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 12
AR595959
LOCUS       AR595959                 1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .1533
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.2e-197        Length:         1533
```

```
ore:                    197.00          Matches:        197
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              88.7%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-33 (1-222) x AR595959 (1-1533)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

SULT 13
595960/c
CUS       AR595960                1533 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 45 from patent US 6818444.
CESSION   AR595960
RSION     AR595960.1  GI:56646941
YWORDS    .
URCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
FERENCE   1  (bases 1 to 1533)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
ATURES              Location/Qualifiers
    source          1. .1533
                    /organism="unknown"
                    /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:                5.2e-197        Length:         1533
ore:                    197.00          Matches:        197
rcent Similarity:       100.0%          Conservative:   0
```

```
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            88.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR595960 (1-1533)

Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 14
AR595956
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.4e-197        Length:         1599
Score:                  197.00          Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            88.7%           Indels:         0
```

```
:                    2             Gaps:          0

-10-821-670A-33 (1-222) x AR595956 (1-1599)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

SULT 15
595957/c
CUS       AR595957              1599 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 40 from patent US 6818444.
CESSION   AR595957
RSION     AR595957.1  GI:56646938
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1599)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
    source         1. .1599
                   /organism="unknown"
                   /mol_type="genomic DNA"
RIGIN

ignment Scores:
ed. No.:              5.4e-197       Length:         1599
core:                 197.00         Matches:        197
ercent Similarity:    100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            88.7%          Indels:         0
:                     2              Gaps:           0
```

```
US-10-821-670A-33 (1-222) x AR595957 (1-1599)

Qy        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 16
AR242439
LOCUS       AR242439               591 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6472509.
ACCESSION   AR242439
VERSION     AR242439.1  GI:27288856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:            2.81e-195      Length:         591
Score:                195.00         Matches:        195
Percent Similarity:   100.0%         Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:          87.8%          Indels:         0
DB:                   2              Gaps:           0
```

```
-10-821-670A-33 (1-222) x AR242439 (1-591)

        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
           |||||||||||||||||||||||||||||||||||||||||||||
       541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

SULT 17
280207
CUS       AR280207                 591 bp    mRNA    linear   PAT 10-APR-2003
FINITION  Sequence 9 from patent US 6518045.
CCESSION  AR280207
RSION     AR280207.1  GI:29715597
YWORDS    .
URCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE  1  (bases 1 to 591)
 AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
 TITLE     Feline cytokine protein
 JOURNAL   Patent: US 6518045-A 9 11-FEB-2003;
           Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
           Kumamoto-ken;
           EPX;
EATURES             Location/Qualifiers
     source         1. .591
                    /organism="unknown"
                    /mol_type="mRNA"
IGIN

lignment Scores:
ed. No.:              2.81e-195      Length:         591
ore:                  195.00         Matches:        195
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            87.8%          Indels:         0
:                     2              Gaps:           0
```

```
US-10-821-670A-33 (1-222) x AR280207 (1-591)

Qy        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
             |||||||||||||||||||||||||||||||||||||||||||||
Db       541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

RESULT 18
AR322422
LOCUS       AR322422                 591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.81e-195      Length:         591
Score:                  195.00         Matches:        195
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            87.8%          Indels:         0
DB:                     2              Gaps:           0
```

```
-10-821-670A-33 (1-222) x AR322422 (1-591)

        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||
       541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

SULT 19
596007
CUS       AR596007                561 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 101 from patent US 6818444.
CESSION   AR596007
RSION     AR596007.1  GI:56646988
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 561)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 101 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
   source          1. .561
                   /organism="unknown"
                   /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:              7.08e-187      Length:         561
ore:                  187.00         Matches:        187
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            84.2%          Indels:         0
:                     2              Gaps:           0

-10-821-670A-33 (1-222) x AR596007 (1-561)

Qy         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        216 MetSerTyrLeuAsnAlaSer 222
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 20
AR596008/c
LOCUS       AR596008                561 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 103 from patent US 6818444.
ACCESSION   AR596008
VERSION     AR596008.1  GI:56646989
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 103 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.08e-187      Length:         561
Score:                  187.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            84.2%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AR596008 (1-561)

Qy         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        216 MetSerTyrLeuAsnAlaSer 222
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

```
SULT 21
U83185
CUS       FCU83185                 669 bp    mRNA    linear   MAM 16-JUL-1999
FINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
CCESSION  U83185
RSION     U83185.1  GI:2735052
YWORDS    .
URCE      Felis catus (cat)
 ORGANISM  Felis catus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
           Felinae; Felis.
FERENCE   1  (bases 1 to 669)
 AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
           Pedersen,N.C. and Lutz,H.
 TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
           (IL-12)
 JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  PUBMED   9522125
FERENCE   2  (bases 1 to 669)
 AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
           Pedersen,N.C. and Lutz,H.
 TITLE     Direct Submission
 JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
           Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
           Zurich, ZH 8057, Switzerland
ATURES             Location/Qualifiers
    source         1. .669
                   /organism="Felis catus"
                   /mol_type="mRNA"
                   /db_xref="taxon:9685"
    CDS            1. .669
                   /note="cytokine"
                   /codon_start=1
                   /product="interleukin-12 p35 subunit"
                   /protein_id="AAB93836.1"
                   /db_xref="GI:2735053"
                   /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                   QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                   REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                   NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                   LNSS"
ORIGIN
```

```
Alignment Scores:
Pred. No.:                4.59e-152       Length:          669
Score:                    154.00          Matches:         154
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              69.4%           Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-33 (1-222) x FCU83185 (1-669)

Qy         67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 258

Qy         87 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

Qy        107 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCys 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGC 378

Qy        127 LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAla 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 438

Qy        147 LysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 498

Qy        167 AspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeu 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTG 558

Qy        187 GluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArg 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618

Qy        207 IleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              |||||||||||||||||||||||||||||||||||||||||||
Db        619 ATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
```

```
RESULT 22
AF054605
LOCUS       AF054605                 285 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION   AF054605
VERSION     AF054605.1  GI:3126818
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
REFERENCE   2  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
```

```
TITLE     Direct Submission
JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
          Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
ATURES              Location/Qualifiers
   source           1. .285
                    /organism="Felis catus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9685"
                    /cell_line="FL4"
                    /cell_type="T cell"
                    /note="persistant FIV infection"
   CDS              <1. .>285
                    /codon_start=3
                    /product="interleukin 12 p35 subunit"
                    /protein_id="AAC15978.1"
                    /db_xref="GI:3126819"
                    /translation="LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLP
                    LELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE"
IGIN

ignment Scores:
ed. No.:              1.06e-78       Length:        285
ore:                  84.00          Matches:       84
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            37.8%          Indels:        0
:                     14             Gaps:          0

-10-821-670A-33 (1-222) x AF054605 (1-285)

        57 LysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAsp 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        33 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 92

        77 IleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsn 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        93 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 152

        97 GluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       153 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 212

       117 ArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMet 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       213 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 272

       137 TyrGlnValGlu 140
           ||||||||||||
       273 TACCAGGTGGAG 284

SULT 23
076201
CUS       AX076201                669 bp    DNA     linear   PAT 06-FEB-2001
FINITION  Sequence 2 from Patent WO0104155.
CESSION   AX076201
RSION     AX076201.1  GI:12710826
YWORDS    .
URCE      synthetic construct
ORGANISM  synthetic construct
          other sequences; artificial sequences.
FERENCE   1
AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
TITLE     Feline interleukin-12 as an immune stimulant
JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
          Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
          Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
          CALIFORNIA (US)
ATURES              Location/Qualifiers
   source           1. .669
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="feline IL-12 p35"
```

```
ORIGIN

Alignment Scores:
Pred. No.:              2.3e-58        Length:        669
Score:                  65.00          Matches:       65
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            29.3%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX076201 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyr 65
              ||||||||||||||||
Db        181 ACTCTAGAATTTTAC 195

RESULT 24
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
ORIGIN

Alignment Scores:
Pred. No.:              2.3e-58        Length:        669
Score:                  65.00          Matches:       65
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            29.3%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX076483 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

        61 ThrLeuGluPheTyr 65
           ||||||||||||||||
       181 ACTCTAGAATTTTAC 195

SULT 25
076477
CUS       AX076477                 4201 bp    DNA     linear   PAT 06-FEB-2001
FINITION  Sequence 3 from Patent WO0104280.
CESSION   AX076477
RSION     AX076477.1  GI:12711029
YWORDS    .
URCE      synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
FERENCE   1
 AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
 TITLE     Vaccine against lentiviral infections, such as the feline immune
           deficiency virus of the cat
 JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
           Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
           Universitaet Zuerich (CH)
ATURES               Location/Qualifiers
    source           1. .4201
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
IGIN

ignment Scores:
ed. No.:              1.21e-57       Length:        4201
ore:                  65.00          Matches:       65
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            29.3%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AX076477 (1-4201)

         1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

        21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

        41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

        61 ThrLeuGluPheTyr 65
           ||||||||||||||||
      3227 ACTCTAGAATTTTAC 3241

SULT 26
154615
CUS       AX154615                 660 bp    DNA     linear   PAT 22-JUN-2001
FINITION  Sequence 19 from Patent WO0140257.
CESSION   AX154615
RSION     AX154615.1  GI:14536190
YWORDS    .
URCE      synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
FERENCE   1
 AUTHORS   Leong,S.R. and Punnonen,J.
 TITLE     Cytokine polypeptides and nucleic acids
 JOURNAL   Patent: WO 0140257-A 19 07-JUN-2001;
           Maxygen, Inc. (US)
ATURES               Location/Qualifiers
    source           1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              4.71e-52       Length:        660
Score:                  59.00          Matches:       59
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX154615 (1-660)

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

Qy        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 27
AX154619
LOCUS       AX154619                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 23 from Patent WO0140257.
ACCESSION   AX154619
VERSION     AX154619.1  GI:14536194
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              4.71e-52       Length:        660
Score:                  59.00          Matches:       59
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            26.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX154619 (1-660)

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACAACC 363

Qy        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

Qy        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480
```

```
SULT 28
154620
CUS       AX154620                 660 bp    DNA     linear   PAT 22-JUN-2001
FINITION  Sequence 24 from Patent WO0140257.
CESSION   AX154620
RSION     AX154620.1  GI:14536195
YWORDS    .
URCE      synthetic construct
ORGANISM  synthetic construct
          other sequences; artificial sequences.
FERENCE   1
AUTHORS   Leong,S.R. and Punnonen,J.
TITLE     Cytokine polypeptides and nucleic acids
JOURNAL   Patent: WO 0140257-A 24 07-JUN-2001;
          Maxygen, Inc. (US)
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
IGIN

ignment Scores:
ed. No.:              4.71e-52       Length:        660
ore:                  59.00          Matches:       59
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            26.6%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AX154620 (1-660)

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 144
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 163
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        424 AATGCAAAGCTGTTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

SULT 29
154616
CUS       AX154616                 660 bp    DNA     linear   PAT 22-JUN-2001
FINITION  Sequence 20 from Patent WO0140257.
CESSION   AX154616
RSION     AX154616.1  GI:14536191
YWORDS    .
URCE      synthetic construct
ORGANISM  synthetic construct
          other sequences; artificial sequences.
FERENCE   1
AUTHORS   Leong,S.R. and Punnonen,J.
TITLE     Cytokine polypeptides and nucleic acids
JOURNAL   Patent: WO 0140257-A 20 07-JUN-2001;
          Maxygen, Inc. (US)
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
IGIN

ignment Scores:
ed. No.:              6.78e-49       Length:        660
ore:                  56.00          Matches:       56
cent Similarity:      100.0%         Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            25.2%        Indels:        0
DB:                     2            Gaps:          0

US-10-821-670A-33 (1-222) x AX154616 (1-660)

Qy        108 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 ATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTT 372

Qy        128 SerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLys 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 432

Qy        148 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 163
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

RESULT 30
BD171284
LOCUS       BD171284                 591 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171284
VERSION     BD171284.1  GI:28412574
KEYWORDS    JP 2002241398-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 4 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/4
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .591
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              9.99e-45       Length:        591
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            23.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x BD171284 (1-591)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||||||||||||||||||||||
Db        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273
```

```
SULT 31
595963
CUS       AR595963                  591 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 49 from patent US 6818444.
CESSION   AR595963
RSION     AR595963.1  GI:56646944
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 591)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 49 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES              Location/Qualifiers
    source          1. .591
                    /organism="unknown"
                    /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:              9.99e-45       Length:        591
ore:                  52.00          Matches:       52
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            23.4%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AR595963 (1-591)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

SULT 32
595964/c
CUS       AR595964                  591 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 51 from patent US 6818444.
CESSION   AR595964
RSION     AR595964.1  GI:56646945
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 591)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 51 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES              Location/Qualifiers
    source          1. .591
                    /organism="unknown"
                    /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:              9.99e-45       Length:        591
ore:                  52.00          Matches:       52
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            23.4%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AR595964 (1-591)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 33
AR595961
LOCUS       AR595961                  666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 46 from patent US 6818444.
ACCESSION   AR595961
VERSION     AR595961.1  GI:56646942
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 46 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .666
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.11e-44       Length:        666
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            23.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AR595961 (1-666)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 34
AR595962/c
LOCUS       AR595962                  666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 48 from patent US 6818444.
ACCESSION   AR595962
VERSION     AR595962.1  GI:56646943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 48 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .666
```

```
                /organism="unknown"
                /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:              1.11e-44        Length:         666
ore:                  52.00           Matches:        52
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            23.4%           Indels:         0
:                     2               Gaps:           0

-10-821-670A-33 (1-222) x AR595962 (1-666)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 35
151062
CUS       AR151062                669 bp    DNA     linear   PAT 08-AUG-2001
FINITION  Sequence 2 from patent US 6231850.
CESSION   AR151062
RSION     AR151062.1  GI:15117112
YWORDS    .
URCE      Unknown.
RGANISM   Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 669)
AUTHORS   Okano,F., Satoh,M. and Yamada,K.
ITLE      Canine interleukin 12
JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
ATURES              Location/Qualifiers
   source           1. .669
                    /organism="unknown"
                    /mol_type="unassigned DNA"
IGIN

ignment Scores:
ed. No.:              1.12e-44        Length:         669
ore:                  52.00           Matches:        52
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            23.4%           Indels:         0
:                     2               Gaps:           0

-10-821-670A-33 (1-222) x AR151062 (1-669)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 36
151072
CUS       AR151072                669 bp    DNA     linear   PAT 08-AUG-2001
FINITION  Sequence 12 from patent US 6231850.
CESSION   AR151072
```

```
VERSION     AR151072.1  GI:15117122
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 12 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.12e-44        Length:         669
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR151072 (1-669)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 37
BD014654
LOCUS       BD014654                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014654
VERSION     BD014654.1  GI:22555437
KEYWORDS    JP 2001161378-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 2 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/2
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
```

```
          FH   Key             Location/Qualifiers
          FT   CDS             (1). .(666)
          FT   mat_peptide     (76). .(666).
ATURES              Location/Qualifiers
    source          1. .669
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
IGIN

ignment Scores:
ed. No.:              1.12e-44       Length:        669
ore:                  52.00          Matches:       52
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            23.4%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x BD014654 (1-669)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 38
014664
CUS         BD014664                669 bp    DNA     linear   PAT 27-AUG-2002
FINITION    Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
CCESSION    BD014664
RSION       BD014664.1  GI:22555447
YWORDS      JP 2001161378-A/12.
URCE        Canis sp.
 ORGANISM   Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
FERENCE     1  (bases 1 to 669)
 AUTHORS    Okano,F.
 TITLE      Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
 JOURNAL    Patent: JP 2001161378-A 12 19-JUN-2001;
            TORAY INDUSTRIES INC
MMENT       OS   Canis sp. (dog)
            PN   JP 2001161378-A/12
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
ATURES              Location/Qualifiers
    source          1. .669
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:            1.12e-44       Length:        669
Score:                52.00          Matches:       52
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          23.4%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-33 (1-222) x BD014664 (1-669)

Qy       65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy       85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy      105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
Db      313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 39
E15018
LOCUS       E15018                  669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES            Location/Qualifiers
     source         1. .669
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:            1.12e-44       Length:        669
Score:                52.00          Matches:       52
Percent Similarity:   100.0%         Conservative:  0
```

```
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            23.4%           Indels:         0
:                     2               Gaps:           0

-10-821-670A-33 (1-222) x E15018 (1-669)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 40
316461
CUS       AR316461                669 bp    mRNA    linear   PAT 17-AUG-2003
FINITION  Sequence 2 from patent US 6562334.
CESSION   AR316461
RSION     AR316461.1  GI:33695289
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 669)
AUTHORS   Okano,F., Satoh,M. and Yamada,K.
TITLE     Canine interleukin 12 administration as an immune disease treatment
JOURNAL   Patent: US 6562334-A 2 13-MAY-2003;
          Toray Industries, Inc.;;
          JPX;
ATURES              Location/Qualifiers
   source           1. .669
                    /organism="unknown"
                    /mol_type="mRNA"
IGIN

ignment Scores:
ed. No.:              1.12e-44        Length:         669
ore:                  52.00           Matches:        52
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            23.4%           Indels:         0
:                     2               Gaps:           0

-10-821-670A-33 (1-222) x AR316461 (1-669)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 41
316471
CUS       AR316471                669 bp    mRNA    linear   PAT 17-AUG-2003
FINITION  Sequence 12 from patent US 6562334.
CESSION   AR316471
RSION     AR316471.1  GI:33695299
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 12 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="unknown"
                      /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.12e-44        Length:         669
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR316471 (1-669)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 42
BD171283
LOCUS       BD171283                1282 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171283
VERSION     BD171283.1  GI:28412573
KEYWORDS    JP 2002241398-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1282)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 3 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/3
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .1282
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              2.01e-44        Length:         1282
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     2               Gaps:           0
```

```
:-10-821-670A-33 (1-222) x BD171283 (1-1282)

r         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:        258 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 317

r         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:        318 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 377

         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
             |||||||||||||||||||||||||||||||||||
:        378 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 413

:SULT 43
:596009
:CUS       AR596009                1455 bp    DNA     linear   PAT 15-DEC-2004
:FINITION  Sequence 104 from patent US 6818444.
:CESSION   AR596009
:RSION     AR596009.1  GI:56646990
:YWORDS    .
:URCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
:FERENCE   1  (bases 1 to 1455)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 104 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
:ATURES              Location/Qualifiers
    source           1. .1455
                     /organism="unknown"
                     /mol_type="genomic DNA"
:IGIN

.ignment Scores:
:ed. No.:               2.25e-44       Length:         1455
:ore:                   52.00          Matches:        52
:rcent Similarity:      100.0%         Conservative:   0
:st Local Similarity:   100.0%         Mismatches:     0
.ery Match:             23.4%          Indels:         0
:                       2              Gaps:           0

:-10-821-670A-33 (1-222) x AR596009 (1-1455)

r         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

r         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

r        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
             |||||||||||||||||||||||||||||||||||
:        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

:SULT 44
:596010/c
:CUS       AR596010                1455 bp    DNA     linear   PAT 15-DEC-2004
:FINITION  Sequence 106 from patent US 6818444.
:CESSION   AR596010
:RSION     AR596010.1  GI:56646991
:YWORDS    .
:URCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
:FERENCE   1  (bases 1 to 1455)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 106 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1455
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.25e-44       Length:         1455
Score:                  52.00          Matches:        52
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            23.4%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AR596010 (1-1455)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db         912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

RESULT 45
AR595973
LOCUS       AR595973                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.36e-44       Length:         1533
Score:                  52.00          Matches:        52
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            23.4%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AR595973 (1-1533)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 46
AR595974/c
```

```
CUS       AR595974                1533 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 68 from patent US 6818444.
CESSION   AR595974
RSION     AR595974.1  GI:56646955
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1533)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
   source          1. .1533
                   /organism="unknown"
                   /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:              2.36e-44       Length:        1533
ore:                  52.00          Matches:       52
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            23.4%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AR595974 (1-1533)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 47
595971
CUS       AR595971                1599 bp    DNA     linear   PAT 15-DEC-2004
FINITION  Sequence 61 from patent US 6818444.
CESSION   AR595971
RSION     AR595971.1  GI:56646952
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 1599)
AUTHORS   Wonderling,R.S. and Boroughs,K.L.
TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
          Heska Corporation; Fort Collins, CO
ATURES             Location/Qualifiers
   source          1. .1599
                   /organism="unknown"
                   /mol_type="genomic DNA"
IGIN

ignment Scores:
ed. No.:              2.45e-44       Length:        1599
ore:                  52.00          Matches:       52
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            23.4%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AR595971 (1-1599)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy       85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy      105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
Db     1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 48
AR595972/c
LOCUS       AR595972                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.45e-44       Length:        1599
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            23.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AR595972 (1-1599)

Qy       65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy       85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy      105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
Db      354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 49
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
```

```
TITLE     Direct Submission
JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
          Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
:ATURES             Location/Qualifiers
    source          1. .669
                    /organism="Canis familiaris"
                    /mol_type="mRNA"
                    /db_xref="taxon:9615"
    CDS             1. .669
                    /codon_start=1
                    /product="interleukin-12 p35 subunit"
                    /protein_id="AAA92058.1"
                    /db_xref="GI:1223906"
                    /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                    QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                    REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                    NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                    LNSS"
:IGIN

:ignment Scores:
:ed. No.:              1.42e-42       Length:        669
:ore:                  50.00          Matches:       50
:rcent Similarity:     100.0%         Conservative:  0
:st Local Similarity:  100.0%         Mismatches:    0
:ery Match:            22.5%          Indels:        0
::                     14             Gaps:          0

-10-821-670A-33 (1-222) x CFU49085 (1-669)

         67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAG 258

         87 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 106
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

        107 LeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||
        319 TTGATAACTAACGGGAGTTGCCTGGCCTCT 348

:SULT 50
:154613
:CUS       AX154613                 666 bp    DNA     linear   PAT 22-JUN-2001
:FINITION  Sequence 17 from Patent WO0140257.
:CESSION   AX154613
:RSION     AX154613.1  GI:14536188
:YWORDS    .
:URCE      synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
:FERENCE   1
 AUTHORS   Leong,S.R. and Punnonen,J.
 TITLE     Cytokine polypeptides and nucleic acids
 JOURNAL   Patent: WO 0140257-A 17 07-JUN-2001;
           Maxygen, Inc. (US)
:ATURES             Location/Qualifiers
    source          1. .666
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
:IGIN

.ignment Scores:
 ed. No.:              3.32e-35       Length:        666
 ore:                  43.00          Matches:       43
 rcent Similarity:     100.0%         Conservative:  0
 st Local Similarity:  100.0%         Mismatches:    0
 ery Match:            19.4%          Indels:        0
 ::                    2              Gaps:          0
```

```
US-10-821-670A-33 (1-222) x AX154613 (1-666)

Qy          96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

Qy         116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAG 402

Qy         136 MetTyrGln 138
               |||||||||
Db         403 ATGTACCAG 411

RESULT 51
AY603407
LOCUS       AY603407                 618 bp    mRNA    linear   MAM 18-JUL-2004
DEFINITION  Capra hircus interleukin 12 p35 subunit precursor, mRNA, partial
            cds.
ACCESSION   AY603407
VERSION     AY603407.1  GI:50261481
KEYWORDS    .
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 618)
  AUTHORS   Rasool,T.J., Shebannavar,S., Hosamani,M., Sreekumar,E., George,A.A.
            and Premraj,A.
  TITLE     cloning and sequencing of goat cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 618)
  AUTHORS   Rasool,T.J., Shebannavar,S., Hosamani,M., Sreekumar,E., George,A.A.
            and Premraj,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2004) Division of Virology, Indian Veterinary
            Research Institute, Mukteswar, Nainital, Uttaranchal 263138, India
FEATURES             Location/Qualifiers
     source          1. .618
                     /organism="Capra hircus"
                     /mol_type="mRNA"
                     /isolation_source="peripheral blood mononuclear cells
                     stimulated with Concanavalin A"
                     /db_xref="taxon:9925"
                     /note="breed: Pashmina"
     CDS             <1. .618
                     /codon_start=1
                     /product="interleukin 12 p35 subunit precursor"
                     /protein_id="AAT72317.1"
                     /db_xref="GI:50261482"
                     /translation="HHLPHLSLGRSLPTTTAGPGRSCLDYSQNLLRAVSNTLQKARQT
                     LEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRETSLITNGHCLASGKT
                     SFMTTLCLRSIYKDLKMYHMEFQAMNAKLLMDPKRQVSLDQNMLAAIAELMQALNFDS
                     ETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYLSSS"
ORIGIN

Alignment Scores:
Pred. No.:             3.51e-34       Length:        618
Score:                 42.00          Matches:       42
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           18.9%          Indels:        0
DB:                    14             Gaps:          0

US-10-821-670A-33 (1-222) x AY603407 (1-618)

Qy          52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         103 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 162

Qy          72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       163 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 222

        92 GluLeu 93
           ||||||
       223 GAATTA 228

SULT 52
173557
CUS       AF173557                 666 bp    mRNA    linear   MAM 13-NOV-2000
FINITION  Ovis aries interleukin-12 p35 subunit precursor, mRNA, complete
          cds.
CESSION   AF173557
RSION     AF173557.1  GI:5805389
YWORDS    .
URCE      Ovis aries (sheep)
RGANISM   Ovis aries
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Caprinae; Ovis.
FERENCE   1  (bases 1 to 666)
AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
TITLE     Ovine interleukin 12 has biological activity on ovine and human
          activated peripheral blood mononuclear cells
JOURNAL   Cytokine 12 (10), 1546-1552 (2000)
 PUBMED   11023671
FERENCE   2  (bases 1 to 666)
AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
TITLE     Direct Submission
JOURNAL   Submitted (29-JUL-1999) Transplantation Immunology Laboratory, The
          Queen Elizabeth Hospital, Woodville Road, Adelaide, South Australia
          5011, Australia
ATURES              Location/Qualifiers
   source           1. .666
                    /organism="Ovis aries"
                    /mol_type="mRNA"
                    /db_xref="taxon:9940"
                    /tissue_type="inflammed renal tissue"
   CDS              1. .666
                    /note="Il-12; cytokine"
                    /codon_start=1
                    /product="interleukin-12 p35 subunit precursor"
                    /protein_id="AAD51976.1"
                    /db_xref="GI:5805390"
                    /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTAGPGTSCLDYSQ
                    NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                    ETSLITNGHCLSSGKTSFMTTLCLRSIYKDLKMYHMEFQAMNAKLLMDPKRQVFLDQN
                    MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                    SSS"
   sig_peptide      1. .75
   mat_peptide      76. .663
                    /product="interleukin-12 p35 subunit"
IGIN

ignment Scores:
ed. No.:              3.75e-34       Length:        666
ore:                  42.00          Matches:       42
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            18.9%          Indels:        0
:                     14             Gaps:          0

-10-821-670A-33 (1-222) x AF173557 (1-666)

        52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

        72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       211 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

        92 GluLeu 93
           ||||||
       Db        271 GAATTA 276

       RESULT 53
       AY232819
       LOCUS       AY232819                 666 bp    mRNA    linear   MAM 09-JUN-2005
       DEFINITION  Bubalus bubalis interleukin-12 p35 subunit precursor, mRNA,
                   complete cds.
       ACCESSION   AY232819
       VERSION     AY232819.1  GI:31322541
       KEYWORDS    .
       SOURCE      Bubalus bubalis (water buffalo)
         ORGANISM  Bubalus bubalis
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                   Pecora; Bovidae; Bovinae; Bubalus.
       REFERENCE   1  (bases 1 to 666)
         AUTHORS   Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
         TITLE     Interleukin-12 subunits p35 and p40 of Indian water buffalo
                   (Bubalus bubalis) maintain high sequence homology with those of
                   other ruminants
         JOURNAL   Eur. J. Immunogenet. 32 (3), 179-186 (2005)
       REFERENCE   2  (bases 1 to 666)
         AUTHORS   Premraj,A., Sreekumar,E. and Rasool,T.J.
         TITLE     Direct Submission
         JOURNAL   Submitted (07-FEB-2003) Animal Biotechnology, Rajiv Gandhi Centre
                   for Biotechnology, Jagathy, Trivandrum, Kerala 695014, India
       FEATURES             Location/Qualifiers
            source          1. .666
                            /organism="Bubalus bubalis"
                            /mol_type="mRNA"
                            /db_xref="taxon:89462"
                            /cell_type="concanavalin A stimulated splenocytes"
            CDS             1. .666
                            /note="cytokine"
                            /codon_start=1
                            /product="interleukin-12 p35 subunit precursor"
                            /protein_id="AAO61417.1"
                            /db_xref="GI:31322542"
                            /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                            NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                            ETSFITNGRCLASGKTSFMTTLCLKSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                            MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                            SSS"
       ORIGIN

       Alignment Scores:
       Pred. No.:              3.75e-34       Length:        666
       Score:                  42.00          Matches:       42
       Percent Similarity:     100.0%         Conservative:  0
       Best Local Similarity:  100.0%         Mismatches:    0
       Query Match:            18.9%          Indels:        0
       DB:                     14             Gaps:          0

       US-10-821-670A-33 (1-222) x AY232819 (1-666)

       Qy         52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       Db        151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

       Qy         72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       Db        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

       Qy         92 GluLeu 93
                     ||||||
       Db        271 GAATTA 276

       RESULT 54
       AB246272
       LOCUS       AB246272                 690 bp    mRNA    linear   MAM 13-JAN-2006
       DEFINITION  Bubalus carabanensis IL-12p35 mRNA for interleukin-12p35, complete
                   cds.
       ACCESSION   AB246272
```

```
:RSION     AB246272.1  GI:84871693
:YWORDS    .
:URCE      Bubalus carabanensis
 ORGANISM  Bubalus carabanensis
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
           Pecora; Bovidae; Bovinae; Bubalus.
·FERENCE   1
 AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
 TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
           buffalo and other bubaline breeds by molecular cloning, sequencing
           and phylogenetics
 JOURNAL   Unpublished
:FERENCE   2  (bases 1 to 690)
 AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
 TITLE     Direct Submission
 JOURNAL   Submitted (06-JAN-2006) Claro N Mingala, Graduate School of
           Veterinary Medicine, Hokkaido University, Department of Disease
           Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
           9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
           Tel:81-11-706-5216, Fax:81-11-706-5217)
:ATURES             Location/Qualifiers
    source          1. .690
                    /organism="Bubalus carabanensis"
                    /mol_type="mRNA"
                    /db_xref="taxon:346063"
                    /sex="female"
                    /cell_type="PBMC"
    gene            1. .690
                    /gene="IL-12p35"
    CDS             1. .666
                    /gene="IL-12p35"
                    /codon_start=1
                    /product="interleukin-12p35"
                    /protein_id="BAE75849.1"
                    /db_xref="GI:84871694"
                    /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                    NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                    ETSFITNGRCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                    MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                    SSS"
:IGIN

.ignment Scores:
 ed. No.:              3.87e-34      Length:         690
 ore:                  42.00         Matches:        42
 rcent Similarity:     100.0%        Conservative:   0
 st Local Similarity:  100.0%        Mismatches:     0
 ery Match:            18.9%         Indels:         0
 :                     14            Gaps:           0

:-10-821-670A-33 (1-222) x AB246272 (1-690)

          52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

          72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

          92 GluLeu 93
             ||||||
         271 GAACTA 276

:SULT 55
:246352
:CUS       AB246352                 690 bp    mRNA    linear   MAM 13-JAN-2006
:FINITION  Bubalus bubalis IL-12p35 mRNA for interleukin-12p35, complete cds.
:CESSION   AB246352
:RSION     AB246352.1  GI:84871715
:YWORDS    .
:URCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES              Location/Qualifiers
     source           1. .690
                      /organism="Bubalus bubalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:89462"
                      /sex="female"
                      /cell_type="PBMC"
                      /note="Bulgarian Murrah buffalo - crossbreed between
                      Mediterranean and Indian buffalo both are Riverine type
                      water buffalo"
     gene             1. .690
                      /gene="IL-12p35"
     CDS              1. .666
                      /gene="IL-12p35"
                      /codon_start=1
                      /product="interleukin-12p35"
                      /protein_id="BAE75857.1"
                      /db_xref="GI:84871716"
                      /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                      NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                      ETSFITNGRCLASGKTSYMTTLCLKSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                      MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                      SSS"
ORIGIN

Alignment Scores:
Pred. No.:              3.87e-34      Length:         690
Score:                  42.00         Matches:        42
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            18.9%         Indels:         0
DB:                     14            Gaps:           0

US-10-821-670A-33 (1-222) x AB246352 (1-690)

Qy          52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy          72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy          92 GluLeu 93
               ||||||
Db         271 GAATTA 276

RESULT 56
AB246359
LOCUS       AB246359                 690 bp    mRNA    linear   MAM 14-JAN-2006
DEFINITION  Bubalus bubalis x Bubalus carabanensis IL-12p35 mRNA for
            interleukin-12p35, complete cds.
ACCESSION   AB246359
VERSION     AB246359.1  GI:84875358
KEYWORDS    .
```

```
URCE      Bubalus bubalis x Bubalus carabanensis
ORGANISM  Bubalus bubalis x Bubalus carabanensis
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bubalus.
FERENCE   1
AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
          buffalo and other bubaline breeds by molecular cloning, sequencing
          and phylogenetics
JOURNAL   Unpublished
FERENCE   2  (bases 1 to 690)
AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
TITLE     Direct Submission
JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
          Veterinary Medicine, Hokkaido University, Department of Disease
          Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
          9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
          Tel:81-11-706-5216, Fax:81-11-706-5217)
ATURES              Location/Qualifiers
   source           1. .690
                    /organism="Bubalus bubalis x Bubalus carabanensis"
                    /mol_type="mRNA"
                    /db_xref="taxon:365610"
                    /sex="female"
                    /cell_type="PBMC"
                    /note="Philippine carabao crossbreed (CB) - crossbreed
                    between Philippine carabao (Swamp type water buffalo) and
                    Indian Murrah buffalo (Riverine type water buffalo)"
   gene             1. .690
                    /gene="IL-12p35"
   CDS              1. .666
                    /gene="IL-12p35"
                    /codon_start=1
                    /product="interleukin-12p35"
                    /protein_id="BAB75893.1"
                    /db_xref="GI:84875359"
                    /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                    NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                    ETSFITNGHCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQVFLDQN
                    MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                    SSS"
IGIN

ignment Scores:
ed. No.:              3.87e-34       Length:        690
ore:                  42.00          Matches:       42
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            18.9%          Indels:        0
:                     14             Gaps:          0

-10-821-670A-33 (1-222) x AB246359 (1-690)

         52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

         72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

         92 GluLeu 93
            ||||||
        271 GAATTA 276

SULT 57
)03542
CUS       AF003542                 690 bp    mRNA    linear   MAM 17-JUN-1997
FINITION  Capra hircus interleukin 12 35kD subunit mRNA, complete cds.
CESSION   AF003542
RSION     AF003542.1  GI:2197070
(WORDS    .
```

```
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Beyer,J.C., Kumpula-McWhirter,N.M. and Cheevers,W.P.
  TITLE     Caprine Interleukin 12 35kD subunit
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Beyer,J.C., Kumpula-McWhirter,N.M. and Cheevers,W.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-1997) Veterinary Microbiology and Pathology,
            Washington State University, P.O Box 647040, Pullman, WA
            99164-7040, USA
FEATURES              Location/Qualifiers
     source           1. .690
                      /organism="Capra hircus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9925"
                      /cell_type="LPS stimulated caprine microglial cells"
     CDS              1. .666
                      /codon_start=1
                      /product="interleukin 12 35kD subunit"
                      /protein_id="AAB61287.1"
                      /db_xref="GI:2197071"
                      /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPITTAGPGRSCLDYSQ
                      NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                      ETSLITNGHCLASGKTSFMTTLCLRSIYKDLKMYHMEFQAINAKLLMDPKRQVSLDQN
                      MLAAIAELMQALNFDSETVPQKPSLEELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                      SSS"
ORIGIN

Alignment Scores:
Pred. No.:              3.87e-34       Length:        690
Score:                  42.00          Matches:       42
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            18.9%          Indels:        0
DB:                     14             Gaps:          0

US-10-821-670A-33 (1-222) x AF003542 (1-690)

Qy          52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         151 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

Qy          72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         211 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

Qy          92 GluLeu 93
               ||||||
Db         271 GAATTA 276

RESULT 58
BTU14416
LOCUS       BTU14416                 690 bp    mRNA    linear   MAM 27-JAN-1996
DEFINITION  Bos taurus interleukin 12 35 kDa subunit mRNA, complete cds.
ACCESSION   U14416
VERSION     U14416.1  GI:555917
KEYWORDS    .
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Zarlenga,D.S., Canals,A., Aschenbrenner,R.A. and Gasbarre,L.C.
  TITLE     Enzymatic amplification and molecular cloning of cDNA encoding the
            small and large subunits of bovine interleukin 12
  JOURNAL   Biochim. Biophys. Acta 1270 (2-3), 215-217 (1995)
   PUBMED   7727547
```

```
:FERENCE   2  (bases 1 to 690)
 AUTHORS   Zarlenga,D.S.
 TITLE     Direct Submission
 JOURNAL   Submitted (06-SEP-1994) Dante S. Zarlenga, U.S. Department of
           Agriculture, ARS, LPSI, PIL, Beltsville, MD 20705, USA
:ATURES             Location/Qualifiers
    source          1. .690
                    /organism="Bos taurus"
                    /mol_type="mRNA"
                    /strain="Holstein"
                    /db_xref="taxon:9913"
                    /clone="BIL12 35"
                    /sex="male"
                    /cell_type="lymphocytes and macrophages"
                    /tissue_type="lymphoid"
    CDS             1. .666
                    /codon_start=1
                    /product="interleukin 12 35 kDa subunit"
                    /protein_id="AAA85810.1"
                    /db_xref="GI:555918"
                    /translation="MCPLRSLLLISTLVLLHHLPHLSLGRSLPTTTASPGRSCLDYSQ
                    NLLRAVSNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASR
                    ETSFITNGHCLASGKTSFMTTLCLRSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQN
                    MLAAIAELMQALNFDSETVPQKPSLKELDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                    SSS"
:IGIN

 ignment Scores:
 ed. No.:              3.87e-34       Length:        690
 ore:                  42.00          Matches:       42
 rcent Similarity:     100.0%         Conservative:  0
 st Local Similarity:  100.0%         Mismatches:    0
 ery Match:            18.9%          Indels:        0
 :                     14             Gaps:          0

 -10-821-670A-33 (1-222) x BTU14416 (1-690)

 r         52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 )        151 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 210

 r         72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 )        211 ATCGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 270

 r         92 GluLeu 93
              ||||||
 :        271 GAATTA 276

:SULT 59
:U57751
)CUS       CEU57751                 666 bp    mRNA    linear   MAM 28-OCT-1999
:FINITION  Cervus elaphus interleukin-12 p35 subunit mRNA, complete cds.
:CESSION   U57751
:RSION     U57751.1  GI:1373385
:YWORDS    .
)URCE      Cervus elaphus (red deer)
 ORGANISM  Cervus elaphus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
           Pecora; Cervidae; Cervinae; Cervus.
:FERENCE   1  (bases 1 to 666)
 AUTHORS   Lockhart,E., Slobbe,L. and Buchan,G.
 TITLE     The characterisation of a cervine immunoregulatory cytokine,
           interleukin 12
 JOURNAL   DNA Seq. 10 (2), 139-148 (1999)
  PUBMED   10376218
:FERENCE   2  (bases 1 to 666)
 AUTHORS   Lockhart,E.A.
 TITLE     Direct Submission
 JOURNAL   Submitted (08-MAY-1996) Euan A. Lockhart, Microbiology, University
           of Otago, Cumberland St, Dunedin, New Zealand
:ATURES             Location/Qualifiers
    source          1. .666
                    /organism="Cervus elaphus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9860"
                    /cell_type="peripheral blood mononuclear cells"
    CDS             1. .666
                    /note="IL-12 p35 subunit"
                    /codon_start=1
                    /product="interleukin-12 p35 subunit"
                    /protein_id="AAB02257.1"
                    /db_xref="GI:1373386"
                    /translation="MCPLRSLLLLSTLVLLHHLPHLSLGRSLPPTTAGPGRSCLNYSQ
                    NLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLVSR
                    ETSLITHGSCLASGKTSFMTTLCLKSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQN
                    MLAAIAELMQALNFNSETVPQKPSLEEMDFYKTKVKLCILLHAFRIRAVTIDRMMSYL
                    SSS"
    primer_bind     1. .17
    primer_bind     complement(658. .666)
ORIGIN

Alignment Scores:
Pred. No.:              4.79e-32       Length:        666
Score:                  40.00          Matches:       40
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            18.0%          Indels:        0
DB:                     14             Gaps:          0

US-10-821-670A-33 (1-222) x CEU57751 (1-666)

Qy         54 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 73
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 ACACTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 216

Qy         74 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 276

RESULT 60
AB107653
LOCUS       AB107653                 669 bp    mRNA    linear   MAM 29-APR-2004
DEFINITION  Lama glama IL-12 p35 mRNA for interleukin 12 p35 subunit, complete
            cds.
ACCESSION   AB107653
VERSION     AB107653.1  GI:29603616
KEYWORDS    .
SOURCE      Lama glama (llama)
  ORGANISM  Lama glama
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
            Camelidae; Lama.
REFERENCE   1
  AUTHORS   Odbileg,R., Lee,S.I., Yoshida,R., Chang,K.S., Ohashi,K.,
            Sugimoto,C. and Onuma,M.
  TITLE     Cloning and sequence analysis of llama cytokines related to
            cell-mediated immunity
  JOURNAL   Vet. Immunol. Immunopathol. 99 (1-2), 1-10 (2004)
  PUBMED    15113649
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Ohashi,K., Raadan,O. and Lee,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2003) Kazuhiko Ohashi, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control; Kita-ku Kita 18 Nishi 9, Sapporo, Hokkaido 060-0818, Japan
            (E-mail:okazu@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
            Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
    source          1. .669
                    /organism="Lama glama"
                    /mol_type="mRNA"
                    /db_xref="taxon:9844"
                    /sex="Female"
                    /cell_type="PBMC"
```

```
                     /country="Japan"
   gene              1. .669
                     /gene="IL-12 p35"
   CDS               1. .669
                     /gene="IL-12 p35"
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="BAC75390.1"
                     /db_xref="GI:29603617"
                     /translation="MCPLRSLFLMATLVFLNHLDHLSLARSLPTTTAGPGMFQCLSHS
                     QNLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLAS
                     RETSLITHGSCLASGKTSFMTTLCLSSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQ
                     NMLVAIAELMQALNVSGETVPQKPSLEEPDFYKTKVKLCILLHAFRIRAVTIDRMMSY
                     LSSS"
IGIN

ignment Scores:
ed. No.:                4.81e-32        Length:         669
ore:                    40.00           Matches:        40
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              18.0%           Indels:         0
:                       14              Gaps:           0

-10-821-670A-33 (1-222) x AB107653 (1-669)

        54 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 73
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       160 ACACTTCAGAAGGCCAGACAAACCCTAGAATTTTACTCTTGCACTTCTGAAGAGATTGAC 219

        74 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       220 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

SULT 61
246672
CUS       AB246672                669 bp    mRNA    linear   MAM 12-JAN-2006
FINITION  Camelus bactrianus IL-12p35 mRNA for interleukin-12p35, complete
          cds.
CESSION   AB246672
RSION     AB246672.1  GI:84794455
YWORDS    .
URCE      Camelus bactrianus (Bactrian camel)
RGANISM   Camelus bactrianus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
          Camelidae; Camelus.
FERENCE   1
UTHORS    Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
ITLE      Molecular cloning and sequence analysis of Th1 and Th2 cytokine
          cDNAs from the bactrian camel (Camelus bactrianus)
OURNAL    Unpublished
FERENCE   2  (bases 1 to 669)
UTHORS    Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
ITLE      Direct Submission
OURNAL    Submitted (10-JAN-2006) Odbileg Raadan, Graduate School of
          Veterinary Medicine, Hokkaido University, Disease Control,
          Laboratory of Infectious Disease; Kita ku, Kita-18, Nishi-9,
          Sapporo, Hokkaido 060-0818, Japan
          (E-mail:odbileg@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
          Fax:81-11-706-5217)
ATURES              Location/Qualifiers
   source           1. .669
                    /organism="Camelus bactrianus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9837"
                    /sex="female"
                    /cell_type="PBMC"
                    /country="Japan"
   gene             1. .669
                    /gene="IL-12p35"
   CDS              1. .669
                    /gene="IL-12p35"
                    /codon_start=1
                    /product="interleukin-12p35"
                    /protein_id="BAE75803.1"
                    /db_xref="GI:84794456"
                    /translation="MCPLRSLFLMATLVFLIHLDHLSLARSLPTTTAGPGMFQCLSHS
                    QNLLRAVSDTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLAS
                    RETSLITHGSCLASGKTPFMTTLCLSSIYEDLKMYHMEFQAMNAKLLMDPKRQIFLDQ
                    NMLVAIAELMQALNVSSETVPQKPSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                    LSSS"
ORIGIN

Alignment Scores:
Pred. No.:              4.81e-32        Length:         669
Score:                  40.00           Matches:        40
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            18.0%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-33 (1-222) x AB246672 (1-669)

Qy         54 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 73
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ACGCTTCAGAAGGCCAGACAAACCCTAGAATTTTACTCTTGCACTTCTGAAGAGATTGAC 219

Qy         74 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

RESULT 62
E35793
LOCUS       E35793                  703 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Process for producing interleukin 12.
ACCESSION   E35793
VERSION     E35793.1  GI:18624617
KEYWORDS    JP 2000157274-A/5.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 703)
  AUTHORS   Nakamura,M., Takehara,K. and Ohara,E.
  TITLE     Process for producing interleukin 12
  JOURNAL   Patent: JP 2000157274-A 5 13-JUN-2000;
            DAI ICHI SEIYAKU CO LTD
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2000157274-A/5
            PD   13-JUN-2000
            PF   20-NOV-1998 JP 1998331052
            PR
            PI   MASAYUKI NAKAMURA,KAZUAKI TAKEHARA,EIJI OHARA PC
            C12N15/09,C07K14/54,C12N5/10,C12P21/02//(C12N15/09,C12R1:91), PC
            (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC
            (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .703
            FT                   /organism='Bos sp. (bovine)'.
FEATURES              Location/Qualifiers
     source           1. .703
                      /organism="Bos sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:29061"
ORIGIN

Alignment Scores:
Pred. No.:              5.03e-32        Length:         703
Score:                  40.00           Matches:        40
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            18.0%           Indels:         0
DB:                     2               Gaps:           0
```

```
:-10-821-670A-33 (1-222) x E35793 (1-703)

         54 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 73
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        168 ACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 227

         74 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        228 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 287

SULT 63
191828
:CUS        AY191828                 657 bp    mRNA    linear   SYN 04-FEB-2003
:FINITION   Synthetic construct evolved IL-12 p35 precursor, mRNA, partial cds.
CESSION    AY191828
:RSION      AY191828.1  GI:27729523
:YWORDS     .
:URCE       synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
:FERENCE    1  (bases 1 to 657)
AUTHORS    Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
           Punnonen,J.
TITLE      Optimized expression and specific activity of IL-12 by directed
           molecular evolution
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
  PUBMED   12529500
:FERENCE    2  (bases 1 to 657)
AUTHORS    Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
           Punnonen,J.
TITLE      Direct Submission
JOURNAL    Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
           Drive, Redwood City, CA 94063, USA
:ATURES             Location/Qualifiers
    source          1. .657
                    /organism="synthetic construct"
                    /mol_type="mRNA"
                    /db_xref="taxon:32630"
    CDS             1. .>657
                    /codon_start=1
                    /transl_table=11
                    /product="evolved IL-12 p35 precursor"
                    /protein_id="AAO19111.1"
                    /db_xref="GI:27729524"
                    /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                    LRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRGI
                    SLITNGSCLASRKTSFMTTLCLGSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNML
                    TAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS
                    S"
    sig_peptide     1. .66
    mat_peptide     67. .657
                    /product="evolved IL-12 p35"
:IGIN

.ignment Scores:
:ed. No.:              5.34e-31       Length:        657
:ore:                  39.00          Matches:       39
:rcent Similarity:     100.0%         Conservative:  0
:st Local Similarity:  100.0%         Mismatches:    0
:ery Match:            17.6%          Indels:        0
:                      8              Gaps:          0

:-10-821-670A-33 (1-222) x AY191828 (1-657)

         55 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 74
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

         75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 270
```

```
RESULT 64
AX154614
LOCUS       AX154614                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              5.36e-31       Length:        660
Score:                  39.00          Matches:       39
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            17.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX154614 (1-660)

Qy          55 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy          75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

RESULT 65
AX154617
LOCUS       AX154617                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              5.36e-31       Length:        660
Score:                  39.00          Matches:       39
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            17.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX154617 (1-660)
```

```
         55 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 74
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

         75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 270

SULT 66
154621
CUS       AX154621                 660 bp    DNA     linear   PAT 22-JUN-2001
FINITION  Sequence 25 from Patent WO0140257.
CESSION   AX154621
RSION     AX154621.1  GI:14536196
YWORDS    .
URCE      synthetic construct
ORGANISM  synthetic construct
          other sequences; artificial sequences.
FERENCE   1
AUTHORS   Leong,S.R. and Punnonen,J.
ITLE      Cytokine polypeptides and nucleic acids
JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
          Maxygen, Inc. (US)
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
IGIN

ignment Scores:
ed. No.:              5.36e-31       Length:         660
ore:                  39.00          Matches:        39
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            17.6%          Indels:         0
:                     2              Gaps:           0

-10-821-670A-33 (1-222) x AX154621 (1-660)

         55 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 74
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

         75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270

SULT 67
154618
CUS       AX154618                 660 bp    DNA     linear   PAT 22-JUN-2001
FINITION  Sequence 22 from Patent WO0140257.
CESSION   AX154618
RSION     AX154618.1  GI:14536193
YWORDS    .
URCE      synthetic construct
ORGANISM  synthetic construct
          other sequences; artificial sequences.
FERENCE   1
AUTHORS   Leong,S.R. and Punnonen,J.
ITLE      Cytokine polypeptides and nucleic acids
JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
          Maxygen, Inc. (US)
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
IGIN
```

```
Alignment Scores:
Pred. No.:              6.84e-29       Length:         660
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            16.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AX154618 (1-660)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        204 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

RESULT 68
PIGIL12PSU
LOCUS       PIGIL12PSU               1426 bp    mRNA    linear   MAM 09-JUL-2001
DEFINITION  Sus scrofa interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   L35765
VERSION     L35765.1  GI:927204
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 1426)
  AUTHORS   Foss,D.L. and Murtaugh,M.P.
  TITLE     Molecular cloning and mRNA expression of porcine interleukin-12
  JOURNAL   Vet. Immunol. Immunopathol. 57 (1-2), 121-134 (1997)
   PUBMED   9239844
COMMENT     On Aug 2, 1995 this sequence version replaced gi:755667.
FEATURES             Location/Qualifiers
     source          1. .1426
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /cell_type="mononuclear"
                     /tissue_type="peripheral blood"
     CDS             108. .878
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAA73897.1"
                     /db_xref="GI:927205"
                     /translation="MCSPGFGLQTSDLTCDVHPSASSRRLAVTAAPLSMCPLRNLLLV
                     ATLVLLNHLDHLSLGRSLPATTAGPGMFKCLNHSQNLLKAVSNTLQKAKQTLEFYSCT
                     SEEIDHEDITKDKTSTVEACLPLELATNESCLAARETSLITNGNCLTSGKTSFMTTLC
                     LSSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQNMLTAITELMQALNFNSETVPQKP
                     SLEELDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS"
     primer_bind     196. .216
     primer_bind     complement(859. .878)
     polyA_site      1426
ORIGIN

Alignment Scores:
Pred. No.:              1.97e-25       Length:         1426
Score:                  34.00          Matches:        34
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            15.3%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-33 (1-222) x PIGIL12PSU (1-1426)

Qy         60 GlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLys 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CAAACCCTAGAATTTTACTCCTGCACTTCAGAAGAGATCGATCATGAAGATATCACCAAA 446

Qy         80 AspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
```

```
                 ||||||||||||||||||||||||||||||||||||||||
        447 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTTGAACTA 488

:SULT 69
:154612
:CUS        AX154612                 666 bp    DNA     linear   PAT 22-JUN-2001
:FINITION   Sequence 16 from Patent WO0140257.
:CESSION    AX154612
:RSION      AX154612.1  GI:14536187
:YWORDS     .
:URCE       synthetic construct
 ORGANISM   synthetic construct
            other sequences; artificial sequences.
:FERENCE    1
 AUTHORS    Leong,S.R. and Punnonen,J.
 TITLE      Cytokine polypeptides and nucleic acids
 JOURNAL    Patent: WO 0140257-A 16 07-JUN-2001;
            Maxygen, Inc. (US)
'ATURES              Location/Qualifiers
    source           1. .666
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
 IGIN

 ignment Scores:
 ed. No.:              1.43e-22       Length:         666
 :ore:                 31.00          Matches:        31
 :rcent Similarity:    100.0%         Conservative:   0
 :st Local Similarity: 100.0%         Mismatches:     0
 :ery Match:           14.0%          Indels:         0
 ::                    2              Gaps:           0

:-10-821-670A-33 (1-222) x AX154612 (1-666)

          96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

         116 SerArgLysThrSerPheMetThrThrLeuCys 126
             |||||||||||||||||||||||||||||||
         343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGC 375

:SULT 70
:IL12P35
:CUS        ECIL12P35                669 bp    mRNA    linear   MAM 18-APR-2005
:FINITION   Equus caballus mRNA for interleukin 12 p35 subunit.
:CESSION    Y11130
:RSION      Y11130.1  GI:5441624
:YWORDS     interleukin-12 subunit p35.
:URCE       Equus caballus (horse)
 ORGANISM   Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
'FERENCE    1
 AUTHORS    Nicolson,L., Penha-Goncalves,M.N., Keanie,J.L., Logan,N.A.,
            Argyle,D.J. and Onions,D.E.
 TITLE      Cloning and sequencing of horse interleukin-12 and interleukin-18
            cDNAs
 JOURNAL    Immunogenetics 50 (1-2), 94-97 (1999)
  PUBMED    10541814
 FERENCE    2  (bases 1 to 669)
 AUTHORS    Nicolson,L.
 TITLE      Direct Submission
 JOURNAL    Submitted (04-FEB-1997) L. Nicolson, Dept. of Vet. Pathology,
            University of Glasgow Vet. School, Bearsden Rd., Glasgow G61 1QH,
            UK
:ATURES              Location/Qualifiers
    source           1. .669
                     /organism="Equus caballus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9796"
                     /cell_line="LPS-stimulated alveolar macrophages"
                     /cell_type="alveolar macrophages"
     gene            1. .669
                     /gene="IL-12 p35"
     CDS             1. .669
                     /gene="IL-12 p35"
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="CAA72012.1"
                     /db_xref="GI:5441625"
                     /db_xref="GOA:Q9XSQ6"
                     /db_xref="InterPro:IPR004281"
                     /db_xref="InterPro:IPR009079"
                     /db_xref="UniProtKB/Swiss-Prot:Q9XSQ6"
                     /translation="MCPPRGLLLVAILVLLNHLDHLSLARNLPTATPGPGMFQCLNHS
                     QNLLRTVSNTLQKARQTLEFYSCTSEEIDHEDITKDKSSTVAACLPLELAPNESCLAS
                     REISFITNGSCLTPGKASSMMTLCLSSIYEDLKMYQVEFKAMNAKLLIDPQRQIFLDE
                     NMLTAIDKLMQALNFNSETVPQKPSLEGLDFYKTKVKLCILLHAFRIRAVTINRMMGY
                     LNAS"
     sig_peptide     1. .69
                     /gene="IL-12 p35"
     misc_feature    1. .16
                     /gene="IL-12 p35"
                     /note="primer-derived sequence"
     misc_feature    651. .669
                     /gene="IL-12 p35"
                     /note="primer-derived sequence"
ORIGIN

Alignment Scores:
Pred. No.:              1.62e-21       Length:         669
Score:                  30.00          Matches:        30
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            13.5%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-33 (1-222) x ECIL12P35 (1-669)

Qy          52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 AGCAACACGCTTCAGAAGGCCAGGCAAACCCTAGAATTCTACTCCTGCACTTCTGAAGAG 213

Qy          72 IleAspHisGluAspIleThrLysAspLys 81
               |||||||||||||||||||||||||||||
Db         214 ATCGATCATGAGGATATCACAAAAGACAAG 243

RESULT 71
AF401989
LOCUS       AF401989                 1626 bp    mRNA    linear   SYN 14-FEB-2002
DEFINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION   AF401989
VERSION     AF401989.1  GI:18656516
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1626)
  AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
            Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
            Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
  PUBMED    11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
```

```
   source          1. .1626
                   /organism="synthetic construct"
                   /mol_type="mRNA"
                   /db_xref="taxon:32630"
   CDS             1. .1626
                   /note="derived from Equus caballus; N-terminal p40 subunit
                   linked by (Gly4Ser)3 linker to signal-peptide deleted p35
                   subunit"
                   /codon_start=1
                   /transl_table=11
                   /product="single chain interleukin-12"
                   /protein_id="AAL77817.1"
                   /db_xref="GI:18656517"
                   /translation="MGHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
                   MVVLTCNTPEEEGITWTLDQSSEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHL
                   LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                   GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                   LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
                   QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCSGGGGS
                   GGGGSGGGGSRNLPTATPGPGMFQCLNHSQNLLRTVSNTLQKARQTLEFYSCTSEEID
                   HEDITKDKSSTVAACLPLELAPNESCLASREISFITNGSCLTPGKASSMMTLCLSSIY
                   EDLKMYQVEFKAMNAKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETVPQKPSLEGL
                   DFYKTKVKLCILLHAFRIRAVTINRMMGYLNAS"
   primer_bind     1. .14
   misc_feature    15. .987
                   /note="interleukin-12 p40 sequence"
   misc_feature    988. .1032
                   /note="linker"
   misc_feature    1033. .1611
                   /note="interleukin-12 p35 sequence"
   primer_bind     complement(1612. .1626)
IGIN

ignment Scores:
ed. No.:              3.61e-21       Length:        1626
ore:                  30.00          Matches:       30
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.5%          Indels:        0
:                     8              Gaps:          0

-10-821-670A-33 (1-222) x AF401989 (1-1626)

        52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1111 AGCAACACGCTTCAGAAGGCCAGGCAAACCCTAGAATTCTACTCCTGCACTTCTGAAGAG 1170

        72 IleAspHisGluAspIleThrLysAspLys 81
           |||||||||||||||||||||||||||||
      1171 ATCGATCATGAGGATATCACAAAAGACAAG 1200

ULT 72
08951
US       AR008951                660 bp    DNA     linear   PAT 04-DEC-1998
FINITION  Sequence 3 from patent US 5756085.
CESSION   AR008951
RSION     AR008951.1  GI:3967756
WORDS     .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 660)
AUTHORS   Sykes,M. and Wolf,S.F.
TITLE     Use of interleukin-12 to prevent graft versus host disease
JOURNAL   Patent: US 5756085-A 3 26-MAY-1998;
ATURES             Location/Qualifiers
   source          1. .660
                   /organism="unknown"
                   /mol_type="unassigned DNA"
IGIN

ignment Scores:
ed. No.:              1.81e-20       Length:        660
```

```
Score:                29.00          Matches:       29
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          13.1%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-33 (1-222) x AR008951 (1-660)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 73
BD007071
LOCUS       BD007071                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007071
VERSION     BD007071.1  GI:18635442
KEYWORDS    JP 2001503257-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 2 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/2
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:            1.81e-20       Length:        660
Score:                29.00          Matches:       29
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          13.1%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-33 (1-222) x BD007071 (1-660)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 74
BD007079
LOCUS       BD007079                660 bp    DNA     linear   PAT 31-JAN-2002
```

```
FINITION  Gene expression and delivery systems and uses.
CESSION   BD007079
RSION     BD007079.1  GI:18635450
YWORDS    JP 2001503258-A/4.
URCE      unidentified
ORGANISM  unidentified
          unclassified sequences.
FERENCE   1  (bases 1 to 660)
AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
TITLE     Gene expression and delivery systems and uses
JOURNAL   Patent: JP 2001503258-A 4 13-MAR-2001;
          BARENTISU INC
MMENT     OS   Unidentified
          PN   JP 2001503258-A/4
          PD   13-MAR-2001
          PF   10-OCT-1997 JP 1998519520
          PR   18-OCT-1996 US    60/028687
          PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
          C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
          C12N15/00
          CC   Strandedness: Single;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers
          FT   source          1. .660
          FT                   /organism='Unidentified'.
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
IGIN

ignment Scores:
ed. No.:                1.81e-20        Length:         660
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-33 (1-222) x BD007079 (1-660)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 75
007080
CUS       BD007080                  660 bp    DNA     linear   PAT 31-JAN-2002
FINITION  Gene expression and delivery systems and uses.
CESSION   BD007080
RSION     BD007080.1  GI:18635451
YWORDS    JP 2001503258-A/5.
URCE      unidentified
 ORGANISM unidentified
          unclassified sequences.
FERENCE   1  (bases 1 to 660)
 AUTHORS  Nodosutoromu,J., Freemark,B. and Dishupande,D.
 TITLE    Gene expression and delivery systems and uses
 JOURNAL  Patent: JP 2001503258-A 5 13-MAR-2001;
          BARENTISU INC
MMENT     OS   Unidentified
          PN   JP 2001503258-A/5
          PD   13-MAR-2001
          PF   10-OCT-1997 JP 1998519520
          PR   18-OCT-1996 US    60/028687
          PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
          C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
          C12N15/00
          CC   Strandedness: Single;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers
          FT   source          1. .660
          FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .660
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.81e-20        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x BD007080 (1-660)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
Db      601 GCCTTCCGCATCCGCGCCGTGACCATC 627

RESULT 76
BD007081
LOCUS       BD007081                  660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007081
VERSION     BD007081.1  GI:18635452
KEYWORDS    JP 2001503258-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 6 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/6
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .660
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.81e-20        Length:         660
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0
```

```
-10-821-670A-33 (1-222) x BD007081 (1-660)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        601 GCCTTCCGCATCCGGGCCGTGACCATC 627

SULT 77
136037
CUS       BD136037                660 bp    DNA     linear   PAT 18-SEP-2002
FINITION  Interferon alpha plasmid and delivery system and method of
          preparing and using the same.
CESSION   BD136037
RSION     BD136037.1  GI:23230982
YWORDS    JP 2002506647-A/4.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 660)
AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
TITLE     Interferon alpha plasmid and delivery system and method of
          preparing and using the same
JOURNAL   Patent: JP 2002506647-A 4 05-MAR-2002;
          VALENTIS INC
MMENT     OS   Homo sapiens (human)
          PN   JP 2002506647-A/4
          PD   05-MAR-2002
          PF   12-MAR-1999 JP 2000536861
          PR   19-MAR-1998 US    60/078654
          PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
          PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
          PC   C12N1/15,
          PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
           C12N5/00
          CC   Interferon alpha plasmid and delivery system and method of  CC
                    preparing and
          CC   using the same
          FH   Key             Location/Qualifiers
          FT   source          1. .660
          FT                   /organism='Homo sapiens (human)'.
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
IGIN

ignment Scores:
ed. No.:              1.81e-20       Length:        660
ore:                  29.00          Matches:       29
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x BD136037 (1-660)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 78
136038
CUS       BD136038                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136038
VERSION     BD136038.1  GI:23230983
KEYWORDS    JP 2002506647-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 5 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/5
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: all optimized codons
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              1.81e-20       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x BD136038 (1-660)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

RESULT 79
BD136039
LOCUS       BD136039                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136039
VERSION     BD136039.1  GI:23230984
KEYWORDS    JP 2002506647-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 6 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/6
            PD   05-MAR-2002
```

```
          PF   12-MAR-1999 JP 2000536861
          PR   19-MAR-1998 US    60/078654
          PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
          PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
          PC   C12N1/15,
          PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
           C12N5/00
          CC   Sequence source: most codons optimized
          FH   Key             Location/Qualifiers
          FT   source          1. .660
          FT                   /organism='Artificial Sequence'.
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
IGIN

ignment Scores:
ed. No.:              1.81e-20       Length:        660
ore:                  29.00          Matches:       29
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x BD136039 (1-660)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        601 GCCTTCCGCATCCGGGCCGTGACCATC 627

SULT 80
8592
CUS       I28592                  660 bp    DNA     linear   PAT 06-FEB-1997
FINITION  Sequence 3 from patent US 5573764.
CCESSION  I28592
RSION     I28592.1  GI:1819368
YWORDS    .
URCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
FERENCE   1  (bases 1 to 660)
 AUTHORS   Sykes,M. and Wolf,S.F.
 TITLE     Use of interleukin-12 to prevent graft versus host disease
 JOURNAL   Patent: US 5573764-A 3 12-NOV-1996;
ATURES              Location/Qualifiers
   source           1. .660
                    /organism="unknown"
                    /mol_type="unassigned DNA"
IGIN

ignment Scores:
 ed. No.:             1.81e-20       Length:        660
 ore:                 29.00          Matches:       29
 rcent Similarity:    100.0%         Conservative:  0
 st Local Similarity: 100.0%         Mismatches:    0
 ery Match:           13.1%          Indels:        0
 :                    2              Gaps:          0

-10-821-670A-33 (1-222) x I28592 (1-660)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

```
RESULT 81
AX154634
LOCUS       AX154634                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 38 from Patent WO0140257.
ACCESSION   AX154634
VERSION     AX154634.1  GI:14536198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 38 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.81e-20       Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX154634 (1-660)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 82
CQ829447
LOCUS       CQ829447                702 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 6 from Patent WO2004052929.
ACCESSION   CQ829447
VERSION     CQ829447.1  GI:49732783
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 6 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES              Location/Qualifiers
     source           1. .702
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="cDNA for alpha chain of IL-12"
ORIGIN

Alignment Scores:
Pred. No.:              1.91e-20       Length:        702
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     2              Gaps:          0
```

```
-10-821-670A-33 (1-222) x CQ829447 (1-702)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        556 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 615

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
        616 GCTTTCAGAATTCGGGCAGTGACTATT 642

SULT 83
052862
CUS       AR052862                721 bp    DNA     linear   PAT 29-SEP-1999
FINITION  Sequence 199 from patent US 5833975.
CESSION   AR052862
RSION     AR052862.1  GI:5977724
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 721)
AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
          DNA sequence
JOURNAL   Patent: US 5833975-A 199 10-NOV-1998;
ATURES              Location/Qualifiers
   source           1. .721
                    /organism="unknown"
                    /mol_type="unassigned DNA"
IGIN

ignment Scores:
ed. No.:              1.96e-20       Length:        721
ore:                  29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AR052862 (1-721)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

SULT 84
288174
CUS       AR288174                721 bp    mRNA    linear   PAT 12-JUN-2003
FINITION  Sequence 199 from patent US 6537594.
CESSION   AR288174
RSION     AR288174.1  GI:31675453
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 721)
AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
          genes
JOURNAL   Patent: US 6537594-A 199 25-MAR-2003;
          Virogenetics Corporation; Troy, NY
ATURES              Location/Qualifiers
   source           1. .721
                    /organism="unknown"
                    /mol_type="mRNA"
IGIN

ignment Scores:
Pred. No.:              1.96e-20       Length:        721
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AR288174 (1-721)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 85
AR567161
LOCUS       AR567161                721 bp    mRNA    linear   PAT 08-OCT-2004
DEFINITION  Sequence 199 from patent US 6780407.
ACCESSION   AR567161
VERSION     AR567161.1  GI:53984803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 199 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES              Location/Qualifiers
     source           1. .721
                      /organism="unknown"
                      /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.96e-20       Length:        721
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AR567161 (1-721)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 86
BD105971
LOCUS       BD105971                762 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Animal model for evaluation of vaccines.
ACCESSION   BD105971
VERSION     BD105971.1  GI:23200789
KEYWORDS    JP 2002501375-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 21 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/21
            PD   15-JAN-2002
```

```
          PF   09-APR-1998 JP 1998543062
          PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
          09-DEC-1997 US    60/069163
          PI   LUNG JI CHANG
          PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
            C12N7/04,
          PC   A61K39/21
          CC   Strandedness: Double;
          CC   Topology: Linear;
          CC   /desc = 'DNA'
          FH   Key             Location/Qualifiers.
ATURES              Location/Qualifiers
    source          1. .762
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
IGIN

ignment Scores:
ed. No.:                2.06e-20        Length:         762
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-33 (1-222) x BD105971 (1-762)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 87
803343
CUS         CQ803343                762 bp    DNA     linear   PAT 10-MAY-2004
FINITION    Sequence 3 from Patent WO2004035799.
CESSION     CQ803343
RSION       CQ803343.1  GI:47110209
YWORDS      .
URCE        Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
FERENCE     1
AUTHORS     Waehler,R. and Schnieders,F.
TITLE       Viral vectors and the use of the same for gene therapy
JOURNAL     Patent: WO 2004035799-A 3 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
ATURES              Location/Qualifiers
    source          1. .762
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
IGIN

ignment Scores:
ed. No.:                2.06e-20        Length:         762
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-33 (1-222) x CQ803343 (1-762)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 88
AR533401
LOCUS       AR533401                762 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 21 from patent US 6730512.
ACCESSION   AR533401
VERSION     AR533401.1  GI:53923067
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.-J.
  TITLE     Combination immunogene therapy
  JOURNAL   Patent: US 6730512-A 21 04-MAY-2004;
            Amdl, Inc.; Tustin, CA
FEATURES            Location/Qualifiers
     source         1. .762
                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.06e-20        Length:         762
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR533401 (1-762)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 89
AF101062
LOCUS       AF101062                762 bp    mRNA    linear   PRI 03-MAR-1999
DEFINITION  Homo sapiens interleukin 12 mRNA, complete cds.
ACCESSION   AF101062
VERSION     AF101062.1  GI:4323578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Liu,y., Guo,Y. and Wu,M.
  TITLE     Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
            Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Liu,Y., Guo,Y. and Wu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1998) Molecular Biology Department, Cancer
            Institute of Second Military Medical University, 800 XianYin Road,
            Shanghai 200433, P.R. China
FEATURES            Location/Qualifiers
     source         1. .762
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /chromosome="3"
```

```
                /map="3p12-q13.2"
                /cell_line="lymphoblastoid B-cell line NC37"
                /note="cells induced by phorbol 12-myristate 13 acetate
                (PMA) and ionophore A23187"
   CDS          1. .762
                /note="natural killer cell stimulatory factor; cytotoxic
                lymphocyte maturation factor 35kDa subunit; p35"
                /codon_start=1
                /product="interleukin 12"
                /protein_id="AAD16432.1"
                /db_xref="GI:4323579"
                /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
   variation    132
                /replace="c"
   variation    732
                /replace="c"
   variation    740
                /replace="c"
IGIN

ignment Scores:
ed. No.:              2.06e-20        Length:         762
ore:                  29.00           Matches:        29
cent Similarity:      100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            13.1%           Indels:         0
:                     5               Gaps:           0

-10-821-670A-33 (1-222) x AF101062 (1-762)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 90
U19842
CUS       MMU19842                 780 bp    mRNA    linear   PRI 03-FEB-1996
FINITION  Macaca mulatta interleukin-12 beta p35 subunit (IL-12b) mRNA,
          complete cds.
CESSION   U19842
RSION     U19842.1  GI:644801
YWORDS    .
URCE      Macaca mulatta (rhesus monkey)
ORGANISM  Macaca mulatta
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Cercopithecidae; Cercopithecinae; Macaca.
FERENCE   1  (bases 1 to 780)
AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
TITLE     Comparative sequence analysis of cytokine genes from human and
          nonhuman primates
JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
 PUBMED   7561102
FERENCE   2  (bases 1 to 780)
AUTHORS   Villinger,F.J.
TITLE     Direct Submission
JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
          Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
ATURES              Location/Qualifiers
   source           1. .780
                    /organism="Macaca mulatta"
                    /mol_type="mRNA"
                    /db_xref="taxon:9544"
                    /clone="RNc IL-12b"
                    /cell_type="peripheral blood mononuclear cells"
                    /tissue_type="blood"
   gene             1. .780
                    /gene="IL-12b"
   CDS              10. .771
                    /gene="IL-12b"
                    /function="NK cell stimulatory factor"
                    /codon_start=1
                    /product="interleukin-12 beta p35 subunit"
                    /protein_id="AAA86707.1"
                    /db_xref="GI:644802"
                    /translation="MWPPGSASQPPPSPATATGLHPAARPEPPQCRLSMCPARSLLLV
                    ATLVLLDYLSLARNLSVATPGPEMFPCLHHSQNLLKAASNTLQKARQILEFYPCTSEE
                    IDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTSFMMALCLRS
                    IYEDLKMYQVEFKTMNAKLLRDPKRQIFLDQNILGVIDELMQALNFNSETVPQKSSLE
                    EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

Alignment Scores:
Pred. No.:              2.1e-20         Length:         780
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-33 (1-222) x MMU19842 (1-780)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 711

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        712 GCTTTCAGAATTCGGGCAGTGACTATT 738

RESULT 91
AF180562
LOCUS       AF180562                 823 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P35 mRNA, complete cds.
ACCESSION   AF180562
VERSION     AF180562.1  GI:5923852
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES              Location/Qualifiers
     source           1. .823
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /chromosome="3"
                      /map="3p12-q13.2"
                      /cell_type="peripheral mononuclear"
     CDS              60. .821
                      /note="NKSF/CLMF; IL12p35; 35kD"
                      /codon_start=1
                      /product="interleukin 12, P35"
                      /protein_id="AAD56385.1"
                      /db_xref="GI:5923853"
                      /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                      ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                      IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
```

```
                IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
IGIN

ignment Scores:
ed. No.:              2.21e-20       Length:        823
ore:                  29.00          Matches:       29
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     5              Gaps:          0

-10-821-670A-33 (1-222) x AF180562 (1-823)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        702 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 761

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        762 GCTTTCAGAATTCGGGCAGTGACTATT 788

SULT 92
165801
CUS       BD165801                856 bp    DNA     linear   PAT 17-JAN-2003
FINITION  Antibody against cytotoxic lymphocyte maturing factors.
CESSION   BD165801
RSION     BD165801.1  GI:27871613
YWORDS    JP 2002167400-A/2.
URCE      unidentified
ORGANISM  unidentified
          unclassified sequences.
FERENCE   1  (bases 1 to 856)
AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
          Podlanski,F.J. and Stern,A.S.
TITLE     Antibody against cytotoxic lymphocyte maturing factors
JOURNAL   Patent: JP 2002167400-A 2 11-JUN-2002;
          PROTEIN DESIGN LABS INC
MMENT     OS   Homo sapiens (human)
          PN   JP 2002167400-A/2
          PD   11-JUN-2002
          PF   14-AUG-2001 JP 2001246031
          PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
          27-AUG-1990 US       572284
          PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
          PI   GUBLER,
          PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
          PI   ALVIN SETH STERN
          PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
            Antibody against cytotoxic lymphocyte maturing factors FH   Key
                  Location/Qualifiers
          FT   CDS                (170). .(826).
ATURES              Location/Qualifiers
   source           1. .856
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
IGIN

ignment Scores:
ed. No.:              2.29e-20       Length:        856
ore:                  29.00          Matches:       29
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x BD165801 (1-856)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769
```

```
Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 93
CQ716168
LOCUS       CQ716168                1020 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 2102 from Patent WO02068579.
ACCESSION   CQ716168
VERSION     CQ716168.1  GI:42277025
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 2102 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1020
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:            2.68e-20       Length:        1020
Score:                29.00          Matches:       29
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          13.1%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-33 (1-222) x CQ716168 (1-1020)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      703 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 762

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      763 GCTTTCAGAATTCGGGCAGTGACTATT 789

RESULT 94
BC104982
LOCUS       BC104982                1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132642 IMAGE:8143985), complete cds.
ACCESSION   BC104982
VERSION     BC104982.1  GI:85397857
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
```

```
                Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
                Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
                Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
                Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
                Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
                Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
                Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
                Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
:ONSRTM         Mammalian Gene Collection Program Team
:ITLE           Generation and initial analysis of more than 15,000 full-length
                human and mouse cDNA sequences
JOURNAL         Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED         12477932
FERENCE         2  (bases 1 to 1021)
AUTHORS         .
:ONSRTM         NIH MGC Project
:ITLE           Direct Submission
JOURNAL         Submitted (13-SEP-2005) National Institutes of Health, Mammalian
                Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK          NIH-MGC Project URL: http://mgc.nci.nih.gov
MMENT           Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Mike Brownstein, NIMH
                cDNA Library Preparation: British Columbia Cancer Research Center
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Genome Sequence Centre,
                BC Cancer Agency, Vancouver, BC, Canada
                info@bcgsc.bc.ca
                Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
                Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
                Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
                Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
                Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
                Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
                Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
                Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
                Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

                Clone distribution: MGC clone distribution information can be found
                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                Series: IRCB Plate: 3 Row: j Column: 15.
ATURES                  Location/Qualifiers
   source               1. .1021
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="MGC:132642 IMAGE:8143985"
                        /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                        /clone_lib="NIH_MGC_287"
                        /note="Vector: pCR4-TOPO with reversed insert; Clone
                        identification sequence tag: TCGTTGCT"
   gene                 1. .1021
                        /gene="IL12A"
                        /note="synonyms: IL-12A, NFSK, CLMF"
                        /db_xref="GeneID:3592"
                        /db_xref="HGNC:5969"
                        /db_xref="IMGT/GENE-DB:5969"
                        /db_xref="MIM:161560"
   CDS                  154. .915
                        /gene="IL12A"
                        /codon_start=1
                        /product="interleukin 12A, precursor"
                        /protein_id="AAI04983.1"
                        /db_xref="GI:85397858"
                        /db_xref="GeneID:3592"
                        /db_xref="HGNC:5969"
                        /db_xref="IMGT/GENE-DB:5969"
                        /db_xref="MIM:161560"
                        /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                        ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                        IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                        IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                        EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
```

```
ORIGIN

Alignment Scores:
Pred. No.:              2.68e-20        Length:         1021
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-33 (1-222) x BC104982 (1-1021)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 855

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db        856 GCTTTCAGAATTCGGGCAGTGACTATT 882

RESULT 95
BC104984
LOCUS       BC104984                1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132644 IMAGE:8143987), complete cds.
ACCESSION   BC104984
VERSION     BC104984.1  GI:85397860
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
```

```
          Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
          Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
          Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
          Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
          Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
          Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
          Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
          Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
          Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRCB Plate: 3 Row: j Column: 17.
ATURES              Location/Qualifiers
    source          1. .1021
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="MGC:132644 IMAGE:8143987"
                    /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                    /clone_lib="NIH_MGC_287"
                    /note="Vector: pCR4-TOPO with reversed insert; Clone
                    identification sequence tag: AAATAGCC"
    gene            1. .1021
                    /gene="IL12A"
                    /note="synonyms: IL-12A, NFSK, CLMF"
                    /db_xref="GeneID:3592"
                    /db_xref="HGNC:5969"
                    /db_xref="IMGT/GENE-DB:5969"
                    /db_xref="MIM:161560"
    CDS             154. .915
                    /gene="IL12A"
                    /codon_start=1
                    /product="interleukin 12A, precursor"
                    /protein_id="AAI04985.1"
                    /db_xref="GI:85397861"
                    /db_xref="GeneID:3592"
                    /db_xref="HGNC:5969"
                    /db_xref="IMGT/GENE-DB:5969"
                    /db_xref="MIM:161560"
                    /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                    ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                    IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                    IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                    EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
IGIN

ignment Scores:
ed. No.:                2.68e-20        Length:         1021
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       5               Gaps:           0

-10-821-670A-33 (1-222) x BC104984 (1-1021)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        796 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 855

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
        856 GCTTTCAGAATTCGGGCAGTGACTATT 882

SULT 96
091390
CUS       AR091390                1026 bp    DNA     linear   PAT 07-SEP-2000
FINITION  Sequence 1 from patent US 5994104.
CESSION   AR091390
RSION     AR091390.1  GI:10018145
YWORDS    .
URCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 1 30-NOV-1999;
FEATURES              Location/Qualifiers
     source           1. .1026
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.69e-20        Length:         1026
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR091390 (1-1026)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 97
AR380496
LOCUS       AR380496                1026 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1041 from patent US 6607879.
ACCESSION   AR380496
VERSION     AR380496.1  GI:40088130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1041 19-AUG-2003;
            Incyte Corporation; Palo Alto, CA
FEATURES              Location/Qualifiers
     source           1. .1026
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.69e-20        Length:         1026
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR380496 (1-1026)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 98
HUMCLMF35
LOCUS       HUMCLMF35               1026 bp    mRNA    linear   PRI 27-APR-1993
```

```
?INITION  Human cytotoxic lymphocyte maturation factor 35 kDa subunit mRNA,
          complete cds.
:ESSION   M65271 M38443
:SION     M65271.1  GI:180623
:WORDS    cytotoxic lymphocyte maturation factor 35 kDa subunit; interleukin.
JRCE      Homo sapiens (human)
)RGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
?ERENCE   1  (bases 1 to 1026)
\UTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
          Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
          and Gately,M.K.
?ITLE     Coexpression of two distinct genes is required to generate secreted
          bioactive cytotoxic lymphocyte maturation factor
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
 PUBMED   1674604
/MENT     Original source text: Human, cDNA to mRNA.
\TURES              Location/Qualifiers
   source           1. .1026
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
   CDS              170. .829
                    /codon_start=1
                    /product="cytotoxic lymphocyte maturation factor 35 kDa
                    subunit"
                    /protein_id="AAA35694.1"
                    /db_xref="GI:180624"
                    /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                    LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
                    SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNML
                    AVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNA
                    S"
IGIN

ignment Scores:
ed. No.:              2.69e-20        Length:         1026
ore:                  29.00           Matches:        29
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            13.1%           Indels:         0
:                     5               Gaps:           0

-10-821-670A-33 (1-222) x HUMCLMF35 (1-1026)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

       204 AlaPheArgIleArgAlaValThrIle 212
           |||||||||||||||||||||||||
       770 GCTTTCAGAATTCGGGCAGTGACTATT 796

SULT 99
393790
:US       AR393790               1287 bp    DNA     linear   PAT 18-DEC-2003
?INITION  Sequence 6 from patent US 6617135.
:ESSION   AR393790
:SION     AR393790.1  GI:40120794
:WORDS    .
JRCE      Unknown.
)RGANISM  Unknown.
          Unclassified.
?ERENCE   1  (bases 1 to 1287)
\UTHORS   Gillies,S.D. and Lo,K.-M.
?ITLE     Multiple cytokine protein complexes
JOURNAL   Patent: US 6617135-A 6 09-SEP-2003;
          EMD Lexigen Research Center Corp.; Billerica, MA
\TURES              Location/Qualifiers
   source           1. .1287
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.3e-20         Length:         1287
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR393790 (1-1287)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254

RESULT 100
AX084108
LOCUS       AX084108               1287 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 6 from Patent WO0110912.
ACCESSION   AX084108
VERSION     AX084108.1  GI:13185658
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 6 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES              Location/Qualifiers
     source           1. .1287
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="human Fc-p35 fusion protein coding sequence"
ORIGIN

Alignment Scores:
Pred. No.:              3.3e-20         Length:         1287
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AX084108 (1-1287)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254


Search completed: June 10, 2006, 12:07:53
Job time : 5072.64 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 01:23:11 ; Search time 537.89 Seconds
(without alignments)
4316.416 Million cell updates/sec

tle: US-10-821-670A-33
rfect score: 222
quence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 5244920 seqs, 3486124231 residues

rd size: 1

tal number of hits satisfying chosen parameters: 10484871

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110446_27507/app_query.fasta_1
B=N_Geneseq -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rng -MINMATCH=0.1
OOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
RANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
LIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
AXLEN=2000000000 -HOST=abss05h
SER=US10821670_@CGN_1_1_1666_@runat_07062006_110446_27507 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description
1	222	100.0	666	6	ABK98947	Abk98947 Feline in
2	222	100.0	666	6	ABK98946	Abk98946 Feline in
3	222	100.0	666	14	ADV34685	Adv34685 Feline si
c 4	222	100.0	666	14	ADV34687	Adv34687 Feline si
5	220	99.1	689	2	AAV56641	Aav56641 Feline FL
6	220	99.1	1441	2	AAV56628	Aav56628 Feline FL
7	197	88.7	591	6	ABK98948	Abk98948 Feline in
c 8	197	88.7	591	6	ABK98949	Abk98949 Feline in
9	197	88.7	591	14	ADV34688	Adv34688 Feline si
c 10	197	88.7	591	14	ADV34690	Adv34690 Feline si
c 11	197	88.7	1533	6	ABK98954	Abk98954 Feline in
12	197	88.7	1533	6	ABK98953	Abk98953 Feline in
c 13	197	88.7	1533	14	ADV34697	Adv34697 Feline si
14	197	88.7	1533	14	ADV34695	Adv34695 Feline si
15	197	88.7	1599	6	ABK98950	Abk98950 Feline in
c 16	197	88.7	1599	6	ABK98951	Abk98951 Feline in
17	197	88.7	1599	14	ADV34691	Adv34691 Feline si
c 18	197	88.7	1599	14	ADV34693	Adv34693 Feline si
19	195	87.8	591	2	AAV56629	Aav56629 Feline FL
20	187	84.2	561	6	ABK99001	Abk99001 Feline in
c 21	187	84.2	561	6	ABK99002	Abk99002 Feline in
22	187	84.2	561	14	ADV34751	Adv34751 Feline N-
c 23	187	84.2	561	14	ADV34753	Adv34753 Feline N-
24	69	31.1	679	4	AAF26097	Aaf26097 Feline fi
25	65	29.3	669	4	AAF26083	Aaf26083 Feline IL
26	65	29.3	669	4	AAF26086	Aaf26086 Feline IL
27	65	29.3	4201	4	AAF26077	Aaf26077 Feline IL
28	59	26.6	660	5	AAD15219	Aad15219 Modified
29	59	26.6	660	5	AAD15214	Aad15214 Modified
30	59	26.6	660	5	AAD15218	Aad15218 Modified
31	56	25.2	660	5	AAD15215	Aad15215 Modified
32	54	24.3	639	4	AAF26098	Aaf26098 Plasmid p
33	52	23.4	591	2	AAX18179	Aax18179 Canine ma
c 34	52	23.4	591	6	ABK98958	Abk98958 Canine in
35	52	23.4	591	6	ABK98957	Abk98957 Canine in
36	52	23.4	591	14	ADV34701	Adv34701 Canine si
c 37	52	23.4	591	14	ADV34703	Adv34703 Canine si
38	52	23.4	666	6	ABK98955	Abk98955 Canine in
c 39	52	23.4	666	6	ABK98956	Abk98956 Canine in
c 40	52	23.4	666	14	ADV34700	Adv34700 Canine si
41	52	23.4	666	14	ADV34698	Adv34698 Canine si
42	52	23.4	669	2	AAV13818	Aav13818 Canine IL
43	52	23.4	669	2	AAV13819	Aav13819 Canine IL
44	52	23.4	669	2	AAX03163	Aax03163 Nucleic a
45	52	23.4	669	2	AAX03153	Aax03153 Nucleic a
46	52	23.4	669	2	AAX35616	Aax35616 Nucleic a
47	52	23.4	669	2	AAX35626	Aax35626 Nucleic a
48	52	23.4	669	4	AAI64389	Aai64389 Canine co
49	52	23.4	669	4	AAI64379	Aai64379 Canine co
50	52	23.4	669	11	ADZ25701	Adz25701 Canine in
51	52	23.4	1282	2	AAX18178	Aax18178 Canine fu
52	52	23.4	1455	6	ABK99003	Abk99003 Canine in
c 53	52	23.4	1455	6	ABK99004	Abk99004 Canine in
c 54	52	23.4	1455	14	ADV34756	Adv34756 Canine si
55	52	23.4	1455	14	ADV34754	Adv34754 Canine si
56	52	23.4	1533	6	ABK98967	Abk98967 Canine in
c 57	52	23.4	1533	6	ABK98968	Abk98968 Canine in
c 58	52	23.4	1533	14	ADV34718	Adv34718 Canine si
59	52	23.4	1533	14	ADV34716	Adv34716 Canine si
60	52	23.4	1599	6	ABK98965	Abk98965 Canine in
c 61	52	23.4	1599	6	ABK98966	Abk98966 Canine in
c 62	52	23.4	1599	14	ADV34715	Adv34715 Canine si
63	52	23.4	1599	14	ADV34713	Adv34713 Canine si
64	50	22.5	669	13	ADT04852	Adt04852 Canine in
65	43	19.4	666	5	AAD15212	Aad15212 Modified
66	42	18.9	554	2	AAT50757	Aat50757 Partial s
67	40	18.0	703	3	AAA70708	Aaa70708 Bovine in
68	39	17.6	660	5	AAD15213	Aad15213 Modified
69	39	17.6	660	5	AAD15216	Aad15216 Modified
70	39	17.6	660	5	AAD15220	Aad15220 Modified
71	37	16.7	660	5	AAD15217	Aad15217 Modified
72	31	14.0	666	5	AAD15211	Aad15211 Modified
73	29	13.1	201	13	ADQ41825	Adq41825 Myocardia
74	29	13.1	201	13	ADQ41824	Adq41824 Myocardia
75	29	13.1	201	13	ADQ41835	Adq41835 Myocardia

76	29	13.1	201	13	ADQ41829	Adq41829 Myocardia
77	29	13.1	201	13	ADQ41838	Adq41838 Myocardia
78	29	13.1	201	13	ADQ41833	Adq41833 Myocardia
79	29	13.1	630	12	ADF77258	Adf77258 Human IL-
80	29	13.1	657	12	ADG39431	Adg39431 Human CLM
81	29	13.1	660	2	AAQ97485	Aaq97485 Human int
82	29	13.1	660	2	AAV07274	Aav07274 Human Int
83	29	13.1	660	2	AAV07218	Aav07218 DNA encod
84	29	13.1	660	2	AAZ40408	Aaz40408 Human int
85	29	13.1	660	2	AAZ40407	Aaz40407 Human int
86	29	13.1	660	2	AAZ40409	Aaz40409 Human int
87	29	13.1	660	5	AAD15221	Aad15221 Human cyt
88	29	13.1	660	6	AAL44226	Aal44226 Human int
89	29	13.1	660	6	ACC47589	Acc47589 Human int
90	29	13.1	660	12	ADF77245	Adf77245 Human IL-
91	29	13.1	660	12	ADF77257	Adf77257 Human IL-
92	29	13.1	660	12	ADF77246	Adf77246 Human IL-
93	29	13.1	660	12	ADF77244	Adf77244 Human IL-
94	29	13.1	683	4	AAF26096	Aaf26096 Human pG-
95	29	13.1	702	12	ADP88401	Adp88401 Human int
96	29	13.1	721	2	AAQ67880	Aaq67880 EPV 42 kD
97	29	13.1	721	2	AAZ08515	Aaz08515 Vaccinia
98	29	13.1	721	13	ADR21891	Adr21891 Vaccinia
99	29	13.1	761	10	ADK98708	Adk98708 Human int
100	29	13.1	761	10	ADK98706	Adk98706 Human int
101	29	13.1	762	2	AAV83207	Aav83207 Interleuk
102	29	13.1	762	3	AAA35201	Aaa35201 Human ade
103	29	13.1	762	3	AAF21323	Aaf21323 Human low
104	29	13.1	762	10	ABZ97017	Abz97017 Human nuc
105	29	13.1	762	11	ABD20866	Abd20866 Human pul
106	29	13.1	762	12	ADO07654	Ado07654 Human int
107	29	13.1	762	13	ADS88021	Ads88021 Tumour tr
108	29	13.1	762	14	ADV42511	Adv42511 Human psy
109	29	13.1	823	10	ACD26420	Acd26420 cDNA enco
110	29	13.1	856	2	AAQ12150	Aaq12150 Cytotoxic
111	29	13.1	856	2	AAT77850	Aat77850 35 kDa su
112	29	13.1	856	2	AAT97970	Aat97970 35 kDa su
113	29	13.1	856	2	AAV00402	Aav00402 35 kDa su
114	29	13.1	856	2	AAV37772	Aav37772 Cytotoxic
115	29	13.1	856	12	ADG39389	Adg39389 Human cyt
116	29	13.1	856	12	ADO03760	Ado03760 Human CLM
117	29	13.1	889	13	ADU04652	Adu04652 Human ext
118	29	13.1	1026	3	AAZ40020	Aaz40020 Human p35
119	29	13.1	1026	8	ACA61266	Aca61266 DNA encod
120	29	13.1	1026	11	ADI31715	Adi31715 Human cDN
121	29	13.1	1026	13	ADS83782	Ads83782 Human lym
122	29	13.1	1172	8	ACC42373	Acc42373 Human ext
123	29	13.1	1200	8	ACF64408	Acf64408 Human IL1
124	29	13.1	1287	4	AAF76882	Aaf76882 DNA encod
125	29	13.1	1289	8	ACC42375	Acc42375 Human ext
126	29	13.1	1316	2	AAT63621	Aat63621 Interleuk
127	29	13.1	1316	6	AAD41639	Aad41639 Human int
128	29	13.1	1364	2	AAT48099	Aat48099 Human int
129	29	13.1	1364	2	AAV42536	Aav42536 Human int
130	29	13.1	1364	2	AAV15228	Aav15228 Heterodim
131	29	13.1	1364	3	AAZ28863	Aaz28863 Human int
132	29	13.1	1364	4	AAF56281	Aaf56281 IL-12 vac
133	29	13.1	1384	15	AEF92723	Aef92723 Human int
134	29	13.1	1396	2	AAQ24371	Aaq24371 Natural k
135	29	13.1	1444	12	ACF57533	Acf57533 Human IL1
136	29	13.1	1444	12	ADJ62891	Adj62891 Human int
137	29	13.1	1444	12	ADN12152	Adn12152 Interleuk
138	29	13.1	1444	14	ADY15785	Ady15785 DNA encod
139	29	13.1	1444	14	ADZ26544	Adz26544 Human IL1
140	29	13.1	1444	14	AEB56478	Aeb56478 Radiochem
141	29	13.1	1494	12	ADQ59495	Adq59495 Human can
142	29	13.1	1526	12	ADQ59549	Adq59549 Human can
143	29	13.1	1532	13	ADQ38388	Adq38388 Human SNP
144	29	13.1	1532	14	ADZ13866	Adz13866 Human can
145	29	13.1	1607	13	ADQ38387	Adq38387 Human SNP
146	29	13.1	1607	14	ADZ13864	Adz13864 Human can
147	29	13.1	2300	3	AAA92406	Aaa92406 Human int
148	29	13.1	2336	14	AEE03207	Aee03207 Human int
149	29	13.1	2390	12	ADM29103	Adm29103 Human int
150	29	13.1	3205	14	AEB48820	Aeb48820 Monoclona
151	29	13.1	4521	3	AAA35204	Aaa35204 Human ade
152	29	13.1	4521	3	AAF21326	Aaf21326 Human low
153	29	13.1	4521	10	ABZ97020	Abz97020 Human nuc
154	29	13.1	4521	11	ABD20869	Abd20869 Human pul
155	29	13.1	5013	14	AEA40941	Aea40941 T-DNA reg
156	29	13.1	5686	2	AAZ40415	Aaz40415 Plasmid p
157	29	13.1	5686	12	ADF77239	Adf77239 Human IL-
158	29	13.1	6139	3	AAZ40023	Aaz40023 Interleuk
159	29	13.1	8578	6	AAD31546	Aad31546 pIRES-hB7
160	29	13.1	8578	6	AAD31545	Aad31545 pIRES-hB7
161	29	13.1	8608	6	AAD31548	Aad31548 pIRES-hB7
162	29	13.1	8623	6	AAD31547	Aad31547 pIRES-hB7
163	29	13.1	8629	6	AAD31552	Aad31552 pIRES-IL1
164	29	13.1	8638	6	AAD31549	Aad31549 pIRES-hB7
165	29	13.1	8644	6	AAD31551	Aad31551 pIRES-IL1
166	29	13.1	8659	6	AAD31550	Aad31550 pIRES-IL1
167	29	13.1	11441	6	AAL44225	Aal44225 Human int
168	29	13.1	11453	10	ADG25152	Adg25152 Vector pS
169	29	13.1	11569	10	ADG25150	Adg25150 Vector pA
170	29	13.1	27277	12	ADQ59494	Adq59494 Human can
171	29	13.1	27277	14	ADZ13863	Adz13863 Human can
172	28	12.6	700	8	ACF64405	Acf64405 Human IL1
173	26	11.7	79	2	AAV56639	Aav56639 Feline FL
174	26	11.7	79	2	AAX18181	Aax18181 Primer fo
175	25	11.3	666	2	AAT50758	Aat50758 Sequence
176	23	10.4	71	4	AAF26092	Aaf26092 Feline IL
177	23	10.4	71	4	AAF26099	Aaf26099 Feline Il
178	23	10.4	95	2	AAV56637	Aav56637 Feline FL
179	20	9.0	201	13	ADQ41830	Adq41830 Myocardia
180	20	9.0	201	13	ADQ41821	Adq41821 Myocardia
181	20	9.0	700	8	ACF64406	Acf64406 Human IL1
182	20	9.0	700	8	ACF64407	Acf64407 Human IL1
183	18	8.1	76	4	AAF26100	Aaf26100 Feline Il
c 184	18	8.1	76	4	AAF26093	Aaf26093 Feline IL
c 185	18	8.1	76	4	AAF26090	Aaf26090 Feline IL
186	16	7.2	95	2	AAX18180	Aax18180 Primer fo
187	13	5.9	60	6	ABN39662	Abn39662 Human spl
188	13	5.9	660	2	AAV31481	Aav31481 Human int
189	13	5.9	660	2	AAZ40421	Aaz40421 Human int
190	13	5.9	660	12	ADF77255	Adf77255 Human IL-
c 191	12	5.4	36	2	AAV56640	Aav56640 Feline FL
c 192	12	5.4	36	2	AAX18182	Aax18182 Primer fo
193	11	5.0	39	6	ABK98991	Abk98991 Synthetic
194	11	5.0	39	14	ADV34741	Adv34741 Feline IL
195	11	5.0	750	8	ACF64404	Acf64404 Human IL1
196	10	4.5	39	2	AAV13830	Aav13830 Primer fo
197	10	4.5	39	2	AAX03166	Aax03166 PCR prime
198	10	4.5	39	2	AAX35629	Aax35629 PCR prime
199	10	4.5	39	4	AAI64392	Aai64392 PCR prime
200	10	4.5	60	6	ABK98983	Abk98983 Feline se

ALIGNMENTS

RESULT 1
ABK98947/c
ID ABK98947 standard; cDNA; 666 BP.
XX
AC ABK98947;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 3; Page 56; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	7.56e-215	Length:	666
ore:	222.00	Matches:	222
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	100.0%	Indels:	0
	6	Gaps:	0

-10-821-670A-33 (1-222) x ABK98947 (1-666)

```
          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247
```

```
Qy      141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy      161 AsnMetLeuThrAlaIleAspGluLeuGluGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy      181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy      201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy      221 AlaSer 222
            ||||||
Db        6 GCTTCC 1
```

RESULT 2
ABK98946
ID ABK98946 standard; cDNA; 666 BP.
XX
AC ABK98946;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69304.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 54-55; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX

Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 7.56e-215 Length: 666
ore: 222.00 Matches: 222
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 100.0% Indels: 0
: 6 Gaps: 0

-10-821-670A-33 (1-222) x ABK98946 (1-666)

```
          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

        221 AlaSer 222
            ||||||
        661 GCTTCC 666
```

ULT 3
734685
ADV34685 standard; cDNA; 666 BP.

ADV34685;

24-FEB-2005 (first entry)

Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; gene; ss.

OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 1. .666
FT /*tag= a
FT /product= "PFeIL-12p35 222 protein "
FT /partial
FT /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34686.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p35 subunit protein
CC encoding full-length cDNA.
XX
SQ Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.56e-215 Length: 666
Score: 222.00 Matches: 222
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-33 (1-222) x ADV34685 (1-666)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
```

```
       101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

       121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

       141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

       161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

       181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

       201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

       221 AlaSer 222
           ||||||
       661 GCTTCC 666
```

SULT 4
V34687/c
ADV34687 standard; DNA; 666 BP.

ADV34687;

24-FEB-2005 (first entry)

Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; ds.

Felis catus.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 3; SEQ ID NO 34; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain IL-12p35 subunit full-length complementary DNA.

XX
SQ Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.56e-215	Length:	666
Score:	222.00	Matches:	222
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-33 (1-222) x ADV34687 (1-666)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
              ||||||
Db          6 GCTTCC 1
```

RESULT 5
AAV56641
ID AAV56641 standard; DNA; 689 BP.
XX
AC AAV56641;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp35 DNA fragment.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ss.

Felis catus.

WO9746583-A1.

11-DEC-1997.

29-MAY-1997; 97WO-JP001824.

04-JUN-1996; 96JP-00165249.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;

WPI; 1998-042118/04.

Novel feline cytokine protein - useful for treating feline auto:immune diseases, e.g. those caused by feline herpes virus or feline calcivirus.

Claim 24; Page 67; 94pp; Japanese.

This sequence encodes a fragment of a novel feline cytokine protein, FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40 heterodimer which can potentiate the cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins are used for treatment of feline autoimmune diseases e.g. as caused by feline herpes virus or feline calcivirus

Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

```
ignment Scores:
ed. No.:              8.27e-213      Length:          689
ore:                  220.00         Matches:         220
cent Similarity:      100.0%         Conservative:    0
st Local Similarity:  100.0%         Mismatches:      0
ery Match:            99.1%          Indels:          0
:                     2              Gaps:            0

-10-821-670A-33 (1-222) x AAV56641 (1-689)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy      161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy      181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy      201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

RESULT 6
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133. .811
FT                   /*tag=  a
FT   sig_peptide     133. .217
FT                   /*tag=  b
FT   mat_peptide     218. .808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.69e-212      Length:          1441
Score:                  220.00         Matches:         220
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            99.1%          Indels:          0
DB:                     2              Gaps:            0
```

```
-10-821-670A-33 (1-222) x AAV56628 (1-1441)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

SULT 7
K98948
    ABK98948 standard; cDNA; 591 BP.

    ABK98948;

    21-OCT-2002  (first entry)

    Feline interleukin-12 nFeIL-12p35-591 coding strand.

    Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
    canine IL-12; autoimmune disease; allergic reaction; infectious disease;
    tumour development; inflammatory disease; graft rejection; gene; ss.

    Felis catus.

    US2002052030-A1.

    02-MAY-2002.

    27-JUL-2001; 2001US-00917265.

    04-AUG-2000; 2000US-0223016P.

    (WOND/) WONDERLING R S.
    (BORO/) BOROUGHS K L.

XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69305.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 56-57; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.38e-189      Length:          591
Score:                  197.00         Matches:         197
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            88.7%          Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-33 (1-222) x ABK98948 (1-591)

Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
```

```
       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

SULT 8
X98949/c
   ABK98949 standard; cDNA; 591 BP.

   ABK98949;

   21-OCT-2002  (first entry)

   Feline interleukin-12 nFeIL-12p35-591 complementary strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; ss.

   Felis catus.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Disclosure; Page 58; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a feline interleukin 12 DNA sequence, as described in
   the invention

   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              1.38e-189      Length:        591
ore:                  197.00         Matches:       197
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            88.7%          Indels:        0
:                     6              Gaps:          0

-10-821-670A-33 (1-222) x ABK98949 (1-591)

        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy      66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy      86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy     106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy     126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy     146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy     166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy     186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy     206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
ADV34688
ID   ADV34688 standard; cDNA; 591 BP.
XX
AC   ADV34688;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34689.
```

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Claim 23; SEQ ID NO 35; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline single chain mature IL-12p35 subunit protein encoding cDNA.

Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	1.38e-189	Length:	591
ore:	197.00	Matches:	197
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	88.7%	Indels:	0
:	14	Gaps:	0

-10-821-670A-33 (1-222) x ADV34688 (1-591)

```
        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

SULT 10
V34690/c
ADV34690 standard; DNA; 591 BP.

ADV34690;

XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 37; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p35 subunit
CC complementary DNA.
XX
SQ Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.38e-189	Length:	591
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	88.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-33 (1-222) x ADV34690 (1-591)

```
Qy        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292
```

```
       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
        51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

SULT 11
K98954/c
ABK98954 standard; cDNA; 1533 BP.

ABK98954;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12-1533 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 66-67; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.48e-189	Length:	1533
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	88.7%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x ABK98954 (1-1533)

```
Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 12
ABK98953
ID ABK98953 standard; cDNA; 1533 BP.
XX
AC ABK98953;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69307.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 63-64; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	3.48e-189	Length:	1533
ore:	197.00	Matches:	197
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	88.7%	Indels:	0
:	6	Gaps:	0

-10-821-670A-33 (1-222) x ABK98953 (1-1533)

```
Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

RESULT 13
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 45; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.48e-189	Length:	1533
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	88.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-33 (1-222) x ADV34697 (1-1533)

```
Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472
```

```
 66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

 86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

SULT 14
/34695
ADV34695 standard; cDNA; 1533 BP.

ADV34695;

24-FEB-2005 (first entry)

Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; gene; ss.

Felis catus.

Key	Location/Qualifiers
CDS	1. .1533
	/*tag= a
	/product= "PFeIL-12 511 protein"
	/partial
	/note= "No start and stop codon"

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.
P-PSDB; ADV34696.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

XX
PS Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.48e-189	Length:	1533
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	88.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-33 (1-222) x ADV34695 (1-1533)

```
Qy        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

RESULT 15
ABK98950
ID ABK98950 standard; cDNA; 1599 BP.
XX
AC ABK98950;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69306.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 6; Page 58-60; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 3.62e-189 Length: 1599
ore: 197.00 Matches: 197
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 88.7% Indels: 0
:: 6 Gaps: 0

:-10-821-670A-33 (1-222) x ABK98950 (1-1599)

```
Qy        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
```

RESULT 16
ABK98951/c
ID ABK98951 standard; cDNA; 1599 BP.
XX
AC ABK98951;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 61-62; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX

Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

:gnment Scores:
:d. No.: 3.62e-189 Length: 1599
:re: 197.00 Matches: 197
:cent Similarity: 100.0% Conservative: 0
:t Local Similarity: 100.0% Mismatches: 0
:ry Match: 88.7% Indels: 0
: 6 Gaps: 0

-10-821-670A-33 (1-222) x ABK98951 (1-1599)

```
 26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

 46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

 66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

 86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

SULT 17
734691
ADV34691 standard; cDNA; 1599 BP.

ADV34691;

24-FEB-2005 (first entry)

Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; gene; ss.

Felis catus.

Key	Location/Qualifiers
CDS	1. .1599
	/*tag= a
	/product= "PFeIL-12p533 protein"
	/partial
	/note= "No stop codon"

XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34692.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.62e-189 Length: 1599
Score: 197.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 88.7% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-33 (1-222) x ADV34691 (1-1599)

```
Qy   26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy   46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy   66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy   86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy  106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy  126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy  146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy  166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

SULT 18
V34693/c
   ADV34693 standard; DNA; 1599 BP.

   ADV34693;

   24-FEB-2005  (first entry)

   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; ds.

   Felis catus.

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Example 3; SEQ ID NO 40; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the feline single chain IL-12 complementary DNA.

   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

ignment Scores:
ed. No.:                3.62e-189       Length:         1599
ore:                    197.00          Matches:        197
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              88.7%           Indels:         0
:                       14              Gaps:           0

-10-821-670A-33 (1-222) x ADV34693 (1-1599)

        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy      66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy      86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy     106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy     126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy     146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy     166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy     186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy     206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 19
AAV56629
ID   AAV56629 standard; cDNA; 591 BP.
XX
AC   AAV56629;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA mature transcript.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76176.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 23; Page 59; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
```

cytotoxic T lymphocyte cells. Such proteins are used for treatment of feline autoimmune diseases e.g. as caused by feline herpes virus or feline calcivirus

Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.46e-187 Length: 591
ore: 195.00 Matches: 195
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 87.8% Indels: 0
: 2 Gaps: 0

10-821-670A-33 (1-222) x AAV56629 (1-591)

```
Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585
```

ULT 20
99001
ABK99001 standard; cDNA; 561 BP.

ABK99001;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12p35-N561 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

Felis catus.

US2002052030-A1.

XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69315.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 92-93; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.75e-179 Length: 561
Score: 187.00 Matches: 187
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 84.2% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-33 (1-222) x ABK99001 (1-561)

```
Qy         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

        216 MetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||
        541 ATGAGCTATCTGAATGCTTCC 561

SULT 21
K99002/c
   ABK99002 standard; cDNA; 561 BP.

   ABK99002;

   21-OCT-2002  (first entry)

   Feline interleukin-12nFeIL-12p35-N561 complementary strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; ss.

   Felis catus.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Disclosure; Page 94; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a feline interleukin 12 DNA sequence, as described in
   the invention

   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              1.75e-179      Length:        561
ore:                  187.00         Matches:       187
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            84.2%          Indels:        0

DB:                   6              Gaps:          0

US-10-821-670A-33 (1-222) x ABK99002 (1-561)

Qy          36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy          56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy          76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy          96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy         136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy         156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy         176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy         196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy         216 MetSerTyrLeuAsnAlaSer 222
               ||||||||||||||||||||
Db          21 ATGAGCTATCTGAATGCTTCC 1

RESULT 22
ADV34751
ID   ADV34751 standard; cDNA; 561 BP.
XX
AC   ADV34751;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal single chain IL-12p35 cDNA, nFeIL-12p35-N561.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .561
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35-N187 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
```

27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.
P-PSDB; ADV34752.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Claim 23; SEQ ID NO 101; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the feline N-terminal single chain IL-12p35 subunit protein encoding cDNA.

Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

:gnment Scores:
:d. No.: 1.75e-179 Length: 561
:re: 187.00 Matches: 187
:cent Similarity: 100.0% Conservative: 0
:t Local Similarity: 100.0% Mismatches: 0
:ry Match: 84.2% Indels: 0
: 14 Gaps: 0

-10-821-670A-33 (1-222) x ADV34751 (1-561)

```
Qy         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        216 MetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
```

RESULT 23
ADV34753/c
ID ADV34753 standard; cDNA; 561 BP.
XX
AC ADV34753;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal IL-12p35 complementary DNA, nFeIL-12p35-N561.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Disclosure; SEQ ID NO 103; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline N-terminal single chain IL-12p35 subunit
CC protein complementary DNA.
XX
SQ Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.75e-179 Length: 561
Score: 187.00 Matches: 187
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 84.2% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-33 (1-222) x ADV34753 (1-561)

```
Qy         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382
```

```
        96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

       116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

       136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

       156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

       176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

       196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

       216 MetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||
        21 ATGAGCTATCTGAATGCTTCC 1
```

SULT 24
AF26097
AAF26097 standard; DNA; 679 BP.

AAF26097;

24-APR-2001 (first entry)

Feline fil12p35a DNA.

Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection; immunostimulant; tumor; antiviral; antitumor; interferon-gamma; Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.

Felis sp.

WO200104155-A2.

18-JAN-2001.

08-JUL-2000; 2000WO-DE002263.

08-JUL-1999; 99CH-00001259.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.
(REGC) UNIV CALIFORNIA.

Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;

WPI; 2001-147178/15.

Recombinant feline interleukin-12, useful as immunostimulant and for treating e.g. viral infections in cats, and related nucleic acid constructs.

Disclosure; Fig 2; 35pp; German.

This invention describes a novel feline interleukin-12 (fIL-12) polypeptide (I) that is expressed, by recombinant gene expression in eukaryotic or prokaryotic cells, in the form of both polypeptide chains of subunits p35 and p40. These proteins are formed so that, in equimolar concentrations and in presence of an immunizing antigen, they can be administered to carnivores, particularly domestic cats. The invention also describes a nucleic acid construct (II) encoding fIL-12 containing sequences at least 95% identical with the p40- and p35-encoding sequences (A, 990 bp and B, 669 bp respectively), reproduced in the specification, as immunostimulants for immunization against infectious diseases and/or for treating infections or tumors in felines, especially domestic cats. The products of the invention have immunostimulatory, antiviral and antitumor activity. Nucleic acid constructs that encode (II) are useful as adjuvants for prophylactic immunization against viral diseases and for treating diseases associated with a Th1 defect. IL-12 induces synthesis of interferon gamma (Th1 response). The feline interleukin-12 polypeptide is useful for carnivores, and particularly domestic cats in the following: (i) as immunostimulant, for preventative or therapeutic use; and (ii) treating tumors and autoimmune diseases, or diseases associated with a Th1 defect, especially pre-existing infections by feline immune deficiency virus (FIV), feline leukemia virus and corona virus

XX
SQ Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	6.2e-60	Length:	679
Score:	69.00	Matches:	69
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	31.1%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-33 (1-222) x AAF26097 (1-679)

```
Qy        114 LeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAsp 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 399

Qy        134 LeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLys 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 459

Qy        154 ArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeu 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 519

Qy        174 AsnValAsnSerValThrValProGln 182
              |||||||||||||||||||||||||||
Db        520 AATGTCAACAGTGTGACTGTGCCACAG 546
```

RESULT 25
AAF26083
ID AAF26083 standard; DNA; 669 BP.
XX
AC AAF26083;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.

Vaccine for treating or preventing lentivirus infection in cats, contains nucleic acid sequence encoding viral protein under control of eukaryotic promoter.

Claim 14; Page 37; 37pp; German.

This invention describes a novel vaccine (A) for prevention or treatment of lentivirus infection in felines which comprises an immunizing nucleic acid sequence (I) that contains, or comprises, at least part of a gene encoding a protein (II) of the virus, under control of a eukaryotic promoter functional in the relevant animal. (II) is especially the envelope (env) protein. The invention also describes (1) vaccine (A) containing an immunizing protein, or fragment, from a lentivirus plus at least one of interleukin (IL)-12 and/or -16; and (2) preparation of a lentivirus protein, or fragment, especially derived from feline immune deficiency virus (FIV), by expressing the corresponding nucleic acid sequence in a host cell. The products of the invention have antiviral activity. The vaccine (A) and related protein-based vaccines, are particularly used to treat or prevent lentivirus infections in domestic cats, especially feline immune deficiency virus (FIV). Vaccination with (A) allows differentiation between vaccinated and infected animals, from the antibody status. The vaccines may be formulated with an adjuvant (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic immune response, particularly a Th1 response

Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 6.86e-56 Length: 669
ore: 65.00 Matches: 65
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 29.3% Indels: 0
: 4 Gaps: 0

-10-821-670A-33 (1-222) x AAF26083 (1-669)

```
          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

         61 ThrLeuGluPheTyr 65
            ||||||||||||||||
        181 ACTCTAGAATTTTAC 195
```

ULT 26
26086
AAF26086 standard; DNA; 669 BP.

AAF26086;

24-APR-2001 (first entry)

Feline IL-12p35 encoding DNA.

Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection; immunostimulant; tumor; antiviral; antitumor; interferon-gamma; Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.

Felis sp.

WO200104155-A2.

18-JAN-2001.

XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Claim 3; Page 31; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.86e-56 Length: 669
Score: 65.00 Matches: 65
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 29.3% Indels: 0
DB: 4 Gaps: 0

US-10-821-670A-33 (1-222) x AAF26086 (1-669)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyr 65
              ||||||||||||||||
Db        181 ACTCTAGAATTTTAC 195
```

RESULT 27
AAF26077
ID AAF26077 standard; DNA; 4201 BP.
XX

AAF26077;

24-APR-2001 (first entry)

Feline IL-12p35 encoding DNA SEQ ID 3.

Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection; interleukin; antiviral; cytotoxic immune response; Th1 response; ds.

Felis sp.

WO200104280-A2.

18-JAN-2001.

08-JUL-2000; 2000WO-DE002262.

08-JUL-1999; 99CH-00001258.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.

Leutenegger C, Schroff M, Wittig B, Lutz H;

WPI; 2001-147190/15.

Vaccine for treating or preventing lentivirus infection in cats, contains nucleic acid sequence encoding viral protein under control of eukaryotic promoter.

Disclosure; Page 31-33; 37pp; German.

This invention describes a novel vaccine (A) for prevention or treatment of lentivirus infection in felines which comprises an immunizing nucleic acid sequence (I) that contains, or comprises, at least part of a gene encoding a protein (II) of the virus, under control of a eukaryotic promoter functional in the relevant animal. (II) is especially the envelope (env) protein. The invention also describes (1) vaccine (A) containing an immunizing protein, or fragment, from a lentivirus plus at least one of interleukin (IL)-12 and/or -16; and (2) preparation of a lentivirus protein, or fragment, especially derived from feline immune deficiency virus (FIV), by expressing the corresponding nucleic acid sequence in a host cell. The products of the invention have antiviral activity. The vaccine (A) and related protein-based vaccines, are particularly used to treat or prevent lentivirus infections in domestic cats, especially feline immune deficiency virus (FIV). Vaccination with (A) allows differentiation between vaccinated and infected animals, from the antibody status. The vaccines may be formulated with an adjuvant (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic immune response, particularly a Th1 response

Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 4.08e-55 Length: 4201
ore: 65.00 Matches: 65
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 29.3% Indels: 0
: 4 Gaps: 0

-10-821-670A-33 (1-222) x AAF26077 (1-4201)

```
          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy         61 ThrLeuGluPheTyr 65
              ||||||||||||||
Db       3227 ACTCTAGAATTTTAC 3241
```

RESULT 28
AAD15219
ID AAD15219 standard; DNA; 660 BP.
XX
AC AAD15219;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-157.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a
FT		/product= "Modified p35 protein precursor"
FT	sig_peptide	1. .66
FT		/*tag= b
FT	mat_peptide	67. .657
FT		/*tag= c
FT		/product= "Mature modified p35 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08612.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 140; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 660 BP; 181 A; 178 C; 144 G; 157 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.04e-50 Length: 660
Score: 59.00 Matches: 59
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

```
ery Match:            26.6%          Indels:        0
:                     5              Gaps:          0

-10-821-670A-33 (1-222) x AAD15219 (1-660)

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 144
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 163
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        424 AATGCAAAGCTGTTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

ESULT 29
)15214
   AAD15214 standard; DNA; 660 BP.

   AAD15214;

   01-NOV-2001  (first entry)

   Modified human cytokine p35 encoding DNA from clone R2-631.

   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
   p35; mutant; ds.

   Homo sapiens.
   Synthetic.

   Key             Location/Qualifiers
   CDS             1. .660
                   /*tag=  a
                   /product= "Modified p35 protein precursor"
   sig_peptide     1. .66
                   /*tag=  b
   mat_peptide     67. .657
                   /*tag=  c
                   /product= "Mature modified p35 protein"

   WO200140257-A2.

   07-JUN-2001.

   30-NOV-2000; 2000WO-US032664.

   02-DEC-1999;   99US-0169035P.
   28-NOV-2000; 2000US-00725324.

   (MAXY-) MAXYGEN INC.

   Leong SR,  Punnonen J;

   WPI; 2001-502381/55.
   P-PSDB; AAE08607.

   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
   and p35 polypeptides), useful for treating various diseases e.g. diabetic
   retinopathy and cancer.

   Claim 87; Page 139; 223pp; English.

   The invention relates to nucleic acids encoding modified cytokine
   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
   gamma induction activities. The polypeptides and polynucleotides of the
   invention are useful for treating various diseases e.g. bacterial
   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
   CC   vaccinated host's cell-mediated immunity for protective response to a
   CC   pathogen. The present sequence is a modified human p35 protein encoding
   CC   DNA
   XX
   SQ   Sequence 660 BP; 182 A; 178 C; 142 G; 158 T; 0 U; 0 Other;

   Alignment Scores:
   Pred. No.:              8.04e-50       Length:        660
   Score:                  59.00          Matches:       59
   Percent Similarity:     100.0%         Conservative:  0
   Best Local Similarity:  100.0%         Mismatches:    0
   Query Match:            26.6%          Indels:        0
   DB:                     5              Gaps:          0

   US-10-821-670A-33 (1-222) x AAD15214 (1-660)

   Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 124
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACC 363

   Qy        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 144
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db        364 CTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

   Qy        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 163
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
   Db        424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480

   RESULT 30
   AAD15218
   ID   AAD15218 standard; DNA; 660 BP.
   XX
   AC   AAD15218;
   XX
   DT   01-NOV-2001  (first entry)
   XX
   DE   Modified human cytokine p35 encoding DNA from clone R2-162.
   XX
   KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
   KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
   KW   p35; mutant; ds.
   XX
   OS   Homo sapiens.
   OS   Synthetic.
   XX
   FH   Key             Location/Qualifiers
   FT   CDS             1. .660
   FT                   /*tag=  a
   FT                   /product= "Modified p35 protein precursor"
   FT   sig_peptide     1. .66
   FT                   /*tag=  b
   FT   mat_peptide     67. .657
   FT                   /*tag=  c
   FT                   /product= "Mature modified p35 protein"
   XX
   PN   WO200140257-A2.
   XX
   PD   07-JUN-2001.
   XX
   PF   30-NOV-2000; 2000WO-US032664.
   XX
   PR   02-DEC-1999;   99US-0169035P.
   PR   28-NOV-2000; 2000US-00725324.
   XX
   PA   (MAXY-) MAXYGEN INC.
   XX
   PI   Leong SR,  Punnonen J;
   XX
   DR   WPI; 2001-502381/55.
   DR   P-PSDB; AAE08611.
   XX
   PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
   PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
```

retinopathy and cancer.

Claim 87; Page 140; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is a modified human p35 protein encoding DNA

Sequence 660 BP; 182 A; 180 C; 144 G; 154 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	8.04e-50	Length:	660
ore:	59.00	Matches:	59
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	26.6%	Indels:	0
:	5	Gaps:	0

-10-821-670A-33 (1-222) x AAD15218 (1-660)

```
        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        304 ATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACAACC 363

        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 144
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        364 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATG 423

        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 163
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        424 AATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480
```

SULT 31
D15215
AAD15215 standard; DNA; 660 BP.

AAD15215;

01-NOV-2001 (first entry)

Modified human cytokine p35 encoding DNA from clone R2-613.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p35; mutant; ds.

Homo sapiens.
Synthetic.

Key	Location/Qualifiers
CDS	1. .660
	/*tag= a
	/product= "Modified p35 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .657
	/*tag= c
	/product= "Mature modified p35 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.

PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08608.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 139-140; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 660 BP; 190 A; 171 C; 137 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.76e-47	Length:	660
Score:	56.00	Matches:	56
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	25.2%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-33 (1-222) x AAD15215 (1-660)

```
Qy      108 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu 127
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      313 ATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTT 372

Qy      128 SerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLys 147
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      373 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 432

Qy      148 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 163
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db      433 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480
```

RESULT 32
AAF26098
ID AAF26098 standard; DNA; 639 BP.
XX
AC AAF26098;
XX
DT 24-APR-2001 (first entry)
XX
DE Plasmid pMOL-fIL12 p35 DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.

(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(UYZU-) UNIV ZUERICH.
(REGC) UNIV CALIFORNIA.

Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;

WPI; 2001-147178/15.

Recombinant feline interleukin-12, useful as immunostimulant and for treating e.g. viral infections in cats, and related nucleic acid constructs.

Disclosure; Fig 2; 35pp; German.

This invention describes a novel feline interleukin-12 (fIL-12) polypeptide (I) that is expressed, by recombinant gene expression in eukaryotic or prokaryotic cells, in the form of both polypeptide chains of subunits p35 and p40. These proteins are formed so that, in equimolar concentrations and in presence of an immunizing antigen, they can be administered to carnivores, particularly domestic cats. The invention also describes a nucleic acid construct (II) encoding fIL-12 containing sequences at least 95% identical with the p40- and p35-encoding sequences (A, 990 bp and B, 669 bp respectively), reproduced in the specification, as immunostimulants for immunization against infectious diseases and/or for treating infections or tumors in felines, especially domestic cats. The products of the invention have immunostimulatory, antiviral and antitumor activity. Nucleic acid constructs that encode (II) are useful as adjuvants for prophylactic immunization against viral diseases and for treating diseases associated with a Th1 defect. IL-12 induces synthesis of interferon gamma (Th1 response). The feline interleukin-12 polypeptide is useful for carnivores, and particularly domestic cats in the following: (i) as immunostimulant, for preventative or therapeutic use; and (ii) treating tumors and autoimmune diseases, or diseases associated with a Th1 defect, especially pre-existing infections by feline immune deficiency virus (FIV), feline leukemia virus and corona virus

Sequence 639 BP; 189 A; 166 C; 133 G; 151 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 8.99e-45 Length: 639
ore: 54.00 Matches: 54
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 24.3% Indels: 0
: 4 Gaps: 0

-10-821-670A-33 (1-222) x AAF26098 (1-639)

```
        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        293 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 352

        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        353 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 412

        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 169
            |||||||||||||||||||||||||||||||||||||||||||
        413 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 454
```

SULT 33
X18179
AAX18179 standard; cDNA; 591 BP.

AAX18179;

07-MAY-1999 (first entry)

Canine mature CLAF p35 subunit coding sequence.

CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog; viral disease; canine distemper; canine parvovirus; autoimmune disease;

KW canine infectious hepatitis; ds.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP002295.
XX
PR 03-JUN-1997; 97JP-00161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Tokiyoshi S, Eda Y;
XX
DR WPI; 1999-070260/06.
DR P-PSDB; AAW74325.
XX
PT Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS Claim 8; Page 34-35; 51pp; Japanese.
XX
CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs
XX
SQ Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.83e-43 Length: 591
Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 23.4% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-33 (1-222) x AAX18179 (1-591)

```
Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               ||||||||||||||||||||||||||||||||||||
Db         238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273
```

RESULT 34
ABK98958/c
ID ABK98958 standard; cDNA; 591 BP.
XX
AC ABK98958;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p35-591 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Disclosure; Page 70; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 8.83e-43 Length: 591
ore: 52.00 Matches: 52
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 23.4% Indels: 0
: 6 Gaps: 0

-10-821-670A-33 (1-222) x ABK98958 (1-591)

```
 65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

 85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
    |||||||||||||||||||||||||||||||||||
354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319
```

SULT 35
K98957
ABK98957 standard; cDNA; 591 BP.

ABK98957;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12p35-591 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69309.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 69; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.83e-43 Length: 591
Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 23.4% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-33 (1-222) x ABK98957 (1-591)

```
Qy   65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy   85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy  105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
        |||||||||||||||||||||||||||||||||||
Db  238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273
```

RESULT 36
ADV34701
ID ADV34701 standard; cDNA; 591 BP.
XX
AC ADV34701;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 591.
XX

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine; infectious disease; antimicrobial; gene; ss.

Canis familiaris.

Key Location/Qualifiers
CDS 1. .591
/*tag= a
/product= "PCaIL-12P35 197 protein"
/partial
/note= "No start and stop codon"

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.
P-PSDB; ADV34702.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 4; SEQ ID NO 49; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the canine single chain IL-12p35 subunit protein encoding cDNA.

Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 8.83e-43 Length: 591
ore: 52.00 Matches: 52
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 23.4% Indels: 0
: 14 Gaps: 0

-10-821-670A-33 (1-222) x ADV34701 (1-591)

```
Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||||||||||||||||||||||
Db        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273
```

SULT 37
/34703/c
ADV34703 standard; DNA; 591 BP.

ADV34703;

XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 51; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p35 subunit
CC complementary DNA.
XX
SQ Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.83e-43 Length: 591
Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 23.4% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-33 (1-222) x ADV34703 (1-591)

```
Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319
```

RESULT 38
ABK98955
ID ABK98955 standard; cDNA; 666 BP.
XX
AC ABK98955;
XX
DT 21-OCT-2002 (first entry)
XX

Canine interleukin-12 nCaIL-12p35-666 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69308.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 1; Page 67-68; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a canine interleukin 12 DNA sequence, as described in the invention

Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

```
ignment Scores:
ed. No.:              9.92e-43       Length:         666
ore:                  52.00          Matches:        52
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            23.4%          Indels:         0
:                     6              Gaps:           0

-10-821-670A-33 (1-222) x ABK98955 (1-666)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 39
K98956/c
   ABK98956 standard; cDNA; 666 BP.

   ABK98956;
```

```
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-66 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 68-69; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.92e-43       Length:         666
Score:                  52.00          Matches:        52
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            23.4%          Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-33 (1-222) x ABK98956 (1-666)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 40
ADV34700/c
ID   ADV34700 standard; DNA; 666 BP.
```

```
ADV34700;

24-FEB-2005  (first entry)

Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 666.

DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
infectious disease; antimicrobial; ds.

Canis familiaris.

US2004248261-A1.

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS,  Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or
p40 subunit protein and a nucleic acid linker, useful in preparing a
vaccine against infectious diseases in feline animals.

Example 4; SEQ ID NO 48; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40
subunit protein and their encoding nucleic acid molecules and a nucleic
acid linker. The invention also provides the feline caspase (casp)-1,
feline IL-18 single chain and canine IL-12 single chain proteins and
their nucleic acid molecules. The nucleic acid molecule is useful in
preparing a vaccine against infectious diseases in feline animals. The
present sequence is the canine single chain IL-12p35 subunit full-length
complementary DNA.

Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

ignment Scores:
ed. No.:               9.92e-43       Length:        666
ore:                   52.00          Matches:       52
cent Similarity:       100.0%         Conservative:  0
st Local Similarity:   100.0%         Mismatches:    0
ery Match:             23.4%          Indels:        0
:                      14             Gaps:          0

-10-821-670A-33 (1-222) x ADV34700 (1-666)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 41
/34698
   ADV34698 standard; cDNA; 666 BP.

   ADV34698;

DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 full-length cDNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PCaIL-12p222 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34699.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 46; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             9.92e-43       Length:        666
Score:                 52.00          Matches:       52
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           23.4%          Indels:        0
DB:                    14             Gaps:          0

US-10-821-670A-33 (1-222) x ADV34698 (1-666)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 42
```

V13818
AAV13818 standard; cDNA to mRNA; 669 BP.

AAV13818;

14-MAY-1998 (first entry)

Canine IL-12 P35 subunit cDNA.

Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour; antiviral; vaccine adjuvant; ds.

Canis sp.

Key	Location/Qualifiers
CDS	1. .669
	/*tag= a
	/product= "interleukin-12_P35_subunit"

JP10036397-A.

10-FEB-1998.

08-NOV-1996; 96JP-00296789.

08-NOV-1995; 95JP-00289729.
23-MAY-1996; 96JP-00128104.

(TORA) TORAY IND INC.

WPI; 1998-174914/16.
P-PSDB; AAW41792.

Canine interleukin 12 - comprises P40 and P35 subunits; useful in veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant activities are expected.

Claim 9; Page 9; 12pp; Japanese.

The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit. A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an antiviral activating factor and the expression of class II MHC molecules in canine tumour cells, stimulating proliferation of canine blastogenic lymphocytes and activating canine leukocytes to inhibit canine tumour cells. The canine IL-12 can be used in veterinary medicines, e.g. antitumour, antivirus and vaccine adjuvant activities are expected

Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	9.96e-43	Length:	669
ore:	52.00	Matches:	52
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	23.4%	Indels:	0
:	2	Gaps:	0

-10-821-670A-33 (1-222) x AAV13818 (1-669)

```
         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

SULT 43
V13819

ID AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC AAV13819;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P35 subunit cDNA.
XX
KW Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .669
FT /*tag= a
FT /product= "interleukin-12_P35_subunit"
XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-00296789.
XX
PR 08-NOV-1995; 95JP-00289729.
PR 23-MAY-1996; 96JP-00128104.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.
DR P-PSDB; AAW41793.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT activities are expected.
XX
PS Claim 11; Page 11-12; 12pp; Japanese.
XX
CC The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC antiviral activating factor and the expression of class II MHC molecules
CC in canine tumour cells, stimulating proliferation of canine blastogenic
CC lymphocytes and activating canine leukocytes to inhibit canine tumour
CC cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.96e-43	Length:	669
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.4%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-33 (1-222) x AAV13819 (1-669)

```
Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

RESULT 44
AAX03163
ID AAX03163 standard; cDNA to mRNA; 669 BP.

AAX03163;

30-MAR-1999 (first entry)

Nucleic acid encoding canine interleukin 12.

Canine; interleukin 12; IL-12; feline; immunological disease; tumour; skin disease; viral infection; allergic disease; breast tumour; oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma; othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour; otitis externa; dermatitis; eczema; fungal skin disease; pyoderma; allergic dermatitis; nettle rash; traumatic dermatitis; hair loss; dog Parvovirus infection; distemper virus; cat plaque virus infection; feline leukaemia; allergy; pollinosis; ds.

Canis sp.

Key	Location/Qualifiers
CDS	1. .669
	/*tag= a
	/product= "interleukin_12"

WO9851327-A1.

19-NOV-1998.

07-MAY-1998; 98WO-JP002031.

16-MAY-1997; 97JP-00127690.

(TORA) TORAY IND INC.

Okano F, Satoh M, Yamada K;

WPI; 1999-070100/06.
P-PSDB; AAW84374.

New therapeutic and prophylactic agents - comprise genetically-engineered canine interleukin 12, used to treat, e.g. canine and feline immunological diseases.

Claim 1; Page 33-34; 45pp; Japanese.

The present sequence encodes a canine interleukin 12 (IL-12) protein. The IL-12 protein can be used in therapeutic or prophylactic agents. The agents can be used to prevent and treat canine and feline immunological diseases including dog and cat tumours, skin diseases, viral infections and allergic diseases, especially tumours, breast tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma, othematoma, pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin diseases, otitis externa, dermatitis, eczema, fungal diseases of the skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis and hair loss; infections; dog Parvovirus infection and distemper virus, cat plaque virus infection and feline leukaemia, and allergic diseases, e.g. pollinosis

Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

ignment Scores:			
ed. No.:	9.96e-43	Length:	669
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	23.4%	Indels:	0
:	2	Gaps:	0

10-821-670A-33 (1-222) x AAX03163 (1-669)

```
Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

RESULT 45
AAX03153
ID AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC AAX03153;
XX
DT 30-MAR-1999 (first entry)
XX
DE Nucleic acid encoding canine interleukin 12.
XX
KW Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;
KW oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW feline leukaemia; allergy; pollinosis; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .669
FT /*tag= a
FT /product= "interleukin_12"
XX
PN WO9851327-A1.
XX
PD 19-NOV-1998.
XX
PF 07-MAY-1998; 98WO-JP002031.
XX
PR 16-MAY-1997; 97JP-00127690.
XX
PA (TORA) TORAY IND INC.
XX
PI Okano F, Satoh M, Yamada K;
XX
DR WPI; 1999-070100/06.
DR P-PSDB; AAW84372.
XX
PT New therapeutic and prophylactic agents - comprise genetically-engineered
PT canine interleukin 12, used to treat, e.g. canine and feline
PT immunological diseases.
XX
PS Claim 1; Page 26-27; 45pp; Japanese.
XX
CC The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC IL-12 protein can be used in therapeutic or prophylactic agents. The
CC agents can be used to prevent and treat canine and feline immunological
CC diseases including dog and cat tumours, skin diseases, viral infections
CC and allergic diseases, especially tumours, breast tumour, oesinophilic
CC granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC and hair loss; infections; dog Parvovirus infection and distemper virus,
CC cat plaque virus infection and feline leukaemia, and allergic diseases,
CC e.g. pollinosis
XX
SQ Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	9.96e-43	Length:	669
Score:	52.00	Matches:	52

```
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            23.4%           Indels:        0
:                     2               Gaps:          0

-10-821-670A-33 (1-222) x AAX03153 (1-669)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 46
X35616
   AAX35616 standard; cDNA to mRNA; 669 BP.

   AAX35616;

   09-JUL-1999  (first entry)

   Nucleic acid encoding canine Interleukin-12 (IL-12).

   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
   tumour; skin disease; infectious disease; allergic disease; ds.

   Canis sp.

   Key             Location/Qualifiers
   CDS             1. .669
                   /*tag=  a

   JP11106350-A.

   20-APR-1999.

   15-MAY-1998;   98JP-00133345.

   16-MAY-1997;   97JP-00127690.
   07-AUG-1997;   97JP-00213755.

   (TORA ) TORAY IND INC.

   WPI; 1999-308068/26.
   P-PSDB; AAY02340.

   A prevention and treating agent containing interleukin 12 (CaIL12) - for
   prevention and treatment of dog and cat immune diseases.

   Claim 1; Page 13; 16pp; Japanese.

   The present sequence encodes canine interleukin-12 (IL-12). The
   specification describes a method for the prevention and treatment of dog
   and cat immune diseases. The treatment used an agent comprising dog IL-12
   (CaIL12) proteins to form a heterodimer. The agent is useful for
   preventing and treating dog and cat immune diseases, including tumours,
   skin diseases, infectious diseases and allergic diseases

   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              9.96e-43        Length:        669
ore:                  52.00           Matches:       52
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            23.4%           Indels:        0
:                     2               Gaps:          0

US-10-821-670A-33 (1-222) x AAX35616 (1-669)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 47
AAX35626
ID   AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35626;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02343.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:            9.96e-43        Length:        669
Score:                52.00           Matches:       52
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          23.4%           Indels:        0
DB:                   2               Gaps:          0

US-10-821-670A-33 (1-222) x AAX35626 (1-669)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAAACCAGCACA 252

       85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

      105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
          |||||||||||||||||||||||||||||||||||||
      313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 48
64389
   AAI64389 standard; DNA; 669 BP.

   AAI64389;

   23-NOV-2001  (first entry)

   Canine coding sequence #4.

   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.

   Canis familiaris.

   Key             Location/Qualifiers
   CDS             1. .669
                   /*tag=  a
                   /product= "Canine protein #4"
   sig_peptide     1. .75
                   /*tag=  b
   mat_peptide     76. .666
                   /*tag=  c

   JP2001161378-A.

   19-JUN-2001.

   26-SEP-2000; 2000JP-00292946.

   01-OCT-1999;   99JP-00281234.

   (TORA ) TORAY IND INC.

   WPI; 2001-592466/67.
   P-PSDB; AAG66483.

   Preparation of a highly pure protein, interleukin 12, a protein
   inhibiting the activity of interleukin 12, and a treating agent and a
   treating method for immunopathy of mammalian.

   Claim 6; Page 18; 21pp; Japanese.

   The present invention relates to a method for the preparation of a highly
   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
   the activity of IL12 is contacted to an ion exchanging carrier and/or a
   pigment carrier to get IL12 and/or a protein inhibiting the activity of
   IL12. The protein is used as a preventive agent for dog immunopathy. The
   present sequence was used in the method of the present invention

   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              9.96e-43      Length:         669
ore:                  52.00         Matches:        52
cent Similarity:      100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            23.4%         Indels:         0
:                     4             Gaps:           0

-10-821-670A-33 (1-222) x AAI64389 (1-669)

          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAAACCAGCACA 252

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
          |||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 49
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1. .75
FT                   /*tag=  b
FT   mat_peptide     76. .666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.96e-43      Length:         669
Score:                  52.00         Matches:        52
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.4%         Indels:         0
DB:                     4             Gaps:           0

US-10-821-670A-33 (1-222) x AAI64379 (1-669)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

       85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

      105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
          ||||||||||||||||||||||||||||||||||||
      313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 50
Z25701
   ADZ25701 standard; cDNA; 669 BP.

   ADZ25701;

   16-JUN-2005  (first entry)

   Canine interleukin 12 P35 encoding cDNA SEQ ID NO:6.

   interleukin-12; antiviral; gene; ss.

   Canis sp.

   Key             Location/Qualifiers
   CDS             1. .669
                   /*tag=  b
                   /product= "interleukin-12 P40"
   sig_peptide     1. .75
                   /*tag=  a
   mat_peptide     76. .666
                   /*tag=  c
                   /product= "interleukin-12 P40"

   JP2003284585-A.

   07-OCT-2003.

   28-MAR-2002; 2002JP-00090161.

   28-MAR-2002; 2002JP-00090161.

   (TORA ) TORAY IND INC.

   WPI; 2003-885430/82.
   P-PSDB; ADZ25703.

   Large scale production of interleukin-12 for pharmaceutical applications,
   comprises infecting an insect cell with a recombinant virus containing
   gene encoding IL-12, and producing IL-12 by carrying out spinner culture
   of insect cell.

   Example; SEQ ID NO 6; 8pp; Japanese.

   The invention related to the large scale production of interleukin-12 (IL
   -12), which involves infecting an insect cell with a recombinant virus
   containing a gene encoding IL-12, and producing IL-12 by carrying out
   spinner culture of insect cell. The method is useful for producing IL-12,
   preferably canine IL-12. IL-12 has pharmaceutical applications. The
   present sequence encodes canine IL-12 P35, which is used in the
   exemplification of the present invention.

   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              9.96e-43        Length:         669
ore:                  52.00           Matches:        52
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            23.4%           Indels:         0
:                     11              Gaps:           0
```

US-10-821-670A-33 (1-222) x ADZ25701 (1-669)

```
Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

```
RESULT 51
AAX18178
ID   AAX18178 standard; cDNA; 1282 BP.
XX
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.87e-42        Length:         1282
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AAX18178 (1-1282)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       258 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 317

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       318 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 377

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||||
       378 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 413

RESULT 52
ABK99003
   ABK99003 standard; cDNA; 1455 BP.

   ABK99003;

   21-OCT-2002  (first entry)

   Canine interleukin-12 nCaIL-12p35-1455 coding strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; gene; ss.

   Canis familiaris.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.
   P-PSDB; ABG69316.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Example 4; Page 94-95; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a canine interleukin 12 DNA sequence, as described in
   the invention

   Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.12e-42        Length:          1455
Score:                    52.00           Matches:         52
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              23.4%           Indels:          0
                          6               Gaps:            0
```

```
US-10-821-670A-33 (1-222) x ABK99003 (1-1455)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||||
Db         544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

RESULT 53
ABK99004/c
ID   ABK99004 standard; cDNA; 1455 BP.
XX
AC   ABK99004;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-1455 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 96; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.12e-42        Length:          1455
Score:                    52.00           Matches:         52
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              23.4%           Indels:          0
```

```
:                    6              Gaps:          0

-10-821-670A-33 (1-222) x ABK99004 (1-1455)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

SULT 54
V34756/c
   ADV34756 standard; DNA; 1455 BP.

   ADV34756;

   24-FEB-2005  (first entry)

   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 1455.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; ds.

   Canis familiaris.

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Example 4; SEQ ID NO 106; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the canine single chain IL-12p35 subunit
   complementary DNA.

   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              2.12e-42       Length:        1455
ore:                  52.00          Matches:       52
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            23.4%          Indels:        0
:                     14             Gaps:          0

-10-821-670A-33 (1-222) x ADV34756 (1-1455)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

RESULT 55
ADV34754
ID   ADV34754 standard; cDNA; 1455 BP.
XX
AC   ADV34754;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 1455.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             232. .900
FT                   /*tag=  a
FT                   /product= "PCaIL-12p35 222 protein"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34755.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 104; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.12e-42       Length:        1455
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            23.4%          Indels:        0
```

```
:                    14            Gaps:          0

-10-821-670A-33 (1-222) x ADV34754 (1-1455)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

SULT 56
<98967
   ABK98967 standard; cDNA; 1533 BP.

   ABK98967;

   21-OCT-2002  (first entry)

   Canine interleukin-12 nCaIL-12-1533 coding strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; gene; ss.

   Canis familiaris.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.
   P-PSDB; ABG69314.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Claim 6; Page 83-85; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a canine interleukin 12 DNA sequence, as described in
   the invention

   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

ignment Scores:
ed. No.:          2.23e-42       Length:        1533
ore:              52.00          Matches:       52
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.4%         Indels:        0
DB:                     6             Gaps:          0

US-10-821-670A-33 (1-222) x ABK98967 (1-1533)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db        1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 57
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 86-87; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:
```

```
ed. No.:              2.23e-42        Length:         1533
ore:                  52.00           Matches:        52
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            23.4%           Indels:         0
:                     6               Gaps:           0

-10-821-670A-33 (1-222) x ABK98968 (1-1533)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 58
V34718/c
   ADV34718 standard; DNA; 1533 BP.

   ADV34718;

   24-FEB-2005  (first entry)

   Canine single chain IL-12 complementary DNA, nCaIL-12 1533.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; ds.

   Canis familiaris.

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Example 4; SEQ ID NO 68; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the canine single chain IL-12 complementary DNA.

   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              2.23e-42        Length:         1533
ore:                  52.00           Matches:        52
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
Query Match:          23.4%           Indels:         0
DB:                   14              Gaps:           0

US-10-821-670A-33 (1-222) x ADV34718 (1-1533)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 59
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:
```

```
ed. No.:              2.23e-42        Length:         1533
ore:                  52.00           Matches:        52
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            23.4%           Indels:         0
:                     14              Gaps:           0

-10-821-670A-33 (1-222) x ADV34716 (1-1533)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

ULT 60
98965
   ABK98965 standard; cDNA; 1599 BP.

   ABK98965;

   21-OCT-2002  (first entry)

   Canine interleukin-12 nCaIL-12-1599 coding strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; gene; ss.

   Canis familiaris.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.
   P-PSDB; ABG69313.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Claim 6; Page 79-80; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a canine interleukin 12 DNA sequence, as described in
   the invention

SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.32e-42        Length:         1599
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-33 (1-222) x ABK98965 (1-1599)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db       1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 61
ABK98966/c
ID   ABK98966 standard; cDNA; 1599 BP.
XX
AC   ABK98966;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 82-83; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
```

the invention

Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

```
ignment Scores:
ed. No.:                2.32e-42        Length:         1599
ore:                    52.00           Matches:        52
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              23.4%           Indels:         0
:                       6               Gaps:           0

-10-821-670A-33 (1-222) x ABK98966 (1-1599)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 62
V34715/c
   ADV34715 standard; DNA; 1599 BP.

   ADV34715;

   24-FEB-2005  (first entry)

   Canine single chain IL-12 complementary DNA, nCaIL-12 1599.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; ds.

   Canis familiaris.

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Example 4; SEQ ID NO 63; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the canine single chain IL-12 complementary DNA.

   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              2.32e-42        Length:         1599
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-33 (1-222) x ADV34715 (1-1599)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 63
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
```

present sequence is the canine single chain IL-12 protein encoding cDNA.

Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 2.32e-42 Length: 1599
ore: 52.00 Matches: 52
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 23.4% Indels: 0
: 14 Gaps: 0

-10-821-670A-33 (1-222) x ADV34713 (1-1599)

```
        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           ||||||||||||||||||||||||||||||||||||
      1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281
```

SULT 64
T04852
ADT04852 standard; DNA; 669 BP.

ADT04852;

13-JAN-2005 (first entry)

Canine interleukin-12 (IL-12) p35 DNA.

gene expression; insect; ds; interleukin-12; IL-12.

Canis familiaris.

JP2004290182-A.

21-OCT-2004.

06-FEB-2004; 2004JP-00030183.

10-MAR-2003; 2003JP-00062907.

(TORA) TORAY IND INC.

WPI; 2004-740760/73.

Novel gene vector for expression in insect useful for expression of foreign gene such as dog interleukin 12 gene, comprises two promoters.

Claim 4; SEQ ID NO 8; 13pp; Japanese.

The invention relates to a novel gene vector for expression in an insect comprising at least two promoters, particularly the polyhedrin promoter and p10 promoter. The vector contains at least two types of foreign protein expression gene and the gene product of the vector is produced using a gene recombinant baculovirus, particularly a recombinant silkworm nuclear polyhedrosis virus. The baculovirus is proliferated in a silkworm. The vector of the invention may be useful for expression of a foreign gene, such as canine interleukin 12. Within the vector, two types of foreign protein expression genes are integrated simultaneously for their simultaneous expression. The current sequence is that of the canine interleukin-12 (IL-12) p35 DNA of the invention.

Sequence 669 BP; 183 A; 177 C; 145 G; 164 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.05e-40 Length: 669
Score: 50.00 Matches: 50
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 22.5% Indels: 0
DB: 13 Gaps: 0

US-10-821-670A-33 (1-222) x ADT04852 (1-669)

```
Qy          67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         199 TGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAG 258

Qy          87 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 106
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         259 GCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCT 318

Qy         107 LeuIleThrAsnGlySerCysLeuAlaSer 116
               ||||||||||||||||||||||||||||||
Db         319 TTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

RESULT 65
AAD15212
ID AAD15212 standard; DNA; 666 BP.
XX
AC AAD15212;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-146.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .666
FT /*tag= a
FT /product= "Modified p35 protein precursor"
FT sig_peptide 1. .75
FT /*tag= b
FT mat_peptide 76. .663
FT /*tag= c
FT /product= "Mature modified p35 protein"
XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08605.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 139; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the

invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is a modified human p35 protein encoding DNA

Sequence 666 BP; 186 A; 179 C; 141 G; 160 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.28e-33 Length: 666
ore: 43.00 Matches: 43
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 19.4% Indels: 0
: 5 Gaps: 0

-10-821-670A-33 (1-222) x AAD15212 (1-666)

```
         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAG 402

        136 MetTyrGln 138
            |||||||||
        403 ATGTACCAG 411
```

SULT 66
T50757
AAT50757 standard; cDNA; 554 BP.

AAT50757;

17-OCT-2003 (revised)
24-SEP-1997 (first entry)

Partial sequence of ovine IL-12 35 kD sununit cDNA.

Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12; livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer; immunosuppression; allergy; reproductive system; growth; early maturity; antibody; diagnosis; immunopotentiator; early haematopoietic progenitor cell; cytotoxic cell; thymocyte; secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.

Ovis aries.

WO9700321-A1.

03-JAN-1997.

14-JUN-1996; 96WO-AU000360.

14-JUN-1995; 95AU-00003502.
27-OCT-1995; 95AU-00006244.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Seow H, Wood P;

WPI; 1997-077528/07.
P-PSDB; AAW08481.

Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine adjuvants and to treat or prevent microbial infections in livestock.

Claim 8; Page 43-44; 78pp; English.

The sequences given in AAT50757-59 encode ovine interleukin-12 (IL-12) 35

CC kD subunit (partial and full length sequence) and the 40 kD subunit.
CC Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC livestock (esp. cows and sheep), particularly where the animals are
CC stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC subunit or synthetic peptide vaccines). They may also be used to treat
CC cancer, immunosuppression and allergy, to enhance/suppress the
CC reproductive system and to promote growth or early maturity. Optionally
CC interleukin can be delivered from constructs or delivery cells and
CC antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC infection. The interleukins are immunopotentiators, especially IL-5
CC promotes growth of early haematopoietic progenitor cells and generation
CC of cytotoxic cells from thymocytes, also it stimulates production and
CC secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC induces production of gamma-interferon by, and proliferation of, T and NK
CC cells and increases the (non-)specific cytolytic lymphocyte response. The
CC genetic constructs can also be used for in vitro production of IL-5 or -
CC 12. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 554 BP; 159 A; 144 C; 124 G; 127 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.1e-32 Length: 554
Score: 42.00 Matches: 42
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 18.9% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-33 (1-222) x AAT50757 (1-554)

```
Qy          52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          96 AGCAACACGCTGCAGAAGGCCAGACAAACCCTAGAATTTTACTCCTGCACTTCTGAGGAG 155

Qy          72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         156 ATTGATCATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTG 215

Qy          92 GluLeu 93
               ||||||
Db         216 GAATTA 221
```

RESULT 67
AAA70708
ID AAA70708 standard; DNA; 703 BP.
XX
AC AAA70708;
XX
DT 15-DEC-2000 (first entry)
XX
DE Bovine interleukin-12 p35 subunit gene.
XX
KW Antiinfective; bovine; interleukin 12; IL12; heterodimer; infection; ss.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT CDS 12. .677
FT /*tag= a
FT /product= "IL-12 p35 subunit"
XX
PN JP2000157274-A.
XX
PD 13-JUN-2000.
XX
PF 20-NOV-1998; 98JP-00331052.
XX
PR 20-NOV-1998; 98JP-00331052.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
XX
DR WPI; 2000-468201/41.

P-PSDB; AAB15391.

Preparation of bovine interleukin 12 comprising using a vector containing the gene encoding it, useful for the prevention and treatment of chronic and opportunistic infections.

Example 1; Page 8-9; 11pp; Japanese.

The invention relates to a method for the preparation of bovine interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35 and p40 subunits. BoIL12 is produced by introducing into a host cell, recombinant vectors containing genes encoding the p35 and p40 subunits. This sequence represents the coding region for the bovine IL12 p35 subunit. Interleukin 12 is used for the prevention and treatment of chronic infections and opportunistic infections

Sequence 703 BP; 188 A; 194 C; 157 G; 164 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.47e-30 Length: 703
ore: 40.00 Matches: 40
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 18.0% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x AAA70708 (1-703)

```
        54 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 73
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       168 ACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAGATCGAT 227

        74 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       228 CATGAAGATATCACCAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 287
```

SULT 68
015213
AAD15213 standard; DNA; 660 BP.

AAD15213;

01-NOV-2001 (first entry)

Modified human cytokine p35 encoding DNA from clone R2-796.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p35; mutant; ds.

Homo sapiens.
Synthetic.

Key	Location/Qualifiers
CDS	1. .660
	/*tag= a
	/product= "Modified p35 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .657
	/*tag= c
	/product= "Mature modified p35 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08606.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 139; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.43e-29 Length: 660
Score: 39.00 Matches: 39
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 17.6% Indels: 0
DB: 5 Gaps: 0

US-10-821-670A-33 (1-222) x AAD15213 (1-660)

```
Qy          55 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy          75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270
```

RESULT 69
AAD15216
ID AAD15216 standard; DNA; 660 BP.
XX
AC AAD15216;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-571.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a
FT		/product= "Modified p35 protein precursor"
FT	sig_peptide	1. .66
FT		/*tag= b
FT	mat_peptide	67. .657
FT		/*tag= c
FT		/product= "Mature modified p35 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR, Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08609.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides), useful for treating various diseases e.g. diabetic retinopathy and cancer.

Claim 87; Page 140; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is a modified human p35 protein encoding DNA

Sequence 660 BP; 184 A; 172 C; 141 G; 163 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.43e-29 Length: 660
ore: 39.00 Matches: 39
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 17.6% Indels: 0
: 5 Gaps: 0

-10-821-670A-33 (1-222) x AAD15216 (1-660)

```
 55 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 74
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

 75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTA 270
```

SULT 70
D15220
AAD15220 standard; DNA; 660 BP.

AAD15220;

01-NOV-2001 (first entry)

Modified human cytokine p35 encoding DNA from clone R1-4-87.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p35; mutant; ds.

Homo sapiens.
Synthetic.

Key	Location/Qualifiers
CDS	1. .660
	/*tag= a
	/product= "Modified p35 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .657
	/*tag= c
	/product= "Mature modified p35 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08613.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 140-141; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.43e-29 Length: 660
Score: 39.00 Matches: 39
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 17.6% Indels: 0
DB: 5 Gaps: 0

US-10-821-670A-33 (1-222) x AAD15220 (1-660)

```
Qy         55 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHis 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CTGCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCAT 213

Qy         75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu 93
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 270
```

RESULT 71
AAD15217
ID AAD15217 standard; DNA; 660 BP.
XX
AC AAD15217;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-555.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.

```
Key             Location/Qualifiers
CDS             1. .660
                /*tag=  a
                /product= "Modified p35 protein precursor"
sig_peptide     1. .66
                /*tag=  b
mat_peptide     67. .657
                /*tag=  c
                /product= "Mature modified p35 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999;  99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR,  Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08610.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
and p35 polypeptides), useful for treating various diseases e.g. diabetic
retinopathy and cancer.

Claim 87; Page 140; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine
polypeptides (i.e. modified p40 and p35 polypeptides). The modified
cytokine polypeptides have T-cell proliferative and interferon (IFN)-
gamma induction activities. The polypeptides and polynucleotides of the
invention are useful for treating various diseases e.g. bacterial
infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
polynucleotide may also be useful as a vaccine adjuvant, to enhance a
vaccinated host's cell-mediated immunity for protective response to a
pathogen. The present sequence is a modified human p35 protein encoding
DNA

Sequence 660 BP; 189 A; 173 C; 136 G; 162 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              1.51e-27      Length:         660
ore:                  37.00         Matches:        37
cent Similarity:      100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            16.7%         Indels:         0
:                     5             Gaps:           0

-10-821-670A-33 (1-222) x AAD15217 (1-660)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

       204 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||
       601 GCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

ULT 72
015211
   AAD15211 standard; DNA; 666 BP.

   AAD15211;

   01-NOV-2001  (first entry)

   Modified human cytokine p35 encoding DNA from clone R2-42.

XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .75
FT                   /*tag=  b
FT   mat_peptide     76. .663
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08604.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 666 BP; 186 A; 181 C; 141 G; 158 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.81e-21      Length:         666
Score:                  31.00         Matches:        31
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            14.0%         Indels:         0
DB:                     5             Gaps:           0

US-10-821-670A-33 (1-222) x AAD15211 (1-666)

Qy          96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         283 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCT 342

Qy         116 SerArgLysThrSerPheMetThrThrLeuCys 126
               |||||||||||||||||||||||||||||||
Db         343 TCCAGAAAGACCTCTTTTATGACAACCCTGTGC 375

RESULT 73
ADQ41825
```

ADQ41825 standard; DNA; 201 BP.

ADQ41825;

18-NOV-2004 (first entry)

Myocardial infarction-associated SNP flanking transcript, SEQ ID 3488.

Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; ds.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin JJ, Iakoubova O;

WPI; 2004-533949/51.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 7; SEQ ID NO 3488; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

ignment Scores:			
ed. No.:	6e-20	Length:	201
ore:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0

DB: 13 Gaps: 0

US-10-821-670A-33 (1-222) x ADQ41825 (1-201)

```
Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98
```

RESULT 74
ADQ41824
ID ADQ41824 standard; DNA; 201 BP.
XX
AC ADQ41824;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3487.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3487; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This

polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

ignment Scores:
ed. No.: 6e-20 Length: 201
ore: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 13 Gaps: 0

-10-821-670A-33 (1-222) x ADQ41824 (1-201)

184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

204 AlaPheArgIleArgAlaValThrIle 212
|||||||||||||||||||||||||
64 GCTTTCAGAATTCGGGCAGTGACTATT 90

SULT 75
241835
ADQ41835 standard; DNA; 201 BP.

ADQ41835;

18-NOV-2004 (first entry)

Myocardial infarction-associated SNP flanking transcript, SEQ ID 3498.

Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; ds.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin JJ, Iakoubova O;

WPI; 2004-533949/51.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 7; SEQ ID NO 3498; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino

CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 6e-20 Length: 201
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 13 Gaps: 0

US-10-821-670A-33 (1-222) x ADQ41835 (1-201)

Qy 184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy 204 AlaPheArgIleArgAlaValThrIle 212
|||||||||||||||||||||||||
Db 72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 76
ADQ41829
ID ADQ41829 standard; DNA; 201 BP.
XX
AC ADQ41829;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3492.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing

myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 7; SEQ ID NO 3492; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

ignment Scores:

ed. No.:	6e-20	Length:	201
ore:	29.00	Matches:	29
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
:	13	Gaps:	0

-10-821-670A-33 (1-222) x ADQ41829 (1-201)

```
       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
       173 GCTTTCAGAATTCGGGCAGTGACTATT 199
```

SULT 77
Q41838
ADQ41838 standard; DNA; 201 BP.

ADQ41838;

18-NOV-2004 (first entry)

Myocardial infarction-associated SNP flanking transcript, SEQ ID 3501.

Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; ds.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3501; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	6e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	13.1%	Indels:	0
DB:	13	Gaps:	0

US-10-821-670A-33 (1-222) x ADQ41838 (1-201)

```
Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199
```

RESULT 78
ADQ41833
ID ADQ41833 standard; DNA; 201 BP.
XX
AC ADQ41833;

18-NOV-2004 (first entry)

Myocardial infarction-associated SNP flanking transcript, SEQ ID 3496.

Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; ds.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin JJ, Iakoubova O;

WPI; 2004-533949/51.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 7; SEQ ID NO 3496; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

ignment Scores:
ed. No.: 6e-20 Length: 201
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 13 Gaps: 0

-10-821-670A-33 (1-222) x ADQ41833 (1-201)

Qy 184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy 204 AlaPheArgIleArgAlaValThrIle 212
||||||||||||||||||||||||||
Db 64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 79
ADF77258
ID ADF77258 standard; DNA; 630 BP.
XX
AC ADF77258;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p35 subunit optimised DNA #5.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; SEQ ID NO 27; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,
CC comprising a promoter and a synthetic 5' intron transcriptionally linked
CC with an interferon alpha coding sequence and a 3' untranslated region.
CC The mammalian interferon alpha expression plasmid is useful for treating
CC tumour growth. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 630 BP; 118 A; 234 C; 141 G; 137 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.82e-19 Length: 630
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 12 Gaps: 0

US-10-821-670A-33 (1-222) x ADF77258 (1-630)

Qy 184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 511 TCCTCCTTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGTTGTGCATCTTGTTGCAC 570

Qy 204 AlaPheArgIleArgAlaValThrIle 212
||||||||||||||||||||||||||
Db 571 GCCTTCCGCATCCGCGCCGTCACCATC 597

SULT 80
G39431
ADG39431 standard; DNA; 657 BP.

ADG39431;

26-FEB-2004 (first entry)

Human CLMF 35 kDa subunit DNA.

human; cytotoxic lymphocyte maturation factor; CLMF; activated T-cell stimulator; natural killer cell stimulator; immunoenhancer; antitumour; tumour; cancer; ds; gene.

Homo sapiens.

Key	Location/Qualifiers
CDS	67. .657
	/*tag= a
	/partial
	/product= "CLMF 35 kDa subunit"
	/note= "No start or stop codon given"

US2003204059-A1.

30-OCT-2003.

08-OCT-2002; 2002US-00267565.

22-DEC-1989; 89US-00455708.
09-MAY-1990; 90US-00520935.
27-AUG-1990; 90US-00572284.
24-MAR-1992; 92US-00857023.
02-MAR-1994; 94US-00205011.
02-JUN-1995; 95US-00459151.
22-SEP-1999; 99US-00401839.

(HOFF) HOFFMANN LA ROCHE & CIE SA F.

Gately MK, Gubler UA, Hulmes JD, Podlaski FJ, Stern AS; Chizzonite RA, Pan YE;

WPI; 2004-010534/01.
P-PSDB; ADG39428.

Novel protein comprising cytotoxic lymphocyte maturation factor in substantially pure form or protein which exhibits cytotoxic lymphocyte maturation factor activity, useful as antitumor and immunoenhancing agent.

Claim 20; Page 29; 74pp; English.

The invention relates to a protein which comprises a cytotoxic lymphocyte maturation factor (CLMF). The protein is useful for stimulating activated T-cells which involves treating T-cells with the protein. The method further involves treating the activated T-cells with IL2 or its biologically active fragment. The protein is useful for stimulating natural killer cells which involves treating the natural killer cells with the protein. The protein has immunoenhancing and antitumour effects when used as single therapeutic agent in vivo. The present sequence is used in the exemplification of the present invention.

Sequence 657 BP; 186 A; 166 C; 139 G; 166 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	1.89e-19	Length:	657
ore:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
:	12	Gaps:	0

US-10-821-670A-33 (1-222) x ADG39431 (1-657)

```
Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

RESULT 81
AAQ97485
ID AAQ97485 standard; cDNA; 660 BP.
XX
AC AAQ97485;
XX
DT 25-MAR-2003 (revised)
DT 22-DEC-1995 (first entry)
XX
DE Human interleukin-12 35 kD subunit.
XX
KW Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW natural killer cell; graft vs. host disease; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a

XX
PN WO9519786-A1.
XX
PD 27-JUL-1995.
XX
PF 20-JAN-1995; 95WO-US000879.
XX
PR 21-JAN-1994; 94US-00186529.
XX
PA (GEMY) GENETICS INST INC.
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Wolf SF, Sykes M;
XX
DR WPI; 1995-269273/35.
DR P-PSDB; AAR79187.
XX
PT Control of graft versus host disease using interleukin 12 - partic.
PT admin. at the time of bone marrow transplant.
XX
PS Disclosure; Page 23-24; 32pp; English.
XX
CC AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC 12 is a heterodimeric cytokine which was originally identified as a
CC factor which induces gamma-interferon from T cells and natural killer
CC cells as set forth in PCT/US91/06332, published April 2 1992, and
CC incorporated by reference. EP 433827, published June 26 1991, disclosed
CC IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC is defined as a heterodimeric glycoprotein comprised of two covalently
CC linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.9e-19	Length:	660
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	13.1%	Indels:	0

```
:                    2             Gaps:          0

-10-821-670A-33 (1-222) x AAQ97485 (1-660)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

3ULT 82
/07274
   AAV07274 standard; cDNA; 660 BP.

   AAV07274;

   25-SEP-1998  (first entry)

   Human Interleukin-12 p35 gene.

   IL-12 subunit; expression construct; treatment; asthma;
   microbial infection; viral infection; cancer; Human; Interleukin; ss.

   Homo sapiens.

   Key             Location/Qualifiers
   CDS             1. .660
                   /*tag=  a
                   /product= "IL-12 p35"
                   /transl_except= (pos:58. .60,aa:Ser)

   WO9817689-A2.

   30-APR-1998.

   10-OCT-1997;   97WO-US018779.

   18-OCT-1996;   96US-0028676P.

   (GENE-) GENEMEDICINE INC.

   Nordstrom J,  Freimark B,  Deshpande D;

   WPI; 1998-261428/23.
   P-PSDB; AAV07274.

   Constructs for expression of interleukin-12 sub-units - are used for
   delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
   infections and certain cancers.

   Claim 1; Page 34-35; 80pp; English.

   The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
   appropriate expression construct engineered into a plasmid. The plasmids
   can provide for efficient expression of IL-12 subunits. The products can
   be used for the treatment of asthma, microbial and viral infections and
   certain cancers

   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              1.9e-19        Length:        660
ore:                  29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AAV07274 (1-660)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 83
AAV07218
ID   AAV07218 standard; DNA; 660 BP.
XX
AC   AAV07218;
XX
DT   12-AUG-1998  (first entry)
XX
DE   DNA encoding human interleukin-12 35kDa subunit.
XX
KW   Interleukin-12; IL-12; graft-versus-host disease;
KW   GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Interleukin-12_35kDa_subunit"
XX
PN   US5756085-A.
XX
PD   26-MAY-1998.
XX
PF   30-APR-1996;   96US-00640386.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Sykes M,  Wolf SF;
XX
DR   WPI; 1998-321459/28.
DR   P-PSDB; AAW51222.
XX
PT   Therapy of graft-versus-host disease - by administration of interleukin-
PT   12 to maintain and/or promote graft-versus-leukaemia effects.
XX
PS   Disclosure; Col 23-24; 20pp; English.
XX
CC   The invention relates to a method for the treatment or prevention of
CC   graft-versus-host disease (GVHD) which comprises the administration of
CC   interleukin-12 (IL-12) at the time of bone-marrow transplantation to
CC   maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC   0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC   the bone marrow transplant. IL-12 is administered daily until there is an
CC   improvement in the condition. Administration is oral, cutaneous,
CC   subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC   intravenous. The present sequence encodes the human interleukin-12 35kDa
CC   subunit
XX
SQ   Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.9e-19        Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AAV07218 (1-660)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 84
Z40408
   AAZ40408 standard; DNA; 660 BP.

   AAZ40408;

   15-FEB-2000  (first entry)

   Human interleukin 12 p35 subunit optimised coding sequence.

   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
   promoter; growth hormone; untranslated region; UTR; mammal; disease;
   cancer; ss.

   Homo sapiens.

   WO9947678-A2.

   23-SEP-1999.

   12-MAR-1999;   99WO-US005394.

   19-MAR-1998;   98US-0078654P.

   (GENE-) GENEMEDICINE INC.

   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;

   WPI; 1999-562116/47.
   P-PSDB; AAY42488.

   New plasmids containing an interferon-alpha coding sequence, used for the
   treatment of a mammalian condition or disease, particularly cancer.

   Claim 11; Page 38-39; 137pp; English.

   This sequence represents an optimised coding region for the human
   interleukin 12 p35 subunit. The invention relates to a novel plasmid
   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
   untranslated region (UTR). The plasmids can be used for treating a
   mammalian condition or disease, particularly cancer

   Sequence 660 BP; 147 A; 237 C; 180 G; 96 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              1.9e-19        Length:        660
ore:                  29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x AAZ40408 (1-660)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

SULT 85
Z40407
   AAZ40407 standard; DNA; 660 BP.

AC   AAZ40407;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p35 subunit wild type coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9947678-A2.
XX
PD   23-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005394.
XX
PR   19-MAR-1998;   98US-0078654P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR   WPI; 1999-562116/47.
DR   P-PSDB; AAY42488.
XX
PT   New plasmids containing an interferon-alpha coding sequence, used for the
PT   treatment of a mammalian condition or disease, particularly cancer.
XX
PS   Claim 11; Page 38-39; 137pp; English.
XX
CC   This sequence represents the wild type coding region for the human
CC   interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC   untranslated region (UTR). The plasmids can be used for treating a
CC   mammalian condition or disease, particularly cancer
XX
SQ   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.9e-19        Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AAZ40407 (1-660)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 86
AAZ40409
ID   AAZ40409 standard; DNA; 660 BP.
XX
AC   AAZ40409;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p35 subunit semi-optimised coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
```

Homo sapiens.

WO9947678-A2.

23-SEP-1999.

12-MAR-1999; 99WO-US005394.

19-MAR-1998; 98US-0078654P.

(GENE-) GENEMEDICINE INC.

Nordstrom J, Pericle F, Rolland A, Ralston R;

WPI; 1999-562116/47.
P-PSDB; AAY42488.

New plasmids containing an interferon-alpha coding sequence, used for the treatment of a mammalian condition or disease, particularly cancer.

Claim 11; Page 38-39; 137pp; English.

This sequence represents a semi-optimised coding region for the human interleukin 12 p35 subunit. The invention relates to a novel plasmid comprising a cytomegalovirus (CMV) promoter transcriptionally linked with an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-untranslated region (UTR). The plasmids can be used for treating a mammalian condition or disease, particularly cancer

Sequence 660 BP; 147 A; 242 C; 170 G; 101 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.9e-19 Length: 660
ore: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 2 Gaps: 0

-10-821-670A-33 (1-222) x AAZ40409 (1-660)

```
       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
       601 GCCTTCCGCATCCGGGCCGTGACCATC 627
```

ULT 87
015221
AAD15221 standard; DNA; 660 BP.

AAD15221;

01-NOV-2001 (first entry)

Human cytokine p35 DNA.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p35; ds.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .660
	/*tag= a
	/product= "p35 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .657
	/*tag= c
	/product= "Mature p35 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08614.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 91; Page 142; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is human p35 protein encoding DNA
XX
SQ Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.9e-19 Length: 660
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 5 Gaps: 0

US-10-821-670A-33 (1-222) x AAD15221 (1-660)

```
Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      601 GCTTTCAGAATTCGGGCAGTGACTATT 627
```

RESULT 88
AAL44226
ID AAL44226 standard; DNA; 660 BP.
XX
AC AAL44226;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human interleukin 12A (IL-12A) coding sequence.
XX
KW Human; gene; ds; interleukin 12A; IL-12A; drug screening; AIDS; malaria;
KW tuberculosis; cancer; haplotyping; genotyping; transgenic animal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .660
FT /*tag= a
FT /product= "Human interleukin 12A (IL-12A)"

variation replace(142, A)
/*tag= b
/standard_name= "Single nucleotide polymorphism"

WO200229115-A1.

11-APR-2002.

05-OCT-2001; 2001WO-US031656.

06-OCT-2000; 2000US-0238693P.

(GENA-) GENAISSANCE PHARM INC.

Armstrong B, Cappola G, Choi JY, Gilson CR, Kliem SE, Koshy B; Parks KE;

WPI; 2002-315865/35.
P-PSDB; AAO15506.

New interleukin 12A (IL-12A) gene polymorphic variants, for studying the expression and function of IL-12A and screening candidate drugs for treating AIDS and cancer.

Claim 28; Fig 2; 72pp; English.

The invention comprises the amino acid and coding sequence of the human interleukin 12A (IL-12A) protein. Specifically the invention relates to the identification of polymorphisms within the human (IL-12A) gene sequence. The polymorphisms identified in the human IL-12A gene sequence are useful in studying the expression and function of IL-12A, and in screening drugs for the treatment of disorders such as AIDS, malaria, tuberculosis and cancer. The IL-12A polymorphisms may be used to haplotype and genotype the IL-12A gene of an individual. The IL-12A DNA sequences of the invention can be used to create transgenic animals for studying expression of the IL-12A isogenes in vivo. The present DNA sequence represents the coding sequence of the human interleukin 12A (IL-12A) gene

Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.9e-19 Length: 660
ore: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 6 Gaps: 0

-10-821-670A-33 (1-222) x AAL44226 (1-660)

184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

204 AlaPheArgIleArgAlaValThrIle 212
||||||||||||||||||||||||||
601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 89
C47589
ACC47589 standard; DNA; 660 BP.

ACC47589;

12-JUN-2003 (first entry)

Human interleukin 12 (hIL-12) P35 subunit gene.

Human; interleukin 12; hIL-12; baculovirus vector;
recombinant production; AcNPV-hIL12;
Autographa california nuclear polyhedrosis virus; tumour; cancer;
infection; bacterial; viral; cytostatic; P35 subunit; gene; ds.

XX
OS Homo sapiens.
XX
PN CN1357622-A.
XX
PD 10-JUL-2002.
XX
PF 02-NOV-2001; 2001CN-00133631.
XX
PR 02-NOV-2001; 2001CN-00133631.
XX
PA (UYWU-) UNIV WUHAN.
XX
PI Meng X, Xu J, Yu Z;
XX
DR WPI; 2002-741792/81.
XX
PT Human interleukin-12 recombinant insect virus strain and its preparation.
XX
PS Claim 4; Fig 6; 17pp; Chinese.
XX
CC The invention relates to a recombinant baculovirus comprising DNA
CC encoding human interleukin 12 (hIL-12) and methods for its preparation.
CC The recombinant baculovirus strain is designated Autographa california
CC nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
CC contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
CC (ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
CC respectively under the control of the viral polyhedrin and P10 promoters.
CC The baculovirus can be used in the recombinant production of human IL-12
CC which is suitable for treating tumours and bacterial, viral and other
CC infections. The present sequence represents the human IL-12 P35 subunit
CC gene used in construction of the baculovirus vector of the invention
XX
SQ Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.9e-19 Length: 660
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-33 (1-222) x ACC47589 (1-660)

Qy 184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy 204 AlaPheArgIleArgAlaValThrIle 212
||||||||||||||||||||||||||
Db 601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 90
ADF77245
ID ADF77245 standard; DNA; 660 BP.
XX
AC ADF77245;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p35 subunit optimised DNA #1.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.

12-MAR-1999; 99US-00268135.

(NORD/) NORDSTROM J L.
(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

Nordstrom JL, Pericle F, Rolland A, Ralston RO;

WPI; 2004-020834/02.

A mammalian interferon alpha expression plasmid is useful in gene therapy to deliver interferon alpha to cells to modulate tumor activity in the treatment of cancer.

Disclosure; SEQ ID NO 7; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 660 BP; 147 A; 237 C; 180 G; 96 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.9e-19 Length: 660
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 12 Gaps: 0

-10-821-670A-33 (1-222) x ADF77245 (1-660)

```
        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        601 GCCTTCCGCATCCGCGCCGTGACCATC 627
```

SULT 91
:77257
ADF77257 standard; DNA; 660 BP.

ADF77257;

26-FEB-2004 (first entry)

Human IL-12 p35 subunit optimised DNA #4.

ds; human; interferon alpha expression plasmid; tumour; IL-12.

Synthetic.
Homo sapiens.

US2003181405-A1.

25-SEP-2003.

29-APR-2002; 2002US-00136837.

12-MAR-1999; 99US-00268135.

(NORD/) NORDSTROM J L.
(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; SEQ ID NO 26; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,
CC comprising a promoter and a synthetic 5' intron transcriptionally linked
CC with an interferon alpha coding sequence and a 3' untranslated region.
CC The mammalian interferon alpha expression plasmid is useful for treating
CC tumour growth. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 660 BP; 197 A; 93 C; 82 G; 288 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.9e-19 Length: 660
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 12 Gaps: 0

US-10-821-670A-33 (1-222) x ADF77257 (1-660)

```
Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCTTCTTTAGAAGAACCTGATTTTTATAAAACTAAAATTAAATTATGTATTTTATTACAT 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        601 GCTTTTCGTATTCGTGCTGTTACTATT 627
```

RESULT 92
ADF77246
ID ADF77246 standard; DNA; 660 BP.
XX
AC ADF77246;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p35 subunit optimised DNA #2.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX

Disclosure; SEQ ID NO 8; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 660 BP; 147 A; 242 C; 170 G; 101 T; 0 U; 0 Other;

```
ignment Scores:
ed. No.:              1.9e-19        Length:        660
ore:                  29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     12             Gaps:          0

-10-821-670A-33 (1-222) x ADF77246 (1-660)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
       601 GCCTTCCGCATCCGGGCCGTGACCATC 627

SULT 93
F77244
   ADF77244 standard; DNA; 660 BP.

   ADF77244;

   26-FEB-2004  (first entry)

   Human IL-12 p35 subunit DNA.

   ds; human; interferon alpha expression plasmid; tumour; IL-12.

   Homo sapiens.

   US2003181405-A1.

   25-SEP-2003.

   29-APR-2002; 2002US-00136837.

   12-MAR-1999;  99US-00268135.

   (NORD/) NORDSTROM J L.
   (PERI/) PERICLE F.
   (ROLL/) ROLLAND A.
   (RALS/) RALSTON R O.

   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;

   WPI; 2004-020834/02.

   A mammalian interferon alpha expression plasmid is useful in gene therapy
   to deliver interferon alpha to cells to modulate tumor activity in the
   treatment of cancer.

   Disclosure; SEQ ID NO 6; 65pp; English.

   The invention relates to a mammalian interferon alpha expression plasmid,
   comprising a promoter and a synthetic 5' intron transcriptionally linked
   with an interferon alpha coding sequence and a 3' untranslated region.
   The mammalian interferon alpha expression plasmid is useful for treating
   tumour growth. The present sequence is used in the exemplification of the
   present invention.
```

SQ Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.:              1.9e-19        Length:        660
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     12             Gaps:          0

US-10-821-670A-33 (1-222) x ADF77244 (1-660)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 94
AAF26096
ID   AAF26096 standard; DNA; 683 BP.
XX
AC   AAF26096;
XX
DT   24-APR-2001  (first entry)
XX
DE   Human pG-hIL12p DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Homo sapiens.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
```

of interferon gamma (Th1 response). The feline interleukin-12 polypeptide is useful for carnivores, and particularly domestic cats in the following: (i) as immunostimulant, for preventative or therapeutic use; and (ii) treating tumors and autoimmune diseases, or diseases associated with a Th1 defect, especially pre-existing infections by feline immune deficiency virus (FIV), feline leukemia virus and corona virus

Sequence 683 BP; 198 A; 171 C; 142 G; 172 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.97e-19 Length: 683
re: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 4 Gaps: 0

-10-821-670A-33 (1-222) x AAF26096 (1-683)

184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

204 AlaPheArgIleArgAlaValThrIle 212
|||||||||||||||||||||||||
601 GCTTTCAGAATACGGGCAGTGACTATT 627

SULT 95
?88401
ADP88401 standard; cDNA; 702 BP.

ADP88401;

09-SEP-2004 (first entry)

Human interleukin-12 alpha chain coding sequence.

antiinflammatory; antiasthmatic; antiallergic; immunosuppressive; antibacterial; protozoacide; gene therapy; expression vector; interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12; human.

Homo sapiens.

WO2004052929-A2.

24-JUN-2004.

08-DEC-2003; 2003WO-IB006404.

06-DEC-2002; 2002GB-00028465.

(UYBE-) UNIV QUEENS BELFAST.

Vandenbroeck K, Alloza I;

WPI; 2004-487887/46.

New expression vector comprising DNA encoding a subunit of a dimeric form of interleukin under transcriptional control of an ecdysone-inducible promoter, useful in preparing a composition for treating e.g., inflammatory disease.

Disclosure; Page 85-86; 87pp; English.

The present invention relates to an expression vector comprising DNA encoding a subunit of a dimeric form of interleukin under transcriptional control of an ecdysone-inducible promoter. The expression vector is useful in preparing a composition for treating a disease having a pathogenesis which includes endogenous production of cytokine IL-12, IL-23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-induced inflammation, epithelial airway inflammation such as asthma, allergic disease, or autoimmune disease such as multiple sclerosis or

CC inflammatory bowel disease. The present sequence is the coding sequence
CC of the human interleukin-12 alpha chain used in the exemplification of
CC the invention.
XX
SQ Sequence 702 BP; 199 A; 184 C; 147 G; 172 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.02e-19 Length: 702
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 12 Gaps: 0

US-10-821-670A-33 (1-222) x ADP88401 (1-702)

Qy 184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 556 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 615

Qy 204 AlaPheArgIleArgAlaValThrIle 212
|||||||||||||||||||||||||
Db 616 GCTTTCAGAATTCGGGCAGTGACTATT 642

RESULT 96
AAQ67880
ID AAQ67880 standard; DNA; 721 BP.
XX
AC AAQ67880;
XX
DT 25-MAR-2003 (revised)
DT 23-MAR-1995 (first entry)
XX
DE EPV 42 kD promoter/Human IL-12 p35 subunit expression cassette.
XX
KW Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW polymerase chain reaction; poxvirus; pSD542; immunological response;
KW pathogen; human; interferon; IFN; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT promoter 1. .61
FT /*tag= a
FT /note= "Vaccinia E3L promoter"
FT CDS 32. .1018
FT /*tag= b
FT /product= "Human IL-12 p35"
XX
PN WO9416716-A1.
XX
PD 04-AUG-1994.
XX
PF 21-JAN-1994; 94WO-US000888.
XX
PR 21-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI Paoletti E, Tartaglia J, Cox WI;
XX
DR WPI; 1994-263767/32.
XX
PT Attenuated recombinant virus used for cancer therapy - comprises DNA
PT encoding cytokine and/or tumour associated antigen.
XX
PS Example 27; Fig 34; 232pp; English.
XX
CC The sequences given in AAQ67879-80 are expression cassettes which contain
CC the p40 and p35 subunits of human interleukin-12 (IL-12) under the

control of the entomopox virus (EPV) promoter and the vaccinia E3L promoter, respectively. These sequences were used in the construction of an ALVAC-based recombinant virus containing the genes for the two subunits of human IL-12. The p40 subunit was amplified using primers JP202 and JP189 and placed under the control of the entomopox virus (EPV) 42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified using primers JP186 and JP201 and placed under the control of the vaccinia E3L promoter using primers JP218 and JP220. The expression cassette was isolated and ligated with pBSSK+ generating plasmid PBSHIL12p35II. The p35 and p40 expression cassettes were excised and assembled in pBSSK+ to give PBSHIL12 in which the two expression cassettes are orientated head-to-head relative to each other. The combination casette containing the poxvirus promoted genes for both IL-12 subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which contains both the human IL-12 genes in the C6 locus. The resulting virus may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	2.07e-19	Length:	721
ore:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
:	2	Gaps:	0

-10-821-670A-33 (1-222) x AAQ67880 (1-721)

```
       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
       662 GCTTTCAGAATTCGGGCAGTGACTATT 688
```

SULT 97
AZ08515
AAZ08515 standard; DNA; 721 BP.

AAZ08515;

19-OCT-1999 (first entry)

Vaccinia E3L/human IL-12 P35 expression cassette.

Attenuated recombinant virus; cytokine; tumour associated antigen; NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies; cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF; interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen; carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza; immunological response; immunotherapy; vaccine; Newcastle Disease; ss.

Synthetic.
Homo sapiens.
Vaccinia virus.

US5942235-A.

24-AUG-1999.

02-JUN-1995; 95US-00458356.

24-DEC-1981; 81US-00334456.
08-DEC-1982; 82US-00446824.
19-JUN-1984; 84US-00622135.
27-AUG-1987; 87US-00090209.
28-AUG-1987; 87US-00090711.
PR 20-OCT-1987; 87US-00110335.
PR 25-APR-1988; 88US-00186054.
PR 23-AUG-1988; 88US-00234390.
PR 14-JUN-1990; 90US-00537882.
PR 14-JUN-1990; 90US-00537890.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 04-MAY-1992; 92US-00881995.
PR 22-JUL-1992; 92US-00918278.
PR 20-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 14-APR-1994; 94US-00228926.
PR 13-SEP-1994; 94US-00306259.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Paoletti E;
XX
DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 27; Fig 34; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC Vaccinia E3L/human IL-12 P35 expression cassette used in the
CC exemplification of the present invention
XX
SQ Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.07e-19	Length:	721
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	13.1%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-33 (1-222) x AAZ08515 (1-721)

```
Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy         204 AlaPheArgIleArgAlaValThrIle 212
               ||||||||||||||||||||||||||||
Db         662 GCTTTCAGAATTCGGGCAGTGACTATT 688
```

RESULT 98
ADR21891
ID ADR21891 standard; DNA; 721 BP.
XX
AC ADR21891;
XX
DT 04-NOV-2004 (first entry)

Vaccinia E3L/human IL-12 expression cassette.

Cytostatic; Vaccine; recombinant poxvirus; nonessential region; attenuated avipox Virus; carcinoembryonic antigen; B7 protein; cancer therapy; ds; human; IL-12; interleukin-12; E3L; expression cassette.

Vaccinia virus.
Homo sapiens.
Synthetic.

US6780407-B1.

24-AUG-2004.

15-SEP-2000; 2000US-00663667.

08-MAR-1989; 89US-00320471.
14-FEB-1990; 90US-00478179.
07-JAN-1991; 91US-00638080.
07-MAR-1991; 91US-00666056.
11-JUN-1991; 91US-00713967.
16-DEC-1991; 91US-00805567.
03-MAR-1992; 92US-00847977.
06-MAR-1992; 92US-00847951.
21-JAN-1993; 93US-00007115.
19-JAN-1994; 94US-00184009.
30-AUG-1995; 95US-00521016.

(AVET) AVENTIS PASTEUR.

Paoletti E, Tartaglia J, Cox WI;

WPI; 2004-601998/58.

New recombinant poxvirus which is an attenuated avipox Virus that expresses an exogenous DNA encoding carcinoembryonic antigen and an exogenous DNA encoding B7 protein, useful for cancer therapy.

Example 27; SEQ ID NO 199; 181pp; English.

The invention describes a recombinant poxvirus containing exogenous DNA in a nonessential region of the poxvirus, where the poxvirus is an attenuated avipox Virus that expresses an exogenous DNA encoding carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also described are: a composition comprising a poxvirus above in admixture with a carrier; and expressing carcinoembryonic antigen and B7 protein in vivo comprising administering to a mammal the composition above. Disclosed are: making recombinant poxvirus defined above; recombinant poxvirus vaccine having an increased level of safety compared to known recombinant poxvirus vaccines; and a modified vector for expressing a gene product in a host. The recombinant poxvirus is useful for providing a recombinant poxvirus vaccine having an increased level of safety compared to known recombinant poxvirus vaccines. The recombinant poxvirus is useful for cancer therapy. This sequence represents a human IL-12 expression cassette used in the creation of NYVAC rescue virus and canarypox virus vector ALVAC comprising the human IL-12 gene.

Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 2.07e-19 Length: 721
re: 29.00 Matches: 29
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 13 Gaps: 0

-10-821-670A-33 (1-222) x ADR21891 (1-721)

184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

204 AlaPheArgIleArgAlaValThrIle 212
|||||||||||||||||||||||||||
662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 99
ADK98708
ID ADK98708 standard; DNA; 761 BP.
XX
AC ADK98708;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human interleukin-12 (IL-12) P35 subunit DNA seqid 3.
XX
KW human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS Homo sapiens.
XX
PN CN1408727-A.
XX
PD 09-APR-2003.
XX
PF 29-SEP-2001; 2001CN-00126923.
XX
PR 29-SEP-2001; 2001CN-00126923.
XX
PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI Wan G, Li C;
XX
DR WPI; 2003-664076/63.
XX
PT Method for efficiently expressing recombinant human interleukin 12 in
PT eukaryotic cell.
XX
PS Claim 6; SEQ ID NO 3; 14pp; Chinese.
XX
CC The invention describes the process of producing human recombinant
CC interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC corresponding to the P35 subunit with the first signal peptide and a
CC nucleotide sequence corresponding to the P40 subunit; inserting the
CC nucleotide sequences into an expression vector; converting the eukaryotic
CC cell with the expression vector; and culturing the transfected eukaryotic
CC cell in condition suitable for recombinant human IL-12 expression. The
CC process balances the expression amount of both P35 and P40 subunits and
CC thus raises the expression amount of IL-12 with bioactivity via raising
CC the expression strength of P35 subunit. This sequence represents the
CC human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ Sequence 761 BP; 205 A; 204 C; 164 G; 187 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.18e-19 Length: 761
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 10 Gaps: 0

US-10-821-670A-33 (1-222) x ADK98708 (1-761)

184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
642 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 701

204 AlaPheArgIleArgAlaValThrIle 212
|||||||||||||||||||||||||||
702 GCTTTCAGAATTCGGGCAGTGACTATT 728

RESULT 100
ADK98706

ADK98706 standard; DNA; 761 BP.

ADK98706;

06-MAY-2004 (first entry)

Human interleukin-12 (IL-12) P35 subunit DNA seqid 1.

human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.

Homo sapiens.

CN1408727-A.

09-APR-2003.

29-SEP-2001; 2001CN-00126923.

29-SEP-2001; 2001CN-00126923.

(ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.

Wan G, Li C;

WPI; 2003-664076/63.

Method for efficiently expressing recombinant human interleukin 12 in eukaryotic cell.

Claim 4; SEQ ID NO 1; 14pp; Chinese.

The invention describes the process of producing human recombinant interleukin-12 (IL-12) includes: providing a nucleotide sequence corresponding to the P35 subunit with the first signal peptide and a nucleotide sequence corresponding to the P40 subunit; inserting the nucleotide sequences into an expression vector; converting the eukaryotic cell with the expression vector; and culturing the transfected eukaryotic cell in condition suitable for recombinant human IL-12 expression. The process balances the expression amount of both P35 and P40 subunits and thus raises the expression amount of IL-12 with bioactivity via raising the expression strength of P35 subunit. This sequence represents the human interleukin-12 (IL-12) P35 subunit polynucleotide.

Sequence 761 BP; 199 A; 209 C; 167 G; 185 T; 0 U; 1 Other;

ignment Scores:

ed. No.:	2.18e-19	Length:	761
ore:	29.00	Matches:	29
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
:	10	Gaps:	0

-10-821-670A-33 (1-222) x ADK98706 (1-761)

```
        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        642 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 701

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        702 GCTTTCAGAATTCGGGCAGTGACTATT 728
```

arch completed: June 10, 2006, 02:27:12
b time : 566.89 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 01:35:52 ; Search time 3076.04 Seconds
(without alignments)
6053.601 Million cell updates/sec

le: US-10-821-670A-33
fect score: 222
quence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 48236798 seqs, 27959665780 residues

d size: 1

al number of hits satisfying chosen parameters: 96471816

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mand line parameters:
ODEL=frame+_p2n.model -DEV=xlp
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110453_27580/app_query.fasta_1
B=EST -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rst -MINMATCH=0.1 -LOOPCL=0
OOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
IST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL
UTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
SER=US10821670_@CGN_1_1_22222_@runat_07062006_110453_27580 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	29	13.1	762	14	DQ033872	DQ033872 Homo sapi
2	29	13.1	863	4	CD013916	CD013916 90138296
3	29	13.1	935	4	CD013914	CD013914 90138124
4	29	13.1	1136	4	CD013915	CD013915 90138132
5	29	13.1	1938	6	BC035571	BC035571 Homo sapi
6	28	12.6	762	14	DQ033873	DQ033873 Pan trogl
7	28	12.6	812	2	BG702253	BG702253 602683459
8	28	12.6	832	2	BI523569	BI523569 603175938
9	24	10.8	581	3	BP260963	BP260963 BP260963
10	24	10.8	777	14	CT080894	CT080894 Sus scrof
11	21	9.5	592	12	CE159257	CE159257 tigr-gss-
c 12	21	9.5	778	1	AJ820622	AJ820622 AJ820622
13	20	9.0	342	2	BM257856	BM257856 521721 MA
14	20	9.0	344	14	BX537236	BX537236 INRA porc
15	18	8.1	447	2	BI824638	BI824638 603033580
c 16	17	7.7	1099	2	BI523344	BI523344 603175938
c 17	16	7.2	777	4	CB168830	CB168830 CWI602769
c 18	13	5.9	528	1	AI332701	AI332701 qq19a07.x
19	11	5.0	463	9	DR007201	DR007201 TC124111
20	11	5.0	508	9	DA505380	DA505380 DA505380
21	11	5.0	571	3	BP261459	BP261459 BP261459
22	10	4.5	373	7	BF552757	BF552757 UI-R-C0-i
23	10	4.5	427	10	DT930939	DT930939 S13.1784
24	10	4.5	456	10	DT913216	DT913216 S13.1426
25	10	4.5	561	3	BU699383	BU699383 LL2in1157
26	10	4.5	563	3	BU698113	BU698113 LL2in1206
27	10	4.5	589	1	AI050362	AI050362 ub30a07.r
c 28	10	4.5	614	11	AZ729972	AZ729972 RPCI-24-1
29	10	4.5	692	5	CJ137697	CJ137697 CJ137697
c 30	10	4.5	941	13	CZ271875	CZ271875 ZMMBF0051
31	10	4.5	1299	6	AK153729	AK153729 Mus muscu
32	9	4.1	87	14	BX655139	BX655139 Arabidops
33	9	4.1	192	4	BY368866	BY368866 BY368866
c 34	9	4.1	194	7	BF366007	BF366007 PM4-NT007
c 35	9	4.1	234	10	DV345207	DV345207 NABWE87TR
c 36	9	4.1	254	8	CR470624	CR470624 CR470624
c 37	9	4.1	276	1	AI136106	AI136106 UI-R-C2p-
38	9	4.1	294	4	BY364595	BY364595 BY364595
39	9	4.1	304	5	CF799003	CF799003 Lr_PAHCF_
40	9	4.1	343	12	CG422132	CG422132 ZMMBBc003
41	9	4.1	372	12	CG396825	CG396825 ZMMBBc001
c 42	9	4.1	374	2	BI296096	BI296096 UI-R-DK0-
c 43	9	4.1	375	12	CL003778	CL003778 ZMMBBb038
44	9	4.1	399	11	AZ036596	AZ036596 RPCI-23-3
45	9	4.1	404	9	DN988885	DN988885 ZEBRA_2F_
46	9	4.1	412	4	CB801533	CB801533 AMGNNUC:S
47	9	4.1	425	5	CF798662	CF798662 Lr_PAHCF_
c 48	9	4.1	437	1	AI750954	AI750954 cn06g05.x
c 49	9	4.1	453	11	AZ215995	AZ215995 Sheared D
50	9	4.1	495	8	CO869708	CO869708 Lr_JV2CF_
51	9	4.1	495	9	DN245766	DN245766 ACAE-aaa4
c 52	9	4.1	501	9	DA587595	DA587595 DA587595
c 53	9	4.1	502	9	DA599473	DA599473 DA599473
54	9	4.1	512	9	DR008986	DR008986 Lr_Cu2CF_
c 55	9	4.1	519	7	BE294832	BE294832 601177293
c 56	9	4.1	521	9	DA598142	DA598142 DA598142
57	9	4.1	539	14	CR813130	CR813130 GR0AAA37C
c 58	9	4.1	549	9	DA956152	DA956152 DA956152
59	9	4.1	551	10	DT919655	DT919655 PCRS30821
c 60	9	4.1	556	9	DA555731	DA555731 DA555731
c 61	9	4.1	556	10	DY063836	DY063836 000403BPP
62	9	4.1	558	9	CX570753	CX570753 RVL1941 W
c 63	9	4.1	562	9	DA552898	DA552898 DA552898
c 64	9	4.1	565	9	DA557449	DA557449 DA557449
c 65	9	4.1	566	1	AI468038	AI468038 tm61g07.x
66	9	4.1	568	14	CR795312	CR795312 GR0AAA12D
c 67	9	4.1	572	7	BE296563	BE296563 601174065
c 68	9	4.1	577	4	CA153972	CA153972 SCVPRZ203
c 69	9	4.1	579	4	BY797655	BY797655 BY797655
70	9	4.1	584	8	CV187969	CV187969 aam01-15m
c 71	9	4.1	585	9	DA541205	DA541205 DA541205
72	9	4.1	592	12	CG452822	CG452822 OG5EE68TV
73	9	4.1	595	13	CW292735	CW292735 104_772_1
c 74	9	4.1	601	2	BI075279	BI075279 IP1_18_D1
c 75	9	4.1	603	4	CA087764	CA087764 SCQSAM209
76	9	4.1	610	7	BB194492	BB194492 BB194492
77	9	4.1	610	11	BH488094	BH488094 BOGBX77TR

78	9	4.1	617	13	CZ102767
79	9	4.1	634	13	CW244996
80	9	4.1	653	13	CW292734
81	9	4.1	660	13	CW244997
82	9	4.1	663	5	CF809729
83	9	4.1	665	10	DR603821
84	9	4.1	671	9	DR008485
85	9	4.1	679	8	CO408614
86	9	4.1	680	5	CF810266
87	9	4.1	685	2	BI922485
88	9	4.1	692	7	BE299956
89	9	4.1	705	11	AZ306792
90	9	4.1	709	5	CD881972
91	9	4.1	709	8	CN736229
92	9	4.1	710	13	CW744074
93	9	4.1	713	12	BZ715412
94	9	4.1	731	5	CF934165
95	9	4.1	731	9	DR009499
96	9	4.1	734	13	CL419793
97	9	4.1	736	10	DR608205
98	9	4.1	750	12	CG395353
99	9	4.1	753	12	CG875642
100	9	4.1	758	1	AJ701803
101	9	4.1	765	7	BE298508
102	9	4.1	770	4	CB670542
103	9	4.1	770	7	BE967024
104	9	4.1	773	2	BI524152
105	9	4.1	773	13	CZ119478
106	9	4.1	784	10	DR666009
107	9	4.1	785	10	DR657389
108	9	4.1	787	10	DR657388
109	9	4.1	788	9	DR008334
110	9	4.1	790	10	DR606214
111	9	4.1	794	2	BM007478
112	9	4.1	794	4	CB899783
113	9	4.1	796	2	BM397339
114	9	4.1	801	10	DR608285
115	9	4.1	817	10	DR666062
116	9	4.1	818	10	DR609392
117	9	4.1	820	10	DR674628
118	9	4.1	822	4	BX835464
119	9	4.1	825	12	CG385421
120	9	4.1	831	14	CT469425
121	9	4.1	832	10	DR609454
122	9	4.1	839	12	CC713587
123	9	4.1	843	11	BZ473305
124	9	4.1	845	5	CD516665
125	9	4.1	847	12	CG681185
126	9	4.1	860	3	BQ707955
127	9	4.1	866	10	DR654811
128	9	4.1	867	10	DR667217
129	9	4.1	870	3	BQ712265
130	9	4.1	873	10	DR637740
131	9	4.1	881	14	AG878338
132	9	4.1	891	10	DR666877
133	9	4.1	900	10	DR641560
134	9	4.1	903	12	CC653054
135	9	4.1	909	3	BQ710906
136	9	4.1	910	10	DR674724
137	9	4.1	911	10	DR667216
138	9	4.1	915	10	DR639416
139	9	4.1	918	14	CNS01EWE
140	9	4.1	927	12	CC713597
141	9	4.1	928	12	CG396548
142	9	4.1	933	10	DR674629
143	9	4.1	933	13	CZ252347
144	9	4.1	936	10	DR666061
145	9	4.1	942	10	DR654810
146	9	4.1	946	10	DR666010
147	9	4.1	947	14	CNS02T8S
148	9	4.1	951	10	DR666876
149	9	4.1	953	10	DR639599
150	9	4.1	963	10	DR666762

CZ102767 OM__Ba011
CW244996 104_706_1
CW292734 104_772_1
CW244997 104_706_1
CF809729 Lr_LC1ED_
DR603821 EST993949
DR008485 Lr_Cu2CF_
CO408614 Lr_CHECF_
CF810266 Lr_LC1ED_
BI922485 EST542389
BE299956 600944512
AZ306792 1M0008F02
CD881972 F1.104O09
CN736229 26RDBNT_U
CW744074 MARC_9128
BZ715412 HSC_00419
CF934165 TrEST-B01
DR009499 Lr_Cu2CF_
CL419793 ZMMBBb042
DR608205 EST998333
CG395353 ZMMBBc001
CG875642 ZMMBBc028
AJ701803 AJ701803
BE298508 601119636
CB670542 OSJNEe03K
BE967024 601660755
BI524152 603051564
CZ119478 OA_BBa000
DR666009 EST105612
DR657389 EST104750
DR657388 EST104750
DR008334 Lr_Cu2CF_
DR606214 EST996342
BM007478 603616745
CB899783 tric019xp
BM397339 5009-0-31
DR608285 EST998413
DR666062 EST105617
DR609392 EST999520
DR674628 EST106474
BX835464 BX835464
CG385421 OGYBY32TV
CT469425 Sus scrof
DR609454 EST999582
CC713587 OGUBP27TH
BZ473305 BONRZ55TR
CD516665 AGENCOURT
CG681185 ZMMBBc014
BQ707955 AGENCOURT
DR654811 EST104492
DR667217 EST105733
BQ712265 AGENCOURT
DR637740 EST102836
AG878338 Oryza sat
DR666877 EST105699
DR641560 EST103218
CC653054 OGVBX05TH
BQ710906 AGENCOURT
DR674724 EST106484
DR667216 EST105733
DR639416 EST103004
AL141087 Anopheles
CC713597 OGUBP27TV
CG396548 ZMMBBc001
DR674629 EST106474
CZ252347 LQCYI32TV
DR666061 EST105617
DR654810 EST104492
DR666010 EST105612
AL212869 Tetraodon
DR666876 EST105699
DR639599 EST103022
DR666762 EST105687

c 151	9	4.1	965	10	DR674723
c 152	9	4.1	991	14	CNS02BA8
153	9	4.1	1006	10	DR666763
c 154	9	4.1	1054	4	BX444783
155	9	4.1	1068	12	CL053527
156	9	4.1	1075	12	CL058505
c 157	9	4.1	1083	12	CL092806
158	9	4.1	1095	12	CL125672
c 159	9	4.1	1145	4	BX418555
c 160	9	4.1	1215	8	CV123647
c 161	9	4.1	1470	6	CR607863
c 162	9	4.1	1762	10	DV790639
c 163	9	4.1	2160	6	CR590609
c 164	9	4.1	2192	14	DQ041206
165	9	4.1	2828	6	AK079629
c 166	9	4.1	3200	6	BC035570
c 167	8	3.6	108	5	CK549365
c 168	8	3.6	131	11	AZ818875
c 169	8	3.6	136	1	AV088513
170	8	3.6	142	10	DR675925
171	8	3.6	144	2	BF751315
c 172	8	3.6	146	2	BG893550
173	8	3.6	147	14	AG218395
c 174	8	3.6	154	13	CZ613100
c 175	8	3.6	156	12	CE383256
176	8	3.6	172	10	DY242424
c 177	8	3.6	181	1	AV093643
178	8	3.6	183	5	CK931475
c 179	8	3.6	191	1	AI996576
180	8	3.6	196	8	CO377743
c 181	8	3.6	197	8	CV324549
182	8	3.6	198	13	CL228836
183	8	3.6	200	13	CL227798
184	8	3.6	201	7	BB588026
185	8	3.6	204	5	CF773702
c 186	8	3.6	207	12	CE180687
c 187	8	3.6	208	5	CF674635
c 188	8	3.6	208	12	CE014974
189	8	3.6	208	12	CG875289
190	8	3.6	212	7	BE398188
c 191	8	3.6	212	12	BZ635858
192	8	3.6	213	12	CL198575
193	8	3.6	214	8	CO376858
194	8	3.6	214	12	CG863507
195	8	3.6	216	5	CD957154
c 196	8	3.6	218	1	AI523278
197	8	3.6	218	13	CZ419338
198	8	3.6	219	12	CG832793
199	8	3.6	222	13	CL230869
200	8	3.6	224	13	CL229028

DR674723 EST106484
AL189593 Tetraodon
DR666763 EST105688
BX444783 BX444783
CL053527 CH216-77N
CL058505 CH216-88C
CL092806 ISB1-22J9
CL125672 ISB1-87H3
BX418555 BX418555
CV123647 OSTF30015
CR607863 full-leng
DV790639 Hw_Liver_
CR590609 full-leng
DQ041206 Homo sapi
AK079629 Mus muscu
BC035570 Homo sapi
CK549365 swkz0_005
AZ818875 2M0089I12
AV088513 AV088513
DR675925 EST106604
BF751315 RC3-BN042
BG893550 kt11a08.y
AG218395 Drosophil
CZ613100 OM__Ba014
CE383256 tigr-gss-
DY242424 CSTAP1D02
AV093643 AV093643
CK931475 p5rmgc_00
AI996576 701667517
CO377743 tah58g03.
CV324549 CM4-ET019
CL228836 ZMMBBc005
CL227798 ZMMBBc002
BB588026 BB588026
CF773702 AG_FSL_21
CE180687 tigr-gss-
CF674635 tac84f07.
CE014974 tigr-gss-
CG875289 ZMMBBc028
BE398188 WHE0002.H
BZ635858 OGAOJ54TC
CL198575 ZMMBBc025
CO376858 tah44b04.
CG863507 ZMMBBc027
CD957154 SCH_190 G
AI523278 ar71b08.x
CZ419338 1015041 R
CG832793 ZMMBBc012
CL230869 ZMMBBc011
CL229028 ZMMBBc014

ALIGNMENTS

RESULT 1
DQ033872
LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

```
JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
 PUBMED   15869325
FERENCE   2  (bases 1 to 762)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
          Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
          White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
ITLE      Direct Submission
JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
MMENT     This sequence was made by sequencing genomic exons and ordering
          them based on alignment.  Translation starts at the beginning of
          alignment.
ATURES              Location/Qualifiers
   source           1. .762
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /chromosome="3"
   gene             <1. .>762
                    /gene="IL12A"
                    /locus_tag="HC3464"
IGIN

ignment Scores:
ed. No.:              5.05e-18        Length:         762
ore:                  29.00           Matches:        29
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            13.1%           Indels:         0
:                     14              Gaps:           0

-10-821-670A-33 (1-222) x DQ033872 (1-762)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 2
013916
CUS       CD013916                  863 bp    mRNA    linear   EST 21-OCT-2003
FINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
CESSION   CD013916
RSION     CD013916.1  GI:37777446
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 863)
AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
          Au-Young,J. and Stuve,L.L.
TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
          drug target genes
JOURNAL   Genomics 83 (4), 566-571 (2004)
 PUBMED   15028279
MMENT     Contact: Jin, P.
          Incyte Corporation
          3160 Porter Drive, Palo Alto, CA 94304, USA
          Tel: 650 621 8639
          Fax: 650 621 8965
          Email: pjin@incyte.com.
ATURES              Location/Qualifiers
   source           1. .863
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone_lib="Single gene library"
                    /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                    using gene-specific primers flanking the open-reading
                    frame. PCR products were subcloned into pDrive Cloning
                    Vector and sequenced completely using M13 forward and
                    reverse primers. Sequencing gaps were closed by
                    re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              5.72e-18        Length:         863
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-33 (1-222) x CD013916 (1-863)

Qy          184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          632 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 691

Qy          204 AlaPheArgIleArgAlaValThrIle 212
                ||||||||||||||||||||||||||
Db          692 GCTTTCAGAATTCGGGCAGTGACTATT 718

RESULT 3
CD013914
LOCUS       CD013914                  935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES              Location/Qualifiers
     source           1. .935
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone_lib="Single gene library"
                      /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                      using gene-specific primers flanking the open-reading
                      frame. PCR products were subcloned into pDrive Cloning
                      Vector and sequenced completely using M13 forward and
                      reverse primers. Sequencing gaps were closed by
                      re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              6.2e-18         Length:         935
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-33 (1-222) x CD013914 (1-935)
```

```
       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       704 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 763

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
       764 GCTTTCAGAATTCGGGCAGTGACTATT 790

3ULT 4
)13915
:US       CD013915                1136 bp    mRNA    linear   EST 21-OCT-2003
:INITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
:ESSION   CD013915
:SION     CD013915.1  GI:37777445
:WORDS    EST.
)RCE      Homo sapiens (human)
:RGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
:ERENCE   1  (bases 1 to 1136)
:UTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
          Au-Young,J. and Stuve,L.L.
:ITLE     PCR isolation and cloning of novel splice variant mRNAs from known
          drug target genes
)URNAL    Genomics 83 (4), 566-571 (2004)
 PUBMED   15028279
:MENT     Contact: Jin, P.
          Incyte Corporation
          3160 Porter Drive, Palo Alto, CA 94304, USA
          Tel: 650 621 8639
          Fax: 650 621 8965
          Email: pjin@incyte.com.
:TURES              Location/Qualifiers
   source           1. .1136
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone_lib="Single gene library"
                    /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                    using gene-specific primers flanking the open-reading
                    frame. PCR products were subcloned into pDrive Cloning
                    Vector and sequenced completely using M13 forward and
                    reverse primers. Sequencing gaps were closed by
                    re-sequencig using primers flanking the gapped areas."
:GIN

ignment Scores:
ed. No.:              7.53e-18       Length:         1136
)re:                  29.00          Matches:        29
:cent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            13.1%          Indels:         0
:                     4              Gaps:           0

-10-821-670A-33 (1-222) x CD013915 (1-1136)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       905 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 964

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
       965 GCTTTCAGAATTCGGGCAGTGACTATT 991

3ULT 5
)35571
:US       BC035571                1938 bp    mRNA    linear   HTC 04-MAR-2003
:INITION  Homo sapiens, clone IMAGE:5240216, mRNA.
:ESSION   BC035571
:SION     BC035571.1  GI:23958681
:WORDS    HTC.
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES              Location/Qualifiers
     source           1. .1938
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5240216"
                      /tissue_type="Brain, fetal, whole pooled"
                      /clone_lib="NIH_MGC_121"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:              1.29e-17       Length:         1938
Score:                  29.00          Matches:        29
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            13.1%          Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-33 (1-222) x BC035571 (1-1938)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1385

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||||
Db       1386 GCTTTCAGAATTCGGGCAGTGACTATT 1412

RESULT 6
DQ033873
LOCUS       DQ033873                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
```

```
CESSION   DQ033873
RSION     DQ033873.1  GI:66885082
YWORDS    GSS.
URCE      Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Pan.
FERENCE   1  (bases 1 to 762)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
          Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
          White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
          Chimpanzees
JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
 PUBMED   15869325
FERENCE   2  (bases 1 to 762)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
          Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
          White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
MMENT     This sequence was made by sequencing genomic exons and ordering
          them based on alignment.  Translation starts at the beginning of
          alignment.
ATURES              Location/Qualifiers
   source           1. .762
                    /organism="Pan troglodytes"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9598"
   gene             <1. .>762
                    /gene="IL12A"
                    /locus_tag="HC3464"
IGIN

ignment Scores:
ed. No.:              5.03e-17       Length:         762
ore:                  28.00          Matches:        28
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            12.6%          Indels:         0
:                     14             Gaps:           0

-10-821-670A-33 (1-222) x DQ033873 (1-762)

         67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        292 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 351

         87 AlaCysLeuProLeuGluLeuThr 94
            |||||||||||||||||||||||
        352 GCCTGTTTACCATTGGAATTAACC 375

SULT 7
702253
CUS       BG702253                812 bp    mRNA    linear   EST 07-MAY-2001
FINITION  602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
          mRNA sequence.
CESSION   BG702253
RSION     BG702253.1  GI:13973409
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 812)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
MMENT     Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
           cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
          Toshiyuki and Piero Carninci (RIKEN)
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM10714  row: e  column: 15
          High quality sequence stop: 804.
FEATURES            Location/Qualifiers
     source         1. .812
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:4816118"
                    /tissue_type="hippocampus"
                    /lab_host="DH10B"
                    /clone_lib="NIH_MGC_95"
                    /note="Organ: brain; Vector: pBluescriptR (modified
                    pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                    (gtcgag); Oligo-dT primed using primer
                    5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                    insert size 2.5 kb and normalized to ROT 5. This is a
                    primary library enriched for  full-length clones and
                    constructed using the Cap-trapper method (Carninci, in
                    preparation).  Library constructed by M. Brownstein
                    (NIMH/NHGRI, National Institutes of Health).  Note: this
                    is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              5.37e-17       Length:         812
Score:                  28.00          Matches:        28
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            12.6%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x BG702253 (1-812)

Qy         67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 665

Qy         87 AlaCysLeuProLeuGluLeuThr 94
              |||||||||||||||||||||||
Db        666 GCCTGTTTACCATTGGAATTAACC 689

RESULT 8
BI523569
LOCUS       BI523569                832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11605 row: 1 column: 09
High quality sequence start: 23
High quality sequence stop: 821.

```
ATURES             Location/Qualifiers
   source          1. .832
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:5240216"
                   /lab_host="DH10B"
                   /clone_lib="NIH_MGC_121"
                   /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                   Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                   fetal brains, female age 20 weeks, female age 24 weeks,
                   and male age 26 weeks. Library is oligo-dT primed and
                   directionally cloned (EcoRV site is destroyed upon
                   cloning). Average insert size 1.7 kb, insert size range
                   0.7-3.5 kb. Library is normalized and enriched for
                   full-length clones and was constructed by C. Gruber
                   (Invitrogen). Research Genetics tracking code 017. Note:
                   this is a NIH_MGC Library."
IGIN

ignment Scores:
ed. No.:              5.5e-17        Length:        832
ore:                  28.00          Matches:       28
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            12.6%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x BI523569 (1-832)

        67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       511 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 570

        87 AlaCysLeuProLeuGluLeuThr 94
           |||||||||||||||||||||||
       571 GCCTGTTTACCATTGGAATTAACC 594

SULT 9
260963
CUS       BP260963                581 bp    mRNA    linear   EST 16-SEP-2004
FINITION  BP260963 Sugano cDNA library, small intestine Homo sapiens cDNA
          clone HSI02082, mRNA sequence.
CESSION   BP260963
RSION     BP260963.1  GI:52176194
YWORDS    EST.
URCE      Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 581)
UTHORS    Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
          Mizushima-Sugano,J., Nakai,K. and Sugano,S.
ITLE      Sequence comparison of human and mouse genes reveals a homologous
          block structure in the promoter regions
OURNAL    Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED   15342556
MMENT     Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Tel: 81-3-5449-5343
          Fax: 81-3-5449-5416
          Email: ysuzuki@hgc.jp.
ATURES             Location/Qualifiers
   source          1. .581
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="HSI02082"
                   /tissue_type="small intestine"
                   /clone_lib="Sugano cDNA library, small intestine"
ORIGIN

Alignment Scores:
Pred. No.:              3.8e-13        Length:        581
Score:                  24.00          Matches:       24
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.8%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-33 (1-222) x BP260963 (1-581)

Qy         67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 567

Qy         87 AlaCysLeuPro 90
              ||||||||||||
Db        568 GCCTGTTTACCA 579

RESULT 10
CT080894
LOCUS       CT080894                777 bp    DNA     linear   GSS 01-NOV-2005
DEFINITION  Sus scrofa genomic clone PigE-253A7, genomic survey sequence.
ACCESSION   CT080894
VERSION     CT080894.1  GI:78647963
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 253A7. 253A7 is
            part of the PigEBAC BAC Library created by Roslin Institute/RFCGR.
            Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="PigE-253A7"
                     /tissue_type="Blood cells"
                     /note="vector pBeloBAC11
                     sex male"
ORIGIN

Alignment Scores:
Pred. No.:              5.08e-13       Length:        777
Score:                  24.00          Matches:       24
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.8%          Indels:        0
DB:                     14             Gaps:          0

US-10-821-670A-33 (1-222) x CT080894 (1-777)

Qy        143 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTGGATCAGAACATG 668

Qy        163 LeuThrAlaIle 166
              ||||||||||||
Db        669 CTCACAGCCATC 680
```

669 CTGACAGCTATT 680

SULT 11
159257
CUS CE159257 592 bp DNA linear GSS 25-SEP-2003
FINITION tigr-gss-dog-17000371408491 Dog Library Canis familiaris genomic, genomic survey sequence.
CESSION CE159257
RSION CE159257.1 GI:35287296
YWORDS GSS.
URCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
FERENCE 1 (bases 1 to 592)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
MMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
ATURES Location/Qualifiers
source 1. .592
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from peripheral blood"
IGIN

lignment Scores:

ed. No.:	3.84e-10	Length:	592
ore:	21.00	Matches:	21
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	9.5%	Indels:	0
:	12	Gaps:	0

-10-821-670A-33 (1-222) x CE159257 (1-592)

```
Qy         75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 GAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACC 110

Qy         95 Met 95
              |||
Db        111 ATG 113
```

SULT 12
820622/c
CUS AJ820622 778 bp mRNA linear EST 12-MAY-2005
FINITION AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
CESSION AJ820622
RSION AJ820622.1 GI:51888098
YWORDS EST.
URCE Bos sp.
ORGANISM Bos sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
FERENCE 1 (bases 1 to 778)
AUTHORS McGuire,K. and Glass,E.J.
TITLE The expanding role of microarrays in the investigation of macrophage responses to pathogens
JOURNAL Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT Contact: McGuire K
Genomics and Genetics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site 1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata.
FEATURES Location/Qualifiers
source 1. .778
/organism="Bos sp."
/mol_type="mRNA"
/db_xref="taxon:29061"
/clone="C0006020h12"
/tissue_type="blood"
/cell_type="bovine monocyte"
/clone_lib="KN206"
/note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost); Site_2: NotI; Normalised library constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata"
ORIGIN

Alignment Scores:

Pred. No.:	5.05e-10	Length:	778
Score:	21.00	Matches:	21
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	9.5%	Indels:	0
DB:	1	Gaps:	0

US-10-821-670A-33 (1-222) x AJ820622 (1-778)

```
Qy        143 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 GCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAAATCTTTCTAGACCAGAACATG 697

Qy        163 Leu 163
              |||
Db        696 CTG 694
```

RESULT 13
BM257856
LOCUS BM257856 342 bp mRNA linear EST 17-DEC-2001
DEFINITION 521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM257856
VERSION BM257856.1 GI:17893455
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 342)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

```
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called and alt_trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -minmatch 12 options.
          PCR PRimers
          FORWARD: AGGAAACAGCTATGACCAT
          BACKWARD: GTTTTCCCAGTCACGACG
          Plate: 125  row: E  column: 18
          Seq primer: ATTTAGGTGACACTATAG.
ATURES              Location/Qualifiers
   source           1. .342
                    /organism="Bos taurus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9913"
                    /tissue_type="pooled"
                    /lab_host="DH10B"
                    /clone_lib="MARC 3BOV"
                    /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                    Library made from pooled tissue from marrow, alveolar
                    macrophage, ovary, fetal semitendonosus muscle, and fetal
                    longissimus muscle."
IGIN

ignment Scores:
ed. No.:              2.21e-09       Length:         342
ore:                  20.00          Matches:        20
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            9.0%           Indels:         0
:                     2              Gaps:           0

10-821-670A-33 (1-222) x BM257856 (1-342)

         52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        282 AGCAACACGCTACAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 341

SULT 14
537236
US        BX537236                344 bp    DNA     linear   GSS 05-JUN-2003
FINITION  INRA porcine BAC library, clone 0849A01 BAC end sequence (Uni M13),
          genomic survey sequence.
CESSION   BX537236
RSION     BX537236.1  GI:31455351
YWORDS    GSS; genome survey sequence.
URCE      Sus scrofa (pig)
RGANISM   Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
          Sus.
FERENCE   1
AUTHORS   Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
          Chardon,P.
ITLE      Construction of a swine BAC library: application to the
          characterization and mapping of porcine type C endoviral elements
JOURNAL   Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
 PUBMED   10449899
FERENCE   2  (bases 1 to 344)
AUTHORS   Robic,A.
ITLE      Direct Submission
JOURNAL   Submitted (05-JUN-2003) Robic A., INRA, Laboratoire de Genetique
          Cellulaire, chemin de Borde rouge, BP27, Auzeville, 31626, FRANCE
          Phone : 05 61 28 51 15 Fax : 05 61 28 53 08 Email :
          arobic@toulouse.inra.fr
ATURES              Location/Qualifiers
   source           1. .344
                    /organism="Sus scrofa"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9823"
                    /clone="0849A01"
                    /note="library Rogel gaillard et al 1999, clone 0849A01
                    Clone distribution : AGENAE Resource center. Francois
                    PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA
                    Radiobiologie et Etude du genome (LREG), Domaine de
                    Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
ORIGIN

Alignment Scores:
Pred. No.:              2.23e-09       Length:         344
Score:                  20.00          Matches:        20
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            9.0%           Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-33 (1-222) x BX537236 (1-344)

Qy        147 LysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIle 166
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTGGATCAGAACATGCTGACAGCTATT 60

RESULT 15
BI824638
LOCUS       BI824638                447 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
            mRNA sequence.
ACCESSION   BI824638
VERSION     BI824638.1  GI:15936188
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11435  row: o  column: 19
            High quality sequence start: 3
            High quality sequence stop: 445.
FEATURES            Location/Qualifiers
     source         1. .447
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5175018"
                    /lab_host="DH10B"
                    /clone_lib="NIH_MGC_115"
                    /note="Organ: pooled brain, lung, testis; Vector:
                    pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                    source anonymous pool of 6 male brains, age range 23-27; 1
                    male lung, age 27; and 1 male testis, age 69.  Library is
                    oligo-dT primed and directionally cloned (EcoRV site is
                    destroyed upon  cloning).  Average insert size 1.8 kb,
                    insert size range 1-3 kb. Library is normalized and
                    enriched for full-length clones and was  constructed by C.
                    Gruber (Invitrogen).  Research Genetics tracking  code
                    021. Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              2.88e-07       Length:         447
Score:                  18.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
```

```
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            8.1%          Indels:        0
:                     2             Gaps:          0

-10-821-670A-33 (1-222) x BI824638 (1-447)

        195 LysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATT 54

SULT 16
523344/c
CUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
FINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
          mRNA sequence.
CESSION   BI523344
RSION     BI523344.1  GI:15348136
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 1099)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
MMENT     Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11605  row: l  column: 09
          High quality sequence start: 40
          High quality sequence stop: 727.
ATURES              Location/Qualifiers
   source           1. .1099
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5240216"
                    /lab_host="DH10B"
                    /clone_lib="NIH_MGC_121"
                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                    fetal brains, female age 20 weeks, female age 24 weeks,
                    and male age 26 weeks.  Library is oligo-dT primed and
                    directionally cloned (EcoRV site is destroyed  upon
                    cloning).  Average insert size 1.7 kb, insert size range
                    0.7-3.5 kb.  Library is normalized and enriched for
                    full-length clones and  was constructed by C. Gruber
                    (Invitrogen).  Research Genetics  tracking code 017. Note:
                    this is a NIH_MGC Library."
IGIN

ignment Scores:
ed. No.:              7.08e-06      Length:        1099
ore:                  17.00         Matches:       17
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            7.7%          Indels:        0
:                     2             Gaps:          0

-10-821-670A-33 (1-222) x BI523344 (1-1099)

        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
        522 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATT 472

RESULT 17
CB168830/c
LOCUS       CB168830                777 bp    mRNA    linear   EST 30-JAN-2003
DEFINITION  CWI602769160.R1 CSEQFXL41 testes Bos taurus cDNA, mRNA sequence.
ACCESSION   CB168830
VERSION     CB168830.1  GI:28154956
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Bovine ESTs (Adelson and Gill)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES              Location/Qualifiers
     source           1. .777
                      /organism="Bos taurus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /tissue_type="testes"
                      /clone_lib="CSEQFXL41 testes"
                      /note="Organ: testes; Vector: pBluescript SK+; Site_1:
                      NotI; Site_2: EcoRI; sequence 5' of the insert
                      (5'-NNN. . .NNNinsert)
                      GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                      the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                      non-normalized library, sequenced 3' with M13R primer."
ORIGIN

Alignment Scores:
Pred. No.:            4.99e-05      Length:        777
Score:                16.00         Matches:       16
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          7.2%          Indels:        0
DB:                   4             Gaps:          0

US-10-821-670A-33 (1-222) x CB168830 (1-777)

Qy        197 LysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 AAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATC 572

RESULT 18
AI332701/c
LOCUS       AI332701                528 bp    mRNA    linear   EST 13-FEB-1999
DEFINITION  qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948
            3' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   AI332701
VERSION     AI332701.1  GI:4069260
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
          Email: cgapbs-r@mail.nih.gov
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Insert Length: 1469    Std Error: 0.00
          Seq primer: -40UP from Gibco
          High quality sequence stop: 451.
ATURES              Location/Qualifiers
   source           1. .528
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:1932948"
                    /tissue_type="Pooled human melanocyte, fetal heart, and
                    pregnant uterus"
                    /lab_host="DH10B"
                    /clone_lib="Soares_NhHMPu_S1"
                    /note="Organ: mixed (see below); Vector: pT7T3D-PacI;
                    Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid
                    DNA from three normalized libraries (melanocyte 2NbHM,
                    pregnant uterus NbHPU, and fetal heart NbHH19W) were
                    mixed, and ss circles were made in vitro. Following HAP
                    purification, this DNA was used as tracer in a subtractive
                    hybridization reaction. The driver was PCR-amplified cDNAs
                    from pools of 5,000 clones made from the same 3 libraries.
                    The pools consisted of I.M.A.G.E. clones 260232-265223,
                    340488-345479, and 484488-489479."
IGIN

ignment Scores:
ed. No.:              0.0336          Length:         528
ore:                  13.00           Matches:        13
cent Similarity:      100.0%          Conservative:   0
t Local Similarity:   100.0%          Mismatches:     0
ery Match:            5.9%            Indels:         0
:                     1               Gaps:           0

-10-821-670A-33 (1-222) x AI332701 (1-528)

        200 IleLeuLeuHisAlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||||||||||||||||
        528 ATACTTCTCCATGCTTTCAGAATTCGGGCAGTGACTATT 490

SULT 19
)07201
CUS         DR007201                463 bp    mRNA    linear   EST 17-MAY-2005
FINITION    TC124111 Human spleen, large insert, pCMV expression library Homo
            sapiens cDNA clone TC124111 5' similar to Homo sapiens interleukin
            12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte
            maturation factor 1, p35) (IL12A), mRNA sequence.
CESSION     DR007201
SION        DR007201.1  GI:66267074
WORDS       EST.
URCE        Homo sapiens (human)
RGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
FERENCE     1  (bases 1 to 463)
AUTHORS     Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
            Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
            Zhang,X., Jay,G. and He,W.
TITLE       High-throughput cloning of full-length human cDNAs directly from
            cDNA libraries optimized for large and rare transcripts
JOURNAL     Unpublished (2005)
MMENT       Contact: Kovacs, KF
            High Throughput cDNA Cloning
            OriGene Technologies, Inc. ( www.origene.com )
            6 Taft Court, Suite 100, Rockville, MD 20850, USA
            Tel: 301 340 3188
            Fax: 301 340 8606
            Email: cDNA@origene.com
            This EST submission is part of an on-going human full-length
            cloning project at OriGene Technologies, Inc.
            Please contact OriGene for access.
            OriGene Technologies, Inc.
            6 Taft Ct. Suite 100
            Rockville, MD 20850
            Tel: (301) 340-3188
            http://www.origene.com
            Seq primer: pCMV6 5prime forward vector primer, OriGene
            Technologies Inc.
FEATURES            Location/Qualifiers
     source         1. .463
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="TC124111"
                    /tissue_type="Spleen"
                    /clone_lib="Human spleen, large insert, pCMV expression
                    library"
                    /note="Organ: Spleen; Vector: pCMV6-XL4; Site_1: EcoR1;
                    Site_2: Xho1/Sal1 compatible end ligatio; Oligo-dT primed
                    reverse transcription optimized for large and GC rich mRNA
                    transcripts, cDNA size selection, optimized ligation for
                    large inserts into mammalian expression vector, random
                    clones selected for end sequence verification of
                    full-length genes"
ORIGIN

Alignment Scores:
Pred. No.:              2.93            Length:         463
Score:                  11.00           Matches:        11
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.0%            Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-33 (1-222) x DR007201 (1-463)

Qy          19 LeuAspHisLeuSerLeuAlaArgAsnLeuPro 29
               |||||||||||||||||||||||||||||||
Db         350 CTGGACCACCTTAGTTTGGCCAGAAACCTCCCC 382

RESULT 20
DA505380
LOCUS       DA505380                508 bp    mRNA    linear   EST 05-NOV-2005
DEFINITION  DA505380 FCBBF3 Homo sapiens cDNA clone FCBBF3020869 5', mRNA
            sequence.
ACCESSION   DA505380
VERSION     DA505380.1  GI:80794577
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
```

Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

ATURES Location/Qualifiers
source 1. .508
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FCBBF3020869"
/tissue_type="brain"
/dev_stage="fetal"
/clone_lib="FCBBF3"
/note="Vector: pME18SFL3"

IGIN

ignment Scores:

ed. No.:	3.22	Length:	508
ore:	11.00	Matches:	11
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	5.0%	Indels:	0
:	9	Gaps:	0

-10-821-670A-33 (1-222) x DA505380 (1-508)

```
         19 LeuAspHisLeuSerLeuAlaArgAsnLeuPro 29
            |||||||||||||||||||||||||||||||
       372 CTGGACCACCTCAGTTTGGCCAGAAACCTCCCC 404
```

SULT 21
261459
CUS BP261459 571 bp mRNA linear EST 16-SEP-2004
FINITION BP261459 Sugano cDNA library, small intestine Homo sapiens cDNA clone HSI03652, mRNA sequence.
CESSION BP261459
RSION BP261459.1 GI:52176690
YWORDS EST.
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
FERENCE 1 (bases 1 to 571)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
ITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
MMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5343
Fax: 81-3-5449-5416
Email: ysuzuki@hgc.jp.

ATURES Location/Qualifiers
source 1. .571
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSI03652"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

IGIN

ignment Scores:

ed. No.:	3.62	Length:	571
ore:	11.00	Matches:	11
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x BP261459 (1-571)

```
Qy         19 LeuAspHisLeuSerLeuAlaArgAsnLeuPro 29
              |||||||||||||||||||||||||||||||
Db        364 CTGGACCACCTCAGTTTGGCCAGAAACCTCCCC 396
```

RESULT 22
BF552757
LOCUS BF552757 373 bp mRNA linear EST 12-DEC-2000
DEFINITION UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION BF552757
VERSION BF552757.1 GI:11662487
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 373)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID= 1782759
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .373
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-iz-d-02-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-C0"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:

791-806, 1996)"
:GIN

ignment Scores:
ed. No.: 23.6 Length: 373
ore: 10.00 Matches: 10
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 4.5% Indels: 0
: 7 Gaps: 0

-10-821-670A-33 (1-222) x BF552757 (1-373)

129 SerIleTyrGluAspLeuLysMetTyrGln 138
||||||||||||||||||||||||||||
98 AGCATCTATGAGGACTTGAAGATGTACCAG 127

SULT 23
930939
:US DT930939 427 bp mRNA linear EST 20-SEP-2005
FINITION S13.1784 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
:ESSION DT930939
RSION DT930939.1 GI:75963455
/WORDS EST.
JRCE Mus musculus (house mouse)
:RGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE 1 (bases 1 to 427)
AUTHORS Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
Lemischka,I.R.
TITLE Diversification of Stem Cell Molecular Repertoire by Alternative
Splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2005) In press
MENT Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657
Fax: 609 258 1704
Email: pritsker@molbio.princeton.edu.
TURES Location/Qualifiers
source 1. .427
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic stem cells"
/cell_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/note="cDNA library was made from FACS-purified
hematopoietic stem cells"
IGIN

ignment Scores:
ed. No.: 27 Length: 427
ore: 10.00 Matches: 10
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 4.5% Indels: 0
: 10 Gaps: 0

-10-821-670A-33 (1-222) x DT930939 (1-427)

129 SerIleTyrGluAspLeuLysMetTyrGln 138
||||||||||||||||||||||||||||
382 AGCATCTATGAGGACTTGAAGATGTACCAG 411

SULT 24
913216
:US DT913216 456 bp mRNA linear EST 19-SEP-2005
FINITION S13.1426 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
:ESSION DT913216

VERSION DT913216.1 GI:75893697
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 456)
AUTHORS Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
Lemischka,I.R.
TITLE Diversification of Stem Cell Molecular Repertoire by Alternative
Splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657
Fax: 609 258 1704
Email: pritsker@molbio.princeton.edu.
FEATURES Location/Qualifiers
source 1. .456
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic stem cells"
/cell_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/note="cDNA library was made from FACS-purified
hematopoietic stem cells"
ORIGIN

Alignment Scores:
Pred. No.: 28.8 Length: 456
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
DB: 10 Gaps: 0

US-10-821-670A-33 (1-222) x DT913216 (1-456)

Qy 129 SerIleTyrGluAspLeuLysMetTyrGln 138
||||||||||||||||||||||||||||
Db 382 AGCATCTATGAGGACTTGAAGATGTACCAG 411

RESULT 25
BU699383
LOCUS BU699383 561 bp mRNA linear EST 09-OCT-2002
DEFINITION LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
sequence.
ACCESSION BU699383
VERSION BU699383.1 GI:23615967
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 561)
AUTHORS Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
TITLE The genetic program of hematopoietic stem cells
JOURNAL Science 288 (5471), 1635-1640 (2000)
PUBMED 10834841
COMMENT Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
Tel: 609 258 2838
Fax: 609 258 2759
Email: ilemischka@molbio.princeton.edu

These ESTs are derived from a subtracted cDNA library enriched for gene products expressed in day 14-14.5 fetal liver hematopoietic stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos
Seq primer: M13Reverse or T7.

ATURES Location/Qualifiers
source 1. .561
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic"
/cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos"
/dev_stage="Embryonic day 14-14.5"
/lab_host="DH10B"
/clone_lib="Hematopoietic Stem Cell Subtracted Library"
/note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site_2: Not I; Two directionally cloned cDNA libraries were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

:GIN

:.gnment Scores:

ed. No.:	35.5	Length:	561
ore:	10.00	Matches:	10
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	4.5%	Indels:	0
:	3	Gaps:	0

-10-821-670A-33 (1-222) x BU699383 (1-561)

```
       129 SerIleTyrGluAspLeuLysMetTyrGln 138
           ||||||||||||||||||||||||||||||
       299 AGCATCTATGAGGACTTGAAGATGTACCAG 328
```

SULT 26
698113
CUS BU698113 563 bp mRNA linear EST 09-OCT-2002
FINITION LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA sequence.
CESSION BU698113
RSION BU698113.1 GI:23610620
YWORDS EST.
URCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE 1 (bases 1 to 563)
AUTHORS Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A., Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
TITLE The genetic program of hematopoietic stem cells
JOURNAL Science 288 (5471), 1635-1640 (2000)
PUBMED 10834841
MMENT Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
Tel: 609 258 2838
Fax: 609 258 2759
Email: ilemischka@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for gene products expressed in day 14-14.5 fetal liver hematopoietic stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos
Seq primer: M13Reverse or T7.

FEATURES Location/Qualifiers
source 1. .563
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic"
/cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos"
/dev_stage="Embryonic day 14-14.5"
/lab_host="DH10B"
/clone_lib="Hematopoietic Stem Cell Subtracted Library"
/note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site_2: Not I; Two directionally cloned cDNA libraries were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

Alignment Scores:

Pred. No.:	35.6	Length:	563
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.5%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x BU698113 (1-563)

```
Qy        129 SerIleTyrGluAspLeuLysMetTyrGln 138
              ||||||||||||||||||||||||||||||
Db        315 AGCATCTATGAGGACTTGAAGATGTACCAG 344
```

RESULT 27
AI050362
LOCUS AI050362 589 bp mRNA linear EST 09-JUL-1998
DEFINITION ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35 subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION AI050362
VERSION AI050362.1 GI:3299479
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 589)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

```
          Email: mouseest@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          MGI:901688
          Seq primer: -28m13 rev2 ET from Amersham
          High quality sequence stop: 60.
ATURES              Location/Qualifiers
   source           1. .589
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:1379220"
                    /sex="male"
                    /tissue_type="Thymus"
                    /dev_stage="4 weeks"
                    /lab_host="DH10B"
                    /clone_lib="Soares_thymus_2NbMT"
                    /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                    1st strand cDNA was primed with a Not I - oligo(dT) primer
                    [5'
                    TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                    3']; double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Not I and cloned into the Not I
                    and Eco RI sites of the modified pT7T3 vector. RNA
                    provided by Dr. Bertrand Jordan. Library went through two
                    rounds of normalization, and was constructed by Bento
                    Soares and M.Fatima Bonaldo."
IGIN

ignment Scores:
ed. No.:                37.2            Length:         589
ore:                    10.00           Matches:        10
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              4.5%            Indels:         0
:                       1               Gaps:           0

-10-821-670A-33 (1-222) x AI050362 (1-589)

        129 SerIleTyrGluAspLeuLysMetTyrGln 138
            |||||||||||||||||||||||||||||
        324 AGCATCTATGAGGACTTGAAGATGTACCAG 353

SULT 28
729972/c
CUS         AZ729972                614 bp    DNA     linear   GSS 25-JAN-2001
FINITION    RPCI-24-117G9.TV RPCI-24 Mus musculus genomic clone RPCI-24-117G9,
            genomic survey sequence.
CESSION     AZ729972
RSION       AZ729972.1  GI:12488267
YWORDS      GSS.
URCE        Mus musculus (house mouse)
RGANISM     Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE     1  (bases 1 to 614)
AUTHORS     Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
TITLE       Mouse BAC End Sequences from Library RPCI-24
JOURNAL     Unpublished (1999)
MMENT       Other_GSSs: RPCI-24-117G9.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 117  row: G  column: 9
            Seq primer: T7
            Class: BAC ends.
FEATURES            Location/Qualifiers
     source         1. .614
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="RPCI-24-117G9"
                    /sex="Male"
                    /cell_type="Spleen/Brain"
                    /clone_lib="RPCI-24"
                    /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                    RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                    library was  cloned in the pTARBAC1 cloning vector at the
                    BamH1 sites using MboI  partially digested male C57BL/6J
                    DNA."
ORIGIN

Alignment Scores:
Pred. No.:              38.8            Length:         614
Score:                  10.00           Matches:        10
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.5%            Indels:         0
DB:                     11              Gaps:           0

US-10-821-670A-33 (1-222) x AZ729972 (1-614)

Qy          99 CysLeuAlaSerArgGluIleSerLeuIle 108
               ||||||||||||||||||||||||||||||
Db         350 TGTTTAGCTTCTAGAGAAATTAGTCTCATC 321

RESULT 29
CJ137697
LOCUS       CJ137697                692 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ137697 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            thymus 3 days neonate Mus musculus cDNA clone A630064E02 5', mRNA
            sequence.
ACCESSION   CJ137697
VERSION     CJ137697.1  GI:76238025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Dr. John Todd (
            Dept. of Medical Genetics Wellcome Trust Centre for Molecular
            Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes
            Hospital Cambridge ) whose assistance we gratefully acknowledge.
```

Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.

ATURES Location/Qualifiers
source 1. .692
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="A630064E02"
/tissue_type="thymus"
/dev_stage="3 days neonate"
/clone_lib="RIKEN full-length enriched mouse cDNA library, C57BL/6J thymus 3 days neonate"

IGIN

ignment Scores:
ed. No.: 43.8 Length: 692
ore: 10.00 Matches: 10
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 4.5% Indels: 0
: 5 Gaps: 0

-10-821-670A-33 (1-222) x CJ137697 (1-692)

129 SerIleTyrGluAspLeuLysMetTyrGln 138
||||||||||||||||||||||||||||
518 AGCATCTATGAGGACTTGAAGATGTACCAG 547

SULT 30
271875/c
CUS CZ271875 941 bp DNA linear GSS 14-MAR-2005
FINITION ZMMBF0051D18f ZMMBF Zea mays genomic clone ZMMBF0051D18 5', genomic survey sequence.
CESSION CZ271875
RSION CZ271875.1 GI:61108687
YWORDS GSS.
URCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
FERENCE 1 (bases 1 to 941)
AUTHORS Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,G. and Messing,J.
ITLE Construction, Sequencing and Characterization of a Fosmid Library of the B73 Maize Genome
JOURNAL Unpublished (2005)
MMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: Fos_F
Class: fosmid ends.

ATURES Location/Qualifiers
source 1. .941
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBF0051D18"
/lab_host="EPI100-T1"
/clone_lib="ZMMBF"
/note="Vector: pEpiFOS-5; Site_1: Eco72I"

IGIN

ignment Scores:
ed. No.: 59.6 Length: 941
ore: 10.00 Matches: 10

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
DB: 13 Gaps: 0

US-10-821-670A-33 (1-222) x CZ271875 (1-941)

Qy 82 ThrSerThrValGluAlaCysLeuProLeu 91
||||||||||||||||||||||||||||
Db 935 ACATCTACTGTTGAAGCATGTTTGCCATTG 906

RESULT 31
AK153729
LOCUS AK153729 1299 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630064E02 product:interleukin 12a, full insert sequence.
ACCESSION AK153729
VERSION AK153729.1 GI:74148962
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851
FERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
FERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 1299)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES	Location/Qualifiers
source	1. .1299
	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="C57BL/6J"
	/db_xref="FANTOM_DB:A630064E02"
	/db_xref="taxon:10090"
	/clone="A630064E02"
	/tissue_type="thymus"
	/clone_lib="RIKEN full-length enriched mouse cDNA library"
	/dev_stage="3 days neonate"
misc_feature	1. .1299
	/note="interleukin 12a (MGD|MGI:96539 GB|NM_008351, evidence: BLASTN, 100%, match=776) putative"

ORIGIN

Alignment Scores:

Pred. No.:	82.3	Length:	1299
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.5%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x AK153729 (1-1299)

```
Qy        129 SerIleTyrGluAspLeuLysMetTyrGln 138
              |||||||||||||||||||||||||||||
Db        518 AGCATCTATGAGGACTTGAAGATGTACCAG 547
```

RESULT 32
BX655139
LOCUS BX655139 87 bp DNA linear GSS 04-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-587A10-021350,

genomic survey sequence.
CESSION BX655139
RSION BX655139.1 GI:37611527
YWORDS GSS.
URCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
FERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
ITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
FERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
ITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
FERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
ITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
FERENCE 4 (bases 1 to 87)
AUTHORS Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
ITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
MENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F11C18. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
ATURES Location/Qualifiers
source 1. .87
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-587A10-021350"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGABI1 (GenBank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
GIN

gnment Scores:

ed. No.:	54.6	Length:	87
ore:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	4.1%	Indels:	0
:	14	Gaps:	0

-10-821-670A-33 (1-222) x BX655139 (1-87)

```
11 ThrIleLeuValLeuLeuAsnHisLeu 19
   ||||||||||||||||||||||||||||
53 ACTATCCTGGTTTTACTAAATCATTTA 79
```

RESULT 33
BY368866
LOCUS BY368866 192 bp mRNA linear EST 12-DEC-2002
DEFINITION BY368866 RIKEN full-length enriched, 6 days neonate spleen Mus musculus cDNA clone F430208H13 3', mRNA sequence.
ACCESSION BY368866
VERSION BY368866.1 GI:26598354
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 192)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

ATURES Location/Qualifiers
source 1. .192
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F430208H13"
/tissue_type="spleen"
/dev_stage="6 days neonate"
/clone_lib="RIKEN full-length enriched, 6 days neonate spleen"

IGIN

ignment Scores:

ed. No.:	121	Length:	192
ore:	9.00	Matches:	9
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	4.1%	Indels:	0
:	4	Gaps:	0

-10-821-670A-33 (1-222) x BY368866 (1-192)

195 LysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||
161 AAAATAAAGTTGTGTATTCTATTACAT 187

SULT 34
366007/c
CUS BF366007 194 bp mRNA linear EST 24-NOV-2000
FINITION PM4-NT0073-230500-002-a01 NT0073 Homo sapiens cDNA, mRNA sequence.
CESSION BF366007
RSION BF366007.1 GI:11328032
/WORDS EST.
URCE Homo sapiens (human)
RGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
FERENCE 1 (bases 1 to 194)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
ITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
OURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
MENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM4&t2=PM4-NT0073-230500-002-a01&t3=2000-05-23&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 30.

ATURES Location/Qualifiers
source 1. .194
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0073"
/note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	122	Length:	194
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x BF366007 (1-194)

Qy 29 ProThrProThrProSerProGlyMet 37
|||||||||||||||||||||||||||
Db 93 CCGACACCAACTCCAAGTCCAGGGATG 67

RESULT 35
DV345207/c
LOCUS DV345207 234 bp mRNA linear EST 17-OCT-2005
DEFINITION NABWE87TR Aedes aegypti infected with Brugia Malayi Aedes aegypti cDNA clone NABWE87, mRNA sequence.
ACCESSION DV345207
VERSION DV345207.1 GI:77794432
KEYWORDS EST.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
REFERENCE 1 (bases 1 to 234)
AUTHORS Loftus,B., Utterback,T., Pertea,G., Koo,H., Mori,A., Schneider,J., Lovin,D., deBruyn,B., Song,Z., Raikhel,A., de Fatima,B.M., Casavant,T., Soares,B. and Severson,D.
TITLE Aedes aegypti cDNA sequencing
JOURNAL Unpublished (2005)
COMMENT Contact: David Severson
The Institute for Genomic Research (TIGR; www.tigr.org); University of Notre Dame, Department of Biological Sciences
9712 Medical Center Drive, Rockville, MD 20850, USA
Sequencing performed at TIGR (http://www.tigr.org) Venter Institute/JTC (JCVIJTC; http://venterinstitute.org) NABWE87TR
Seq primer: REVERSE-CAGGAAACAGCTATGACC.
FEATURES Location/Qualifiers
source 1. .234
/organism="Aedes aegypti"
/mol_type="mRNA"
/db_xref="taxon:7159"
/clone="NABWE87"
/sex="Female"
/tissue_type="adult females at 24 h, 3 days and 12 days post feeding on a Brugia malayi infected blood meal"
/dev_stage="Adult"
/clone_lib="Aedes aegypti infected with Brugia Malayi"
ORIGIN

Alignment Scores:

Pred. No.:	147	Length:	234
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	10	Gaps:	0

```
-10-821-670A-33 (1-222) x DV345207 (1-234)

        46 ThrLeuLeuArgAlaIleSerAsnThr 54
           ||||||||||||||||||||||||||
        28 ACACTTTTGAGAGCCATATCGAACACA 2

SULT 36
470624/c
CUS       CR470624                  254 bp    mRNA    linear   EST 01-JUL-2004
FINITION  CR470624 Rat pBluescript Lion Rattus norvegicus cDNA clone
          LIONp463F03352 3', mRNA sequence.
CESSION   CR470624
RSION     CR470624.1  GI:49604381
YWORDS    EST.
URCE      Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
FERENCE   1  (bases 1 to 254)
AUTHORS   Henrich,J., Hermanns,J., Kranz,H., Loebbert,R., Schlueter,T.,
          Schuette,D., Weindel,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
          Radelof,U., Schneider,D. and Korn,B.
TITLE     Rat ArrayTAG cDNA
JOURNAL   Unpublished (2004)
MMENT     Contact: Inge Arlart
          RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
          Heubnerweg 6, D-14059 Berlin, Germany
          Email: www.rzpd.de
          RZPD; LIONp463F03352.
          RZPDLIB;
          Rat ArrayTAG cDNA
          http://www.rzpd.de/cgi-
          bin/products/showLib.pl.cgi/response?libNo=463 Contact: Inge Arlart
          RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
          Heubnerweg 6, D-14059 Berlin, Germany
          Tel: +49 30 32639 100
          Fax: +49 30 32639 111
          www.rzpd.de
          This clone is available royalty-free from RZPD;
          contact RZPD (clone@rzpd.de) for further information. Seq primer:
          RP: CAGGAAACAGCTATGAC.
ATURES              Location/Qualifiers
   source           1. .254
                    /organism="Rattus norvegicus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10116"
                    /clone="LIONp463F03352"
                    /lab_host="DH10B"
                    /clone_lib="Rat pBluescript Lion"
IGIN

lignment Scores:
ed. No.:              160           Length:        254
ore:                  9.00          Matches:       9
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     8             Gaps:          0

-10-821-670A-33 (1-222) x CR470624 (1-254)

          6 GlyLeuLeuLeuValThrIleLeuVal 14
            |||||||||||||||||||||||||||
        159 GGCCTCTTGCTTGTCACCATCCTGGTG 133

SULT 37
136106/c
CUS       AI136106                  276 bp    mRNA    linear   EST 05-JUL-1999
FINITION  UI-R-C2p-ny-b-11-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone
          UI-R-C2p-ny-b-11-0-UI 3', mRNA sequence.
CESSION   AI136106
```

```
VERSION     AI136106.1  GI:3636883
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 276)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            The sequence tag present in the cDNA between the NotI site and the
            oligo-dT track served to identify it as a clone from the normalized
            adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima
            Bonaldo, Ph.D. Clone distribution: clones will be available through
            Research Genetics This clone is also available through the
            I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
            ID=1787041
            Seq primer: M13 Forward
            POLYA=No.
FEATURES                Location/Qualifiers
     source             1. .276
                        /organism="Rattus norvegicus"
                        /mol_type="mRNA"
                        /strain="Sprague-Dawley"
                        /db_xref="taxon:10116"
                        /clone="UI-R-C2p-ny-b-11-0-UI"
                        /dev_stage="adult"
                        /lab_host="DH10B (Life Technologies)"
                        /clone_lib="UI-R-C2p"
                        /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                        The UI-R-C2p library is a subtracted library derived from
                        the UI-R-C1 library, which is a subtracted library derived
                        from the UI-R-C0 library.  The UI-R-C0 library consisted
                        of a mixture of individually tagged normalized  libraries
                        constructed from rat placenta, adult lung, brain, liver,
                        kidney,  heart, spleen, ovary, muscle, 8, 12 and 18-day
                        embryo. The tag is a string of  3-5 nucleotides present
                        between the Not I site and the oligo-dT track which allows
                        identification of the library of origin of a clone within
                        the mixture. The subtracted library (UI-R-C2p) was
                        constructed as follows: PCR amplified cDNA inserts from
                        UI-R-C1 clones from which 3' ESTs had been derived was
                        used as a driver in a hybridization with the UI-R-C1
                        library in the form of single-stranded circles. The
                        remaining single-stranded circles (subtracted library) was
                        purified by hydroxyapatite column chromatography,
                        converted to double-stranded circles and electroporated
                        into DH10B bacteria (Life Technologies) to generate the
                        UI-R-C2p library. This procedure has been previously
                        described (Bonaldo, Lennon and Soares, Genome Research 6:
                        791-806, 1996)"
ORIGIN

Alignment Scores:
Pred. No.:              174           Length:        276
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     1             Gaps:          0

US-10-821-670A-33 (1-222) x AI136106 (1-276)
```

```
          6 GlyLeuLeuLeuValThrIleLeuVal 14
            ||||||||||||||||||||||||||||
        177 GGCCTCTTGCTTGTCACCATCCTGGTG 151

SULT 38
364595
CUS        BY364595                294 bp    mRNA    linear   EST 12-DEC-2002
FINITION   BY364595 RIKEN full-length enriched, 8 cells embryo Mus musculus
           cDNA clone E860025O10 3', mRNA sequence.
CESSION    BY364595
RSION      BY364595.1  GI:26594083
YWORDS     EST.
URCE       Mus musculus (house mouse)
RGANISM    Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE    1  (bases 1 to 294)
AUTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
           Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
           Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
           Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
           Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
           Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
           Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
           Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
           Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
           Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
           Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
           Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
           Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
           Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
           Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
           Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
           Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
           Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
           Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
           Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
           Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
           Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
           Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
           Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
           Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
           Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
           Rogers,J., Birney,E. and Hayashizaki,Y.
ITLE       Analysis of the mouse transcriptome based on functional annotation
           of 60,770 full-length cDNAs
JOURNAL    Nature 420, 563-573 (2002)
 PUBMED    12466851
MENT       Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
           Sciences Center(GSC), Yokohama Institute
           The Institute of Physical and Chemical Research (RIKEN)
           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
           Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
           Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
           Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
           Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
           Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
           Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
           Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
           prepare full-length cDNA libraries for rapid discovery of new
           genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
           sequencing pipeline with 384 multicapillary sequencer. Genome Res.
           10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
           encyclopedia: real-time sequence clustering for construction of a
           nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
           Encyclopedia Project of Genome Exploration Research Group in Riken
           Genomic Sciences Center and Genome Science Laboratory in RIKEN.
           Division of Experimental Animal Research in Riken contributed to
           prepare mouse tissues.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
           further details.
FEATURES             Location/Qualifiers
     source          1. .294
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="E860025O10"
                     /cell_type="8 cells"
                     /dev_stage="8 cells embryo"
                     /clone_lib="RIKEN full-length enriched, 8 cells embryo"
ORIGIN

Alignment Scores:
Pred. No.:                185             Length:          294
Score:                    9.00            Matches:         9
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              4.1%            Indels:          0
DB:                       4               Gaps:            0

US-10-821-670A-33 (1-222) x BY364595 (1-294)

Qy          28 LeuProThrProThrProSerProGly 36
               ||||||||||||||||||||||||||||
Db         165 CTCCCCACCCCCACCCCCAGCCCGGGC 191

RESULT 39
CF799003
LOCUS      CF799003                304 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION Lr_PAHCF_12D05_M13R Earthworm Fluorantene Exposure Library
           Lumbricus rubellus cDNA clone Lr_PAHCF_12D05 5' similar to
           ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
           terrestris, mRNA sequence.
ACCESSION  CF799003
VERSION    CF799003.1  GI:37803573
KEYWORDS   EST.
SOURCE     Lumbricus rubellus (humus earthworm)
  ORGANISM Lumbricus rubellus
           Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
           Lumbricina; Lumbricidae; Lumbricus.
REFERENCE  1  (bases 1 to 304)
  AUTHORS  Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S., Kille,P. and
           Blaxter,M.
  TITLE    The Lumbricus rubellus EST program - Sequences from a Fluorantene
           Exposure library
  JOURNAL  Unpublished (2003)
COMMENT    Contact: Jennifer Chaseley
           BIOSI 1
           Cardiff University
           Main College, Museum Avenue, Cardiff, CF11 3TL, UK
           Tel: +44 2920876680
           Fax: +44 2920874305
           Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
           Sequencing was performed in Cardiff using the pBluescriptII XR cDNA
           library (Stratagene) protocol.
           PCR PRimers
           FORWARD: gttttcccagtcacgacg
           BACKWARD: caggaaacagctatgaccatg
           Plate: 12  row: D  column: 05
           Seq primer: caggaaacagctatgaccatg
           High quality sequence stop: 304.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
```

```
                /db_xref="taxon:35632"
                /clone="Lr_PAHCF_12D05"
                /tissue_type="Whole worm"
                /dev_stage="Adult"
                /clone_lib="Earthworm Fluorantene Exposure Library"
                /note="Vector: pBluescript II SK+; The library was
                prepared using protocols given by the supplier
                (Stratagene)."
:GIN

:gnment Scores:
ed. No.:              191           Length:        304
ore:                  9.00          Matches:       9
:cent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     5             Gaps:          0

-10-821-670A-33 (1-222) x CF799003 (1-304)

         40 CysLeuAsnHisSerGlnThrLeuLeu 48
            ||||||||||||||||||||||||||||
        107 TGCCTCAACCATTCGCAGACGCTATTA 133

SULT 40
422132
CUS       CG422132                343 bp    DNA     linear   GSS 22-SEP-2003
FINITION  ZMMBBc0037M17f ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0037M17
          5', genomic survey sequence.
CESSION   CG422132
RSION     CG422132.1  GI:34566977
YWORDS    GSS.
URCE      Zea mays
ORGANISM  Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
FERENCE   1  (bases 1 to 343)
AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
          Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
:ITLE     Sequencing of the maize genome at PGIR (2003c)
JOURNAL   Unpublished (2003)
MMENT     Contact: Bharti,A.K.
          Dr.Joachim Messing's lab
          The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
          University
          190 Frelinghuysen Road, Piscataway, NJ 08854, USA
          Tel: 732 445 3801
          Fax: 732 445 5735
          Email: bharti@waksman.rutgers.edu
          Seq primer: T7
          Class: BAC ends
          High quality sequence start: 137.
ATURES              Location/Qualifiers
   source           1. .343
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /cultivar="B73"
                    /db_xref="taxon:4577"
                    /clone="ZMMBBc0037M17"
                    /lab_host="E. coli DH10B"
                    /clone_lib="ZMMBBc (EcoRI)"
                    /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
:GIN

:gnment Scores:
ed. No.:              216           Length:        343
ore:                  9.00          Matches:       9
:cent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
                      12            Gaps:          0
```

```
US-10-821-670A-33 (1-222) x CG422132 (1-343)

Qy          28 LeuProThrProThrProSerProGly 36
               ||||||||||||||||||||||||||||
Db         182 CTGCCAACCCCGACACCATCACCTGGG 208

RESULT 41
CG396825
LOCUS       CG396825                372 bp    DNA     linear   GSS 22-SEP-2003
DEFINITION  ZMMBBc0014O04r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0014O04
            3', genomic survey sequence.
ACCESSION   CG396825
VERSION     CG396825.1  GI:34340050
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003b)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
            Class: BAC ends
            High quality sequence start: 154.
FEATURES              Location/Qualifiers
     source           1. .372
                      /organism="Zea mays"
                      /mol_type="genomic DNA"
                      /cultivar="B73"
                      /db_xref="taxon:4577"
                      /clone="ZMMBBc0014O04"
                      /lab_host="E. coli DH10B"
                      /clone_lib="ZMMBBc (EcoRI)"
                      /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Alignment Scores:
Pred. No.:            234           Length:        372
Score:                9.00          Matches:       9
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          4.1%          Indels:        0
DB:                   12            Gaps:          0

US-10-821-670A-33 (1-222) x CG396825 (1-372)

Qy          28 LeuProThrProThrProSerProGly 36
               ||||||||||||||||||||||||||||
Db         149 CTGCCCACCCCGACACCATCACCTGGG 175

RESULT 42
BI296096/c
LOCUS       BI296096                374 bp    mRNA    linear   EST 19-JUL-2001
DEFINITION  UI-R-DK0-cew-c-08-0-UI.s1 UI-R-DK0 Rattus norvegicus cDNA clone
            UI-R-DK0-cew-c-08-0-UI 3', mRNA sequence.
ACCESSION   BI296096
VERSION     BI296096.1  GI:14960195
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
```

```
          Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
FERENCE   1  (bases 1 to 374)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
ITLE      Normalization and subtraction: two approaches to facilitate gene
          discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
 PUBMED   8889548
MMENT     Contact: Soares, MB
          Coordinated Laboratory for Computational Genomics
          University of Iowa
          375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: bento-soares@uiowa.edu
          The sequence contained an oligo-dT track that was present in the
          oligonucleotide that was used to prime the synthesis of first
          strand cDNA and therefore this may represent a bonafide poly A
          tail. The sequence tag present in the cDNA between the NotI site
          and the oligo-dT track served to identify it as a clone from the
          normalized rat placenta pool library cDNA Library Preparation: M.B.
          Soares Lab Clone distribution: clones will be available through
          Research Genetics (www.resgen.com)
          Seq primer: M13 Forward
          POLYA=Yes.
ATURES              Location/Qualifiers
   source           1. .374
                    /organism="Rattus norvegicus"
                    /mol_type="mRNA"
                    /strain="Sprague-Dawley"
                    /db_xref="taxon:10116"
                    /clone="UI-R-DK0-cew-c-08-0-UI"
                    /dev_stage="ADULT"
                    /lab_host="DH10B (Life Technologies)"
                    /clone_lib="UI-R-DK0"
                    /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                    The UI-R-DK0 library is a subtracted library derived from
                    a mixture of five individually tagged normalized rat
                    libraries: brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP
                    (20%), aorta-nRAP (20%), and placenta-nRPP (20%). Each
                    original library was constructed from a mixture of equal
                    amounts of RNA from seven different developmental
                    time-points: embryonic day 17, embryonic day 19, embryonic
                    day 21, adult day 1, adult day 12, adult day 75, and adult
                    day 200. (Exception: the aorta pool does not contain
                    embryonic day 17 RNA and the placenta pool contains only
                    the three embryonic stages). Each library was normalized
                    individually according to the procedure described by
                    Bonaldo, Lennon & Soares (Genome Research Genome 6:
                    791-806, 1996). For construction of the DK0 subtracted
                    library, plasmid DNA from each of the five individually
                    tagged normalized libraries was mixed in the proportions
                    specified above and electroporated into competent bacteria
                    for production of single-stranded circular DNA
                    representing the pool of libraries. Single-stranded
                    circular DNA representing these five normalized libraries
                    was then used as a tracer in a subtractive hybridization
                    with a driver (PCR amplified inserts from a plasmid DNA
                    template preparation) comprising: a) a set of about 1,000
                    arrayed clones from each of the five non-normalized
                    libraries of brain (CT0s), heart (CS0s), kidney (CU0s),
                    aorta (CW0s), and placenta (CX0s). The resulting pool of
                    approximately 5,000 clones represented about 33.3% of the
                    final driver population. A set of about 2,000 arrayed
                    clones from each of the five normalized libraries of brain
                    (CT0), heart (CS0), kidney (CU0), aorta (CW0), and
                    placenta (CX0). The resulting pool of about 10,000 clones
                    represented about 66.6% of the final driver population.
                    TAG_TISSUE=rat placenta pool
                    TAG_LIB=UI-R-DK0
                    TAG_SEQ=TCACGACAGT"
IGIN

ignment Scores:

Pred. No.:                236             Length:         374
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.1%            Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-33 (1-222) x BI296096 (1-374)

Qy          6 GlyLeuLeuLeuValThrIleLeuVal 14
              |||||||||||||||||||||||||||
Db        172 GGCCTCTTGCTTGTCACCATCCTGGTG 146

RESULT 43
CL003778/c
LOCUS       CL003778                375 bp    DNA     linear   GSS 23-DEC-2003
DEFINITION  ZMMBBb0384A14.r ZMMBBb Zea mays genomic clone ZMMBBb0384A14 3',
            genomic survey sequence.
ACCESSION   CL003778
VERSION     CL003778.1  GI:40317677
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
            and Wing,R.
  TITLE     Sequencing of the maize genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: T7
            BACKWARD: M13r
            Plate: 0384  row: A  column: 14
            Seq primer: M13r
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .375
                      /organism="Zea mays"
                      /mol_type="genomic DNA"
                      /cultivar="B73"
                      /db_xref="taxon:4577"
                      /clone="ZMMBBb0384A14"
                      /lab_host="DH10B"
                      /clone_lib="ZMMBBb"
                      /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                      HindIII; Zea mays L. ssp. mays"
ORIGIN

Alignment Scores:
Pred. No.:                236             Length:         375
Score:                    9.00            Matches:        9
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              4.1%            Indels:         0
DB:                       12              Gaps:           0

US-10-821-670A-33 (1-222) x CL003778 (1-375)

Qy          3 ProProArgGlyLeuLeuLeuValThr 11
              |||||||||||||||||||||||||||
Db        194 CCACCACGTGGCTTGTTGCTCGTGACA 168

RESULT 44
```

```
036596
CUS       AZ036596                 399 bp    DNA     linear   GSS 01-MAR-2000
FINITION  RPCI-23-327M17.TV RPCI-23 Mus musculus genomic clone
          RPCI-23-327M17, genomic survey sequence.
CESSION   AZ036596
RSION     AZ036596.1  GI:7124047
YWORDS    GSS.
URCE      Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE   1  (bases 1 to 399)
AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
          Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
          Jong,P. and Fraser,C.M.
ITLE      Mouse BAC End Sequences from Library RPCI-23
JOURNAL   Unpublished (1999)
MMENT     Other_GSSs: RPCI-23-327M17.TJB
          Contact: Shaying Zhao
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: szhao@tigr.org
          Clones are derived from the mouse BAC library RPCI-23. For BAC
          library availability, please contact Pieter de Jong
          (pieter@dejong.med.buffalo.edu). Clones may be purchased from
          BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
          or from Resea ch Genetics (info@resgen.com). BAC end page:
          http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
          Plate: 327  row: M  column: 17
          Seq primer: T7
          Class: BAC ends.
ATURES              Location/Qualifiers
   source           1. .399
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="RPCI-23-327M17"
                    /sex="Female"
                    /lab_host="DH10B"
                    /clone_lib="RPCI-23"
                    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                    EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                    brain genomic DNA was isolated and  partially digested
                    with a combination of EcoRI and EcoRI Methylase.   Size
                    selected DNA was cloned into the pBACe3.6 vector at the
                    EcoRI  sites.  The ligation products were transformed into
                    DH10B  electrocompetent cells (BRL Life Technologies).   "
IGIN

ignment Scores:
ed. No.:               251            Length:        399
ore:                   9.00           Matches:       9
cent Similarity:       100.0%         Conservative:  0
st Local Similarity:   100.0%         Mismatches:    0
ery Match:             4.1%           Indels:        0
:                      11             Gaps:          0

-10-821-670A-33 (1-222) x AZ036596 (1-399)

          8 LeuLeuValThrIleLeuValLeuLeu 16
            ||||||||||||||||||||||||||||
         94 CTGCTTGTCACAATACTAGTCCTTCTA 120

SULT 45
988885
CUS       DN988885                 404 bp    mRNA    linear   EST 17-MAY-2005
FINITION  ZEBRA_2F_2-II_05_ZEBRA_2F_2-II_05_G04.ab1 Bermudagrass line Zebra
          subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
          ZEBRA_2F_2-II_05_ZEBRA_2F_2-II_05_G04.ab1, mRNA sequence.
ACCESSION DN988885
VERSION   DN988885.1  GI:66248712
KEYWORDS  EST.
SOURCE    Cynodon dactylon (Bermuda grass)
  ORGANISM Cynodon dactylon
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Chloridoideae; Cynodonteae; Cynodon.
REFERENCE 1  (bases 1 to 404)
  AUTHORS Melmaiee,K., Elavarthi,S. and Guenzi,A.C.
  TITLE   Identification of differentially expressed genes associated with
          cold acclimation using suppression subtraction hybridization (SSH)
          and cDNA microarrays
  JOURNAL Unpublished (2005)
COMMENT   Contact: Guenzi AC
          Dep. of Plant and Soil Sciences
          Oklahoma State University
          368 Agriculture Hall, Stillwater, OK 74078-6028, USA
          Tel: 405-744-6028
          Fax: 405 744 6039
          Email: acg@mail.pss.okstate.edu
          PCR PRimers
          FORWARD: M13 forward
          BACKWARD: M13 Reverse
          Seq primer: M13 Forward.
FEATURES            Location/Qualifiers
     source         1. .404
                    /organism="Cynodon dactylon"
                    /mol_type="mRNA"
                    /cultivar="Zebra"
                    /db_xref="taxon:28909"
                    /clone="ZEBRA_2F_2-II_05_ZEBRA_2F_2-II_05_G04.ab1"
                    /tissue_type="Crown"
                    /lab_host="E. coli"
                    /clone_lib="Bermudagrass line Zebra subtracted cold
                    acclimated cDNA library"
                    /note="Vector: Qiagen's pDrive; Messenger RNA was
                    extracted from control and cold acclimated bermudagrass
                    crown tissue at 2 and 28 days after acclimation and cDNA
                    library was constructed following Clontech PCR- select
                    cDNA subtraction procedure."
ORIGIN

Alignment Scores:
Pred. No.:               255            Length:        404
Score:                   9.00           Matches:       9
Percent Similarity:      100.0%         Conservative:  0
Best Local Similarity:   100.0%         Mismatches:    0
Query Match:             4.1%           Indels:        0
DB:                      9              Gaps:          0

US-10-821-670A-33 (1-222) x DN988885 (1-404)

Qy          29 ProThrProThrProSerProGlyMet 37
               |||||||||||||||||||||||||||
Db         368 CCCACCCCCACCCCCTCGCCGGGGATG 394

RESULT 46
CB801533
LOCUS       CB801533                 412 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  AMGNNUC:SRPB2-00244-H1-A srpb2 (10220) Rattus norvegicus cDNA clone
          srpb2-00244-h1 5', mRNA sequence.
ACCESSION   CB801533
VERSION     CB801533.1  GI:29914888
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   Amgen EST Program.
```

```
TITLE     Amgen Rat EST Program
JOURNAL   Unpublished (2003)
MENT      Contact: Dan Fitzpatrick
          Amgen, Inc
          One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
          Tel: 805 447-4881
          Plate: 00244  row: h  column: 1.
TURES             Location/Qualifiers
   source         1. .412
                  /organism="Rattus norvegicus"
                  /mol_type="mRNA"
                  /db_xref="taxon:10116"
                  /clone="srpb2-00244-h1"
                  /tissue_type="prostate tissue"
                  /clone_lib="srpb2 (10220)"
                  /note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; rat
                  prostate normalized double selected poly(A+) mRNA size
                  fraction > 1 kb"
IGIN

ignment Scores:
ed. No.:              260           Length:        412
ore:                  9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     4             Gaps:          0

-10-821-670A-33 (1-222) x CB801533 (1-412)

       197 LysLeuCysIleLeuLeuHisAlaPhe 205
           |||||||||||||||||||||||||||
       283 AAGCTCTGTATCCTGCTCCATGCCTTC 309

SULT 47
798662
CUS       CF798662                425 bp    mRNA    linear   EST 21-OCT-2003
FINITION  Lr_PAHCF_05D11_M13R Earthworm Fluorantene Exposure Library
          Lumbricus rubellus cDNA clone Lr_PAHCF_05D11 5' similar to
          ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
          terrestris, mRNA sequence.
CESSION   CF798662
RSION     CF798662.1  GI:37803232
YWORDS    EST.
URCE      Lumbricus rubellus (humus earthworm)
RGANISM   Lumbricus rubellus
          Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
          Lumbricina; Lumbricidae; Lumbricus.
FERENCE   1  (bases 1 to 425)
AUTHORS   Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S., Kille,P. and
          Blaxter,M.
TITLE     The Lumbricus rubellus EST program - Sequences from a Fluorantene
          Exposure library
JOURNAL   Unpublished (2003)
MMENT     Contact: Jennifer Chaseley
          BIOSI 1
          Cardiff University
          Main College, Museum Avenue, Cardiff, CF11 3TL, UK
          Tel: +44 2920876680
          Fax: +44 2920874305
          Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
          Sequencing was performed in Cardiff using the pBluescriptII XR cDNA
          library (Stratagene) protocol.
          PCR PRimers
          FORWARD: gttttcccagtcacgacg
          BACKWARD: caggaaacagctatgaccatg
          Plate: 05  row: D  column: 11
          Seq primer: caggaaacagctatgaccatg
          High quality sequence stop: 374.
ATURES            Location/Qualifiers
   source         1. .425
                  /organism="Lumbricus rubellus"
                  /mol_type="mRNA"
                  /db_xref="taxon:35632"
                  /clone="Lr_PAHCF_05D11"
                  /tissue_type="Whole worm"
                  /dev_stage="Adult"
                  /clone_lib="Earthworm Fluorantene Exposure Library"
                  /note="Vector: pBluescript II SK+; The library was
                  prepared using protocols given by the supplier
                  (Stratagene)."
ORIGIN

Alignment Scores:
Pred. No.:              268           Length:        425
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     5             Gaps:          0

US-10-821-670A-33 (1-222) x CF798662 (1-425)

Qy          40 CysLeuAsnHisSerGlnThrLeuLeu 48
               |||||||||||||||||||||||||||
Db         109 TGCCTCAACCATTCGCAGACGCTATTA 135

RESULT 48
AI750954/c
LOCUS       AI750954                437 bp    mRNA    linear   EST 20-JUN-2002
DEFINITION  cn06g05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA
            clone NHTBC_cn06g05 random, mRNA sequence.
ACCESSION   AI750954
VERSION     AI750954.1  GI:5129218
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
            Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M.,
            Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.
  TITLE     SGAP: The Skeletal Genome Anatomy Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Libin Jia
            Medical Genetics Branch
            National Human Genome Research Institute
            10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
            Tel: 301-402-4877
            Fax: 301-496-7157
            Email: libin@helix.nih.gov
            DNA Sequencing and analyses by National Institutes of Health
            Intramural Sequencing Center (NISC).
            Plate: 06  row: g  column: 05
            Seq primer: -21M13 forward primer (ABI).
FEATURES              Location/Qualifiers
     source           1. .437
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="NHTBC_cn06g05"
                      /sex="Female"
                      /tissue_type="Bone"
                      /cell_type="Trabecular Bone Cells"
                      /lab_host="SURE"
                      /clone_lib="Normal Human Trabecular Bone Cells"
                      /note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI;
                      Library constructed by Dr. Marian Young and Dr. Pamela
                      Gehron Robey (NIDCR)"
ORIGIN

Alignment Scores:
Pred. No.:              275           Length:        437
Score:                  9.00          Matches:       9
```

```
:cent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            4.1%            Indels:        0
:                     1               Gaps:          0

-10-821-670A-33 (1-222) x AI750954 (1-437)

        29 ProThrProThrProSerProGlyMet 37
           |||||||||||||||||||||||||||
       295 CCGACACCAACTCCAAGTCCAGGGATG 269

SULT 49
215995/c
CUS       AZ215995                453 bp    DNA     linear   GSS 09-JUN-2000
FINITION  Sheared DNA-84C4.TF Sheared DNA Trypanosoma brucei genomic clone
          Sheared DNA-84C4, genomic survey sequence.
CESSION   AZ215995
RSION     AZ215995.1  GI:8433795
YWORDS    GSS.
URCE      Trypanosoma brucei
ORGANISM  Trypanosoma brucei
          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
          Trypanosoma.
FERENCE   1  (bases 1 to 453)
AUTHORS   El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
          Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
          Donelson,J., Fraser,C. and Adams,M.
ITLE      Determination of clone end sequences from Trypanosoma brucei GUTat
          10.1 sheared DNA library
JOURNAL   Unpublished (1999)
MMENT     Other_GSSs: Sheared DNA-84C4.TR
          Contact: Najib M. El-Sayed
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: nelsayed@tigr.org
          Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
          DNA library constructed at TIGR. Clones will be available for
          distribution through Research Genetics, Alabama, USA. Sheared DNA
          end sequences search page: http://www.tigr.org/tdb/mdb/tdbb/.
          Seq primer: M13-Forward
          Class: shotgun.
ATURES              Location/Qualifiers
   source           1. .453
                    /organism="Trypanosoma brucei"
                    /mol_type="genomic DNA"
                    /strain="TREU927/4 GUTat 10.1"
                    /db_xref="taxon:5691"
                    /clone="Sheared DNA-84C4"
                    /clone_lib="Sheared DNA"
                    /note="Vector: pUC18; Site_1: SmaI; Constructed at The
                    Institute for Genomic Research (TIGR), Rockville, MD.
                    Genomic DNA isolated from a cloned population of
                    Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                    sheared to give a tight size distribution (approx 2 kb).
                    The v + i method used for the library construction is
                    described in detail in Smith, H.O. and Venter, J.C.
                    (Making small insert libraries for whole genome shotgun
                    sequencing projects.  In Genome Sequencing: A Practical
                    Approach, eds. M. Vaudin and B. Barell, Oxford University
                    Press, 1999)."
IGIN

lignment Scores:
ed. No.:              286             Length:        453
ore:                  9.00            Matches:       9
:cent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            4.1%            Indels:        0
                      11              Gaps:          0
```

```
US-10-821-670A-33 (1-222) x AZ215995 (1-453)

Qy        111 GlySerCysLeuAlaSerArgLysThr 119
              |||||||||||||||||||||||||||
Db        332 GGGAGCTGTCTCGCCTCGCGAAAAACG 306

RESULT 50
CO869708
LOCUS       CO869708                495 bp    mRNA    linear   EST 10-AUG-2004
DEFINITION  Lr_JV2CF_06B01_SKplus Juvenile Earthworm Library Lumbricus rubellus
            cDNA clone Lr_JV2CF_06B01 similar to
            gi|3122450|sp|Q37546|NU1M_LUMTE NADH-UBIQUINONE OXIDOREDUCTASE.
            Score = 263 bits (671), Expect = 2e-70, mRNA sequence.
ACCESSION   CO869708
VERSION     CO869708.1  GI:51099550
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   Chaseley,J., Hedley,B.A., Morgan,A.J., Sturzenbaum,S., Kille,P. and
            Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Juvenile
            library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Jennifer Chaseley
            BIOSI 1
            Cardiff University
            Main College, Museum Avenue, Cardiff, CF11 3TL, UK
            Tel: +44 2920876680
            Fax: +44 2920874305
            Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
            Sequencing was performed in Edinburgh using the pBluescript II XR
            cDNA library (Stratagene) protocol.
            PCR PRimers
            FORWARD: M13F (gttttcccagtcacgacg)
            BACKWARD: M13R (caggaaacagctatgaccatg)
            Plate: 06  row: B  column: 01
            Seq primer: SKplus
            High quality sequence start: 3
            High quality sequence stop: 474.
FEATURES              Location/Qualifiers
     source           1. .495
                      /organism="Lumbricus rubellus"
                      /mol_type="mRNA"
                      /db_xref="taxon:35632"
                      /clone="Lr_JV2CF_06B01"
                      /sex="mixed"
                      /tissue_type="Whole worm"
                      /dev_stage="Juvenile"
                      /clone_lib="Juvenile Earthworm Library"
                      /note="Organ: Whole worm"
ORIGIN

Alignment Scores:
Pred. No.:            312             Length:        495
Score:                9.00            Matches:       9
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          4.1%            Indels:        0
DB:                   8               Gaps:          0

US-10-821-670A-33 (1-222) x CO869708 (1-495)

Qy         40 CysLeuAsnHisSerGlnThrLeuLeu 48
              ||||||||||||||||||||||||||
Db        117 TGCCTCAACCATTCGCAGACGCTATTA 143

RESULT 51
DN245766
LOCUS       DN245766                495 bp    mRNA    linear   EST 29-JUN-2005
DEFINITION  ACAE-aaa46c17.g1 Hydra EST UCI 5 Hydra magnipapillata cDNA 5'
```

```
          similar to sp|Q90YS3|RS2_ICTPU 40S ribosomal protein S2
          >gb|AAK95183.1|AF402809_1 40S ribosomal protein S2 [Ictalurus
          punctatus], mRNA sequence.
CESSION   DN245766
RSION     DN245766.2  GI:68340520
WORDS     EST.
URCE      Hydra magnipapillata
RGANISM   Hydra magnipapillata
          Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
          Hydridae; Hydra.
FERENCE   1  (bases 1 to 495)
UTHORS    Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
          Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
          Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
          Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
          Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
ITLE      WashU Hydra EST Project
OURNAL    Unpublished (2002)
MENT      On Mar 1, 2005 this sequence version replaced gi:60408221.
          Contact: Hans Bode
          WashU Hydra EST Project
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          Library material provided by Hans Bode & Dirk Lindgens, Univ. of
          Calif., Irvine Library constructed by Dirk Lindgens, Univ. of
          Calif. Irvine Library sequenced by Washington University Genome
          Sequencing Center For information on obtaining a clone please
          contact: Hans Bode (hrbode@uci.edu)
          This trace has been recalled with phred
          original value before phred recall for SL was 88
          original value before phred recall for SR was 600
          Seq primer: -40RP from Gibco.
TURES                Location/Qualifiers
   source            1. .495
                     /organism="Hydra magnipapillata"
                     /mol_type="mRNA"
                     /strain="105"
                     /db_xref="taxon:6085"
                     /lab_host="DH10B"
                     /clone_lib="Hydra EST UCI 5"
                     /note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I;
                     a.1st strand cDNA was primed with a Not I primer-adapter
                     (5' - pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3')
                     b.Double-stranded cDNA was ligated to Sal I adapter,
                     digested with Not I and cloned into the pSPORT 1-vector
                     pre-cut with Not I and Sal I. c.The ligation mix was
                     transformed into DH10B cells. d.The cells were grown in
                     SOC = 5g yeast, 20g tryptone, 0.5 g NaCl, 10 mM MgSO4, 10
                     mM MgCl, 0.2% glucose/Liter, (no antibiotic). e.DMSO was
                     added to a final conc. of 10% as a cryoprotectant.and
                     frozen f.The titre before freezing was determined as
                     ~2400/100 ul. Assuming a 10% loss upon freezing, the titre
                     is probably ~2100/ 100 ul. g.9 tubes each containing ~
                     2100 clones/100 ul [ = total of ~19,000] are enclosed.
                     h.The frequency of vectors containing inserts is 96% as
                     determined by digestion check after picking 24 clones,
                     miniprep and subsequent digestion with Not I and Sal I.
                     i.A low level of 32P was used in the cDNA synthesis
                     procedure. The level measured by holding a Geiger Counter
                     next to a tube was background."
IGIN

ignment Scores:
ed. No.:              312          Length:        495
ore:                  9.00         Matches:       9
cent Similarity:      100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            4.1%         Indels:        0
:                     9            Gaps:          0
```

```
US-10-821-670A-33 (1-222) x DN245766 (1-495)

Qy          7 LeuLeuLeuValThrIleLeuValLeu 15
              ||||||||||||||||||||||||||||
Db        363 TTGCTATTGGTGACTATACTTGTCTTG 389

RESULT 52
DA587595/c
LOCUS       DA587595                501 bp    mRNA    linear   EST 06-NOV-2005
DEFINITION  DA587595 HLUNG2 Homo sapiens cDNA clone HLUNG2008655 5', mRNA
            sequence.
ACCESSION   DA587595
VERSION     DA587595.1  GI:80880623
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
  PUBMED    16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES              Location/Qualifiers
     source           1. .501
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="HLUNG2008655"
                      /tissue_type="lung"
                      /clone_lib="HLUNG2"
                      /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              316          Length:        501
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            4.1%         Indels:        0
DB:                     9            Gaps:          0

US-10-821-670A-33 (1-222) x DA587595 (1-501)

Qy          29 ProThrProThrProSerProGlyMet 37
               |||||||||||||||||||||||||||
Db        427 CCGACACCAACTCCAAGTCCAGGGATG 401

RESULT 53
DA599473/c
LOCUS       DA599473                502 bp    mRNA    linear   EST 07-NOV-2005
DEFINITION  DA599473 HSYRA2 Homo sapiens cDNA clone HSYRA2004329 5', mRNA
```

```
          sequence.
CESSION   DA599473
RSION     DA599473.1  GI:81141689
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 502)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
ITLE      Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
JOURNAL   Genome Res. 16 (1), 55-65 (2006)
 PUBMED   16344560
MMENT     Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
ATURES              Location/Qualifiers
   source           1. .502
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="HSYRA2004329"
                    /cell_type="synoviocytes from rheumatioid arthritis
                    (HS-RA)"
                    /clone_lib="HSYRA2"
                    /note="Vector: pME18SFL3; primary culture, synoviocytes
                    from rheumatioid arthritis"
IGIN

lignment Scores:
ed. No.:              316            Length:        502
ore:                  9.00           Matches:       9
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            4.1%           Indels:        0
:                     9              Gaps:          0

-10-821-670A-33 (1-222) x DA599473 (1-502)

        29 ProThrProThrProSerProGlyMet 37
           |||||||||||||||||||||||||||
       265 CCGACACCAACTCCAAGTCCAGGGATG 239

SULT 54
008986
CUS       DR008986                512 bp    mRNA    linear   EST 18-MAY-2005
FINITION  Lr_Cu2CF_12A07 Earthworm Copper Exposure Library Lumbricus rubellus
          cDNA clone Lr_Cu2CF_12A07 similar to UniRef100_Q37546
          NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
          Score = 250 bits (638), Expect = 1e-65, mRNA sequence.
CESSION   DR008986
RSION     DR008986.1  GI:66273130
YWORDS    EST.
URCE      Lumbricus rubellus (humus earthworm)
ORGANISM  Lumbricus rubellus
          Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
          Lumbricina; Lumbricidae; Lumbricus.
REFERENCE 1  (bases 1 to 512)
  AUTHORS Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
          Sturzenbaum,S., Kille,P. and Blaxter,M.
  TITLE   The Lumbricus rubellus EST program - Sequences from a Copper
          exposure library
  JOURNAL Unpublished (2005)
COMMENT   Contact: Jennifer Chaseley
          BIOSI 1
          Cardiff University
          Main College, Museum Avenue, Cardiff, CF11 3TL, UK
          Tel: +44 2920876680
          Fax: +44 2920874305
          Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
          Sequencing was performed in Cardiff using the pBluescript II XR
          cDNA library (Stratagene) protocol.
          PCR PRimers
          FORWARD: M13(gttttcccagtcacgacgtt)
          BACKWARD: M13R(caggaaacagctatgaccatg)
          Plate: 12  row: A  column: 07
          Seq primer: caggaaacagctatgaccatg
          High quality sequence start: 17
          High quality sequence stop: 323.
FEATURES            Location/Qualifiers
     source         1. .512
                    /organism="Lumbricus rubellus"
                    /mol_type="mRNA"
                    /db_xref="taxon:35632"
                    /clone="Lr_Cu2CF_12A07"
                    /sex="mixed"
                    /tissue_type="whole worm"
                    /dev_stage="Adult"
                    /clone_lib="Earthworm Copper Exposure Library"
                    /note="Vector: pbluescript II SK; The library was prepared
                    using protocols given by the supplier (Clontech)."
ORIGIN

Alignment Scores:
Pred. No.:              323            Length:        512
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.1%           Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-33 (1-222) x DR008986 (1-512)

Qy         40 CysLeuAsnHisSerGlnThrLeuLeu 48
              ||||||||||||||||||||||||||
Db        135 TGCCTCAACCATTCGCAGACGCTATTA 161

RESULT 55
BE294832/c
LOCUS       BE294832                519 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  601177293F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532535 5',
            mRNA sequence.
ACCESSION   BE294832
VERSION     BE294832.1  GI:9178374
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 519)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
```

```
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          Plate: LLCM208  row: j  column: 24
          High quality sequence stop: 517.
ATURES              Location/Qualifiers
   source           1. .519
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:3532535"
                    /tissue_type="rhabdomyosarcoma"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_17"
                    /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                    Site_2: XhoI; cDNA made by oligo-dT priming.
                    Directionally cloned into EcoRI/XhoI sites using the
                    following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                    for average insert size 1.8kb.  Library constructed by
                    Ling Hong in the laboratory of Gerald M. Rubin (University
                    of California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."
IGIN

ignment Scores:
ed. No.:              327           Length:         519
ore:                  9.00          Matches:        9
cent Similarity:      100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            4.1%          Indels:         0
:                     7             Gaps:           0

-10-821-670A-33 (1-222) x BE294832 (1-519)

        29 ProThrProThrProSerProGlyMet 37
           |||||||||||||||||||||||||||
       363 CCGACACCAACTCCAAGTCCAGGGATG 337

SULT 56
598142/c
CUS         DA598142                  521 bp    mRNA    linear   EST 07-NOV-2005
FINITION    DA598142 HSYRA2 Homo sapiens cDNA clone HSYRA2002676 5', mRNA
            sequence.
CESSION     DA598142
RSION       DA598142.1  GI:81116153
YWORDS      EST.
URCE        Homo sapiens (human)
RGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
FERENCE     1  (bases 1 to 521)
AUTHORS     Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE       Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
JOURNAL     Genome Res. 16 (1), 55-65 (2006)
 PUBMED     16344560
MMENT       Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES            Location/Qualifiers
     source         1. .521
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="HSYRA2002676"
                    /cell_type="synoviocytes from rheumatioid arthritis
                    (HS-RA)"
                    /clone_lib="HSYRA2"
                    /note="Vector: pME18SFL3; primary culture, synoviocytes
                    from rheumatioid arthritis"
ORIGIN

Alignment Scores:
Pred. No.:              329           Length:         521
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.1%          Indels:         0
DB:                     9             Gaps:           0

US-10-821-670A-33 (1-222) x DA598142 (1-521)

Qy         29 ProThrProThrProSerProGlyMet 37
              |||||||||||||||||||||||||||
Db        454 CCGACACCAACTCCAAGTCCAGGGATG 428

RESULT 57
CR813130
LOCUS       CR813130                  539 bp    DNA     linear   GSS 27-SEP-2004
DEFINITION  GR0AAA37CD06RM1 INRA BAC Bos taurus genomic clone INRAb_622G01, DNA
            sequence, genomic survey sequence.
ACCESSION   CR813130
VERSION     CR813130.1  GI:52749218
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 539)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work  was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 622 row: G column: 01
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES            Location/Qualifiers
     source         1. .539
                    /organism="Bos taurus"
                    /mol_type="genomic DNA"
```

```
                /strain="breed: Holstein"
                /db_xref="taxon:9913"
                /clone="INRAb_622G01"
                /sex="Male"
                /cell_type="fibroblast"
                /clone_lib="INRA bovine BAC"
                /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                INRA Bovine BAC library (Male) produced by Andre Eggen
                Genoscope sequence ID : GR0AAA37CD06RM1"
:GIN

:gnment Scores:
ed. No.:              340           Length:        539
ore:                  9.00          Matches:       9
:cent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     14            Gaps:          0

-10-821-670A-33 (1-222) x CR813130 (1-539)

         96 AsnGluSerCysLeuAlaSerArgGlu 104
            |||||||||||||||||||||||||||
        331 AATGAGAGTTGCCTGGCTTCCAGAGAG 357

SULT 58
956152/c
:US       DA956152                549 bp    mRNA    linear   EST 09-NOV-2005
FINITION  DA956152 SPLEN2 Homo sapiens cDNA clone SPLEN2035001 5', mRNA
          sequence.
:CESSION  DA956152
RSION     DA956152.1  GI:81288557
:WORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 549)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
:ITLE     Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
JOURNAL   Genome Res. 16 (1), 55-65 (2006)
 PUBMED   16344560
MMENT     Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
ATURES                Location/Qualifiers
   source             1. .549
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="SPLEN2035001"
                      /tissue_type="spleen"
                      /clone_lib="SPLEN2"
                      /note="Vector: pME18SFL3"
:GIN
```

```
Alignment Scores:
Pred. No.:              346           Length:        549
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     9             Gaps:          0

US-10-821-670A-33 (1-222) x DA956152 (1-549)

Qy          29 ProThrProThrProSerProGlyMet 37
               |||||||||||||||||||||||||||
Db         539 CCGACACCAACTCCAAGTCCAGGGATG 513

RESULT 59
DT919655
LOCUS       DT919655                551 bp    mRNA    linear   EST 19-SEP-2005
DEFINITION  PCRS30821 Hematopoietic stem cells Mus musculus cDNA, mRNA
            sequence.
ACCESSION   DT919655
VERSION     DT919655.1  GI:75900136
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES              Location/Qualifiers
     source           1. .551
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10090"
                      /tissue_type="Hematopoietic stem cells"
                      /cell_type="Hematopoietic stem cells"
                      /clone_lib="Hematopoietic stem cells"
                      /note="cDNA library was made from FACS-purified
                      hematopoietic stem cells"
ORIGIN

Alignment Scores:
Pred. No.:              347           Length:        551
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     10            Gaps:          0

US-10-821-670A-33 (1-222) x DT919655 (1-551)

Qy         197 LysLeuCysIleLeuLeuHisAlaPhe 205
               |||||||||||||||||||||||||||
Db         180 AAGCTCTGCATCCTGCTTCACGCCTTC 206

RESULT 60
DA555731/c
LOCUS       DA555731                556 bp    mRNA    linear   EST 06-NOV-2005
DEFINITION  DA555731 HCHON2 Homo sapiens cDNA clone HCHON2006006 5', mRNA
            sequence.
ACCESSION   DA555731
```

```
SION      DA555731.1  GI:80908037
WORDS     EST.
URCE      Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 556)
UTHORS    Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
ITLE      Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
OURNAL    Genome Res. 16 (1), 55-65 (2006)
PUBMED    16344560
MENT      Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
TURES               Location/Qualifiers
   source           1. .556
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="HCHON2006006"
                    /cell_type="chondrocytes (HC)"
                    /clone_lib="HCHON2"
                    /note="Vector: pME18SFL3; primary culture, chondrocytes"
IGIN

ignment Scores:
ed. No.:              351           Length:        556
ore:                  9.00          Matches:       9
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     9             Gaps:          0

-10-821-670A-33 (1-222) x DA555731 (1-556)

         29 ProThrProThrProSerProGlyMet 37
            |||||||||||||||||||||||||||
        468 CCGACACCAACTCCAAGTCCAGGGATG 442

ULT 61
63836/c
US        DY063836                 556 bp    mRNA    linear   EST 31-JAN-2006
INITION   000403BPPA001687HT BPPA Bos taurus cDNA, mRNA sequence.
ESSION    DY063836
SION      DY063836.1  GI:86208958
WORDS     EST.
URCE      Bos taurus (cattle)
RGANISM   Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bos.
ERENCE    1  (bases 1 to 556)
UTHORS    McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
          Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
          Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C.,
          McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
          Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
          Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
          Atkinson,P.
  TITLE   AgResearch, Genesis and Primary Industry Victoria Bovine EST
          project
  JOURNAL Unpublished (2006)
COMMENT   Contact: Maqbool N
          AgResearch Ltd.
          Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
          Mosgiel, New Zealand
          Email: nauman.maqbool@agresearch.co.nz.
FEATURES            Location/Qualifiers
     source         1. .556
                    /organism="Bos taurus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9913"
                    /tissue_type="Peyers Patch"
                    /clone_lib="BPPA"
                    /note="Vector: pBK-CMV; Bovine peyers patch cDNA library
                    derived from tissue harvested from a Friesian cross animal
                    by Wayne Hein on 27/01/00"
ORIGIN

Alignment Scores:
Pred. No.:              351           Length:        556
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     10            Gaps:          0

US-10-821-670A-33 (1-222) x DY063836 (1-556)

Qy          28 LeuProThrProThrProSerProGly 36
               |||||||||||||||||||||||||||
Db         414 CTACCAACTCCCACTCCCTCTCCTGGC 388

RESULT 62
CX570753
LOCUS       CX570753                 558 bp    mRNA    linear   EST 12-JAN-2005
DEFINITION  RVL1941 Wackym-Soares normalized rat vestibular cDNA library Rattus
            norvegicus cDNA 5', mRNA sequence.
ACCESSION   CX570753
VERSION     CX570753.1  GI:57597784
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Wackym,P.A. and Cioffi,J.A.
  TITLE     In silico analysis of the rat vestibular periphery transcriptome
            using a normalized cDNA library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Wackym, P.A.
            Department of Otolaryngology and Communication Sciences
            9200 W. Wisconsin Ave, Milwaukee, WI, 53226, USA
            Tel: 414.266.3750
            Fax: 414.266.2693
            Email: wackym@mcw.edu
            Insert Length: 559   Std Error: 0.00
            Seq primer: T7.
FEATURES            Location/Qualifiers
     source         1. .558
                    /organism="Rattus norvegicus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10116"
                    /tissue_type="Vestibular end organs, primary afferent
                    neurons"
                    /clone_lib="Wackym-Soares normalized rat vestibular cDNA
                    library"
```

/note="Vector: pT7T3Pac; The library was constructed and normalized according Bonaldo and Soares, Genome Analysis - A Laboratory Manual, Vol. 2: 49 - 157. Inserts are directionally cloned into the EcoRI and NotI sites. The library tag located between the NotI site and the polyA tail is TAGGTTACAC."

:GIN

:gnment Scores:

ed. No.:	352	Length:	558
ore:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.1%	Indels:	0
	9	Gaps:	0

-10-821-670A-33 (1-222) x CX570753 (1-558)

```
       197 LysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||
        68 AAGCTCTGTATCCTGCTCCATGCCTTC 94
```

SULT 63
552898/c
CUS DA552898 562 bp mRNA linear EST 05-NOV-2005
FINITION DA552898 HCHON2 Homo sapiens cDNA clone HCHON2002588 5', mRNA sequence.
CESSION DA552898
RSION DA552898.1 GI:80836243
YWORDS EST.
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
FERENCE 1 (bases 1 to 562)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
:ITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
MMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
ATURES Location/Qualifiers
source 1. .562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCHON2002588"
/cell_type="chondrocytes (HC)"
/clone_lib="HCHON2"
/note="Vector: pME18SFL3; primary culture, chondrocytes"

:GIN

:gnment Scores:

ed. No.:	354	Length:	562
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-33 (1-222) x DA552898 (1-562)

```
Qy          29 ProThrProThrProSerProGlyMet 37
               |||||||||||||||||||||||||||
Db         390 CCGACACCAACTCCAAGTCCAGGGATG 364
```

RESULT 64
DA557449/c
LOCUS DA557449 565 bp mRNA linear EST 06-NOV-2005
DEFINITION DA557449 HCHON2 Homo sapiens cDNA clone HCHON2008119 5', mRNA sequence.
ACCESSION DA557449
VERSION DA557449.1 GI:80952829
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 565)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
FEATURES Location/Qualifiers
source 1. .565
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCHON2008119"
/cell_type="chondrocytes (HC)"
/clone_lib="HCHON2"
/note="Vector: pME18SFL3; primary culture, chondrocytes"
ORIGIN

Alignment Scores:

Pred. No.:	356	Length:	565
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-33 (1-222) x DA557449 (1-565)

```
Qy          29 ProThrProThrProSerProGlyMet 37
               |||||||||||||||||||||||||||
```

```
       473 CCGACACCAACTCCAAGTCCAGGGATG 447

SULT 65
168038/c
CUS       AI468038                 566 bp    mRNA    linear   EST 14-APR-1999
FINITION  tm61g07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162652 3'
          similar to gb:M58458 40S RIBOSOMAL PROTEIN S4, X ISOFORM (HUMAN);,
          mRNA sequence.
CESSION   AI468038
RSION     AI468038.1  GI:4330128
WORDS     EST.
URCE      Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 566)
UTHORS    NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
ITLE      National Cancer Institute / National Institute of Neurological
          Disorders and Stroke, Brain Tumor Genome Anatomy Project
          (CGAP/BTGAP), Tumor Gene Index
URNAL     Unpublished (1998)
MMENT     Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
          Ph.D.
           cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
          Bonaldo, Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Insert Length: 547   Std Error: 0.00
          Seq primer: -40UP from Gibco
          High quality sequence stop: 210.
TURES             Location/Qualifiers
   source         1. .566
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:2162652"
                  /tissue_type="anaplastic oligodendroglioma"
                  /lab_host="DH10B"
                  /clone_lib="NCI_CGAP_Brn25"
                  /note="Organ: brain; Vector: pT7T3D-PacI; Site_1: Not I;
                  Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                  oligo(dT) primer (5'
                  TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTTTTTTTTTTTTTTTTT
                  T 3']; double-stranded cDNA was ligated to Eco RI
                  adaptors (Pharmacia), digested with Not I and cloned into
                  the Not I and Eco RI sites of the modified pT7T3 vector.
                  Library is normalized, and was constructed by Bento
                  Soares and M.Fatima Bonaldo."
IGIN

ignment Scores:
ed. No.:              357           Length:        566
ore:                  9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     1             Gaps:          0

-10-821-670A-33 (1-222) x AI468038 (1-566)

          4 ProArgGlyLeuLeuLeuValThrIle 12
            ||||||||||||||||||||||||||||
        458 CCAAGAGGACTCCTTCTTGTTACTATT 432

SULT 66
795312
CUS       CR795312                 568 bp    DNA     linear   GSS 24-SEP-2004
```

```
DEFINITION  GR0AAA12DG09RM1 INRA BAC Bos taurus genomic clone INRAb_238E06, DNA
            sequence, genomic survey sequence.
ACCESSION   CR795312
VERSION     CR795312.1  GI:52676311
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 568)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 568)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 238 row: E column: 06
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .568
                      /organism="Bos taurus"
                      /mol_type="genomic DNA"
                      /strain="breed: Holstein"
                      /db_xref="taxon:9913"
                      /clone="INRAb_238E06"
                      /sex="Male"
                      /cell_type="fibroblast"
                      /clone_lib="INRA bovine BAC"
                      /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                      INRA Bovine BAC library (Male) produced by Andre Eggen
                      Genoscope sequence ID : GR0AAA12DG09RM1"
ORIGIN

Alignment Scores:
Pred. No.:              358           Length:        568
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     14            Gaps:          0

US-10-821-670A-33 (1-222) x CR795312 (1-568)

Qy          96 AsnGluSerCysLeuAlaSerArgGlu 104
               |||||||||||||||||||||||||||
Db         330 AATGAGAGTTGCCTGGCTTCCAGAGAG 356

RESULT 67
BE296563/c
LOCUS       BE296563                 572 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  601174065F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529265 5',
            mRNA sequence.
ACCESSION   BE296563
VERSION     BE296563.1  GI:9180127
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
```

```
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 572)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
MMENT     Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          Plate: LLCM200  row: b  column: 18
          High quality sequence start: 18
          High quality sequence stop: 572.
ATURES              Location/Qualifiers
   source           1. .572
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:3529265"
                    /tissue_type="rhabdomyosarcoma"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_17"
                    /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                    Site_2: XhoI; cDNA made by oligo-dT priming.
                    Directionally cloned into EcoRI/XhoI sites using the
                    following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                    for average insert size 1.8kb.  Library constructed by
                    Ling Hong in the laboratory of Gerald M. Rubin (University
                    of California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."
IGIN

lgnment Scores:
ed. No.:              361          Length:        572
ore:                  9.00         Matches:       9
rcent Similarity:     100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            4.1%         Indels:        0
:                     7            Gaps:          0

-10-821-670A-33 (1-222) x BE296563 (1-572)

        29 ProThrProThrProSerProGlyMet 37
           |||||||||||||||||||||||||||||
       456 CCGACACCAACTCCAAGTCCAGGGATG 430

SULT 68
53972/c
CUS       CA153972                 577 bp    mRNA    linear   EST 24-SEP-2003
FINITION  SCVPRZ2038B02.g RZ2 Saccharum officinarum cDNA clone SCVPRZ2038B02
          5', mRNA sequence.
CESSION   CA153972
RSION     CA153972.1  GI:35060583
YWORDS    EST.
URCE      Saccharum officinarum
ORGANISM  Saccharum officinarum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
          complex.
FERENCE   1  (bases 1 to 577)
AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
ITLE      The libraries that made SUCEST
JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
MMENT     Contact: Arruda P
          Centro de Biologia Molecular e Engenharia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parruda@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian Clone Collection Center (BCCC) at
          http://www.bcccenter.fcav.unesp.br
          Plate: 038  row: B  column: 02
          Seq primer: T7 Promoter Primer.
FEATURES            Location/Qualifiers
     source         1. .577
                    /organism="Saccharum officinarum"
                    /mol_type="mRNA"
                    /db_xref="taxon:4547"
                    /clone="SCVPRZ2038B02"
                    /lab_host="DH10B"
                    /clone_lib="RZ2"
                    /note="Organ: Shoot-root transition zone from young plants
                    (small insert library); Vector: pSport1; Site_1: SalI;
                    Site_2: NotI; An unidirectional cDNA library generated
                    from [Shoot-root transition zone  from young plants (small
                    insert library)]. cDNA was prepared from polyA+  mRNA
                    using SuperScript Plasmid System Kit (Invitrogen). The
                    double-strand  cDNAs were fractionated in a sepharose
                    CL-2B 40cm-columns and fragments  sizing between 0.8 and
                    1.5 Kb were directionally cloned into the vector.  Details
                    of each source of RNA and library construction can be
                    obtained at  http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Alignment Scores:
Pred. No.:              364          Length:        577
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            4.1%         Indels:        0
DB:                     4            Gaps:          0

US-10-821-670A-33 (1-222) x CA153972 (1-577)

Qy        169 LeuLeuGlnAlaLeuAsnValAsnSer 177
                ||||||||||||||||||||||||||
Db         51 CTTCTCCAAGCTCTCAACGTCAACTCC 25

RESULT 69
BY797655/c
LOCUS       BY797655                 579 bp    mRNA    linear   EST 16-AUG-2005
DEFINITION  BY797655 Homo sapiens eye Homo sapiens cDNA clone
            HEmEye2086A07_049.ab1 5', mRNA sequence.
ACCESSION   BY797655
VERSION     BY797655.1  GI:73475674
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Choy,K., Wang,C., Ogura,A., Lau,T., Rogers,M., Ikeo,K.,
            Gojobori,T., Lam,D. and Pang,C.
  TITLE     Comparative annotation of 15,809 ESTs identified from pooled early
            gestation human eyes
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Kw Choy
            National Institute of Genetics, Center for Information Biology and
            DDBJ
            Yata1111, Mishima, 411-8540, Japan
            Tel: 852-2632-3099
            Email: richardchoy@cuhk.edu.hk
            This sequence is assembled via IDEA. This clone was obtained from
            National Institute of Genetics and Chinese University of HongKong.
FEATURES            Location/Qualifiers
     source         1. .579
```

```
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="HEmEye2086A07_049.ab1"
                /tissue_type="eye"
                /clone_lib="Homo sapiens eye"
IGIN

ignment Scores:
ed. No.:              365           Length:        579
ore:                  9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     4             Gaps:          0

-10-821-670A-33 (1-222) x BY797655 (1-579)

        29 ProThrProThrProSerProGlyMet 37
           |||||||||||||||||||||||||||
       240 CCGACACCAACTCCAAGTCCAGGGATG 214

SULT 70
187969
CUS       CV187969                 584 bp    mRNA    linear   EST 09-JUN-2005
FINITION  aam01-15ms3-g12 Aam01 Acorus americanus cDNA clone aam01-15ms3-g12
          5', mRNA sequence.
CESSION   CV187969
RSION     CV187969.1  GI:52026762
YWORDS    EST.
URCE      Acorus americanus
RGANISM   Acorus americanus
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Acoraceae; Acorus.
FERENCE   1  (bases 1 to 584)
AUTHORS   dePamphilis,C., Carlson,J., Ma,H., Soltis,D., Soltis,P.,
          Oppenheimer,D., Frohlich,M., Doyle,J., Tanksley,S., Webb,M.,
          Leebens-Mack,J., McNeal,J., Landherr,L., Ilut,D. and Wall,K.
ITLE      Generation of ESTs from early flower buds of Acorus americanus
URNAL     Unpublished (2003)
MMENT     Contact: Claude dePamphilis or James Leebens-Mack
          Mueller Laboratory
          Penn State University
          208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
          State University, University Park, PA 16802, USA
          Tel: 814 863 6413
          Fax: 814 865 9131
          Email: cwd3@psu.edu or jhl10@psu.edu
          The sequence provided is trimmed of vector and low quality regions.
          Full sequence and original trace file are available from the Plant
          Genome Network website (http://pgn.cornell.edu)
          Plate: aam01-15ms3  row: g  column: 12
          Seq primer: M13F.
ATURES              Location/Qualifiers
   source           1. .584
                    /organism="Acorus americanus"
                    /mol_type="mRNA"
                    /db_xref="PGN:aam01-15ms3-g12"
                    /db_xref="taxon:263995"
                    /clone="aam01-15ms3-g12"
                    /tissue_type="inflorescence"
                    /dev_stage="10mm buds"
                    /lab_host="SOLR"
                    /clone_lib="Aam01"
                    /note="Vector: pBluescript SK (+/-); Site_1: EcoRI;
                    Site_2: XhoI; This is a directionally cloned,
                    non-normalized library. This library has been generated by
                    the Floral Genome Project (FGP). The Floral Genome Project
                    is funded by NSF's Plant Genome Research Program
                    (DBI-0115684). More information about the project can be
                    obtained at http://fgp.bio.psu.edu"
IGIN
```

```
Alignment Scores:
Pred. No.:              368           Length:        584
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     8             Gaps:          0

US-10-821-670A-33 (1-222) x CV187969 (1-584)

Qy          3 ProProArgGlyLeuLeuLeuValThr 11
              |||||||||||||||||||||||||||
Db         84 CCTCCAAGGGGCCTGCTCTTAGTCACA 110

RESULT 71
DA541205/c
LOCUS       DA541205                 585 bp    mRNA    linear   EST 04-NOV-2005
DEFINITION  DA541205 FELNG2 Homo sapiens cDNA clone FELNG2001238 5', mRNA
            sequence.
ACCESSION   DA541205
VERSION     DA541205.1  GI:80523474
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
  PUBMED    16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES              Location/Qualifiers
     source           1. .585
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="FELNG2001238"
                      /tissue_type="lung"
                      /dev_stage="fetal"
                      /clone_lib="FELNG2"
                      /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              369           Length:        585
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     9             Gaps:          0

US-10-821-670A-33 (1-222) x DA541205 (1-585)
```

```
        29 ProThrProThrProSerProGlyMet 37
           ||||||||||||||||||||||||||||
       456 CCGACACCAACTCCAAGTCCAGGGATG 430

SULT 72
452822
CUS       CG452822                 592 bp    DNA     linear   GSS 17-SEP-2003
FINITION  OG5EE68TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0845K15,
          genomic survey sequence.
CESSION   CG452822
RSION     CG452822.1  GI:34837822
YWORDS    GSS.
URCE      Zea mays
ORGANISM  Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
FERENCE   1  (bases 1 to 592)
AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
          Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
          Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
CITLE     Consortium for Maize Genomics
JOURNAL   Unpublished (2002)
MMENT     Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TF
          Class: methylation filtered.
ATURES              Location/Qualifiers
   source           1. .592
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /strain="B73"
                    /db_xref="taxon:4577"
                    /clone="ZMMBMa0845K15"
                    /clone_lib="ZM_0.7_1.5_KB"
                    /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                    methylation filtered genomic DNA library"
IGIN

lignment Scores:
ed. No.:               373            Length:        592
ore:                   9.00           Matches:       9
rcent Similarity:      100.0%         Conservative:  0
st Local Similarity:   100.0%         Mismatches:    0
ery Match:             4.1%           Indels:        0
                       12             Gaps:          0

-10-821-670A-33 (1-222) x CG452822 (1-592)

         5 ArgGlyLeuLeuLeuValThrIleLeu 13
           |||||||||||||||||||||||||||
       255 CGGGGCTTGCTCTTGGTGACCATCCTC 281

SULT 73
292735
CUS       CW292735                 595 bp    DNA     linear   GSS 31-OCT-2004
FINITION  104_772_11414243_148_35583_034 Sorghum methylation filtered library
          (LibID: 104) Sorghum bicolor genomic clone 11414243, genomic survey
          sequence.
CESSION   CW292735
RSION     CW292735.1  GI:55008923
YWORDS    GSS.
URCE      Sorghum bicolor (sorghum)
ORGANISM  Sorghum bicolor
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Sorghum.
FERENCE   1  (bases 1 to 595)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 772  row: p  column: 11
            Seq primer: SWfor Forward
            Class: methylation filtered
            High quality sequence stop: 595.
FEATURES              Location/Qualifiers
     source           1. .595
                      /organism="Sorghum bicolor"
                      /mol_type="genomic DNA"
                      /cultivar="ATx623"
                      /db_xref="taxon:4558"
                      /clone="11414243"
                      /clone_lib="Sorghum methylation filtered library (LibID:
                      104)"
                      /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                      prepared from purified nuclei was randomly sheared,
                      end-repaired, size fractionated to enrich for the 0.5 to 5
                      kb fraction, ligated into HincII-digested pBCSK(-) vector
                      and electroporated into E. coli cells. This is a
                      methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:               375            Length:        595
Score:                   9.00           Matches:       9
Percent Similarity:      100.0%         Conservative:  0
Best Local Similarity:   100.0%         Mismatches:    0
Query Match:             4.1%           Indels:        0
DB:                      13             Gaps:          0

US-10-821-670A-33 (1-222) x CW292735 (1-595)

Qy          7 LeuLeuLeuValThrIleLeuValLeu 15
              ||||||||||||||||||||||||||
Db        377 TTATTACTAGTAACTATATTGGTGTTG 403

RESULT 74
BI075279/c
LOCUS       BI075279                 601 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  IP1_18_D10.b1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
            mRNA sequence.
ACCESSION   BI075279
VERSION     BI075279.1  GI:14513936
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and
            Pratt,L.H.
  TITLE     An EST database from Sorghum: developing preanthesis pannicles
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
```

```
          Email: mmpratt@uga.edu
          Sequences have been trimmed to exclude PolyA, vector and regions
          below Phred quality 16. The threshold for high quality sequence is
          20. Three-prime sequences, which are obtained with PolyTMix or T7
          sequencing primer, are presented as the reverse complement.
          Seq primer: JEN REV
          High quality sequence stop: 469
          POLYA=No.
ATURES              Location/Qualifiers
   source           1. .601
                    /organism="Sorghum bicolor"
                    /mol_type="mRNA"
                    /cultivar="BTx623"
                    /db_xref="taxon:4558"
                    /clone_lib="Immature pannicle 1 (IP1)"
                    /note="Organ: Developing preanthesis pannicles; Vector:
                    pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
                    Site_2: EcoRI; The library was made from poly-A RNA in the
                    cloning vector lambda ZAP II.  Clones to be sequenced were
                    prepared by mass excision."
IGIN

ignment Scores:
ed. No.:              379             Length:         601
ore:                  9.00            Matches:        9
cent Similarity:      100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            4.1%            Indels:         0
:                     2               Gaps:           0

-10-821-670A-33 (1-222) x BI075279 (1-601)

          6 GlyLeuLeuLeuValThrIleLeuVal 14
            ||||||||||||||||||||||||||||
         28 GGCTTGCTGCTAGTGACAATCCTCGTG 2

ULT 75
087764/c
US          CA087764                603 bp    mRNA    linear   EST 23-SEP-2003
FINITION    SCQSAM2098D07.g AM2 Saccharum officinarum cDNA clone SCQSAM2098D07
            5', mRNA sequence.
CESSION     CA087764
RSION       CA087764.1  GI:34941071
YWORDS      EST.
URCE        Saccharum officinarum
RGANISM     Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
            complex.
FERENCE     1  (bases 1 to 603)
AUTHORS     Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
ITLE        The libraries that made SUCEST
OURNAL      Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
MMENT       Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 098  row: D  column: 07
            Seq primer: T7 Promoter Primer.
ATURES              Location/Qualifiers
   source           1. .603
                    /organism="Saccharum officinarum"
                    /mol_type="mRNA"
                    /db_xref="taxon:4547"
                    /clone="SCQSAM2098D07"
                    /lab_host="DH10B"
                    /clone_lib="AM2"
                    /note="Organ: Apical meristem and tissues surrounding of
                    immature plants; Vector: pSport1; Site_1: SalI; Site_2:
                    NotI; An unidirectional cDNA library generated from
                    [Apical meristem and  tissues surrounding of immature
                    plants]. cDNA was prepared from polyA+  mRNA using
                    SuperScript Plasmid System Kit (Invitrogen). The
                    double-strand  cDNAs were fractionated in a sepharose
                    CL-2B 40cm-columns and fragments  sizing between 0.8 and
                    1.5 Kb were directionally cloned into the vector.  Details
                    of each source of RNA and library construction can be
                    obtained at  http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Alignment Scores:
Pred. No.:              380             Length:         603
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.1%            Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-33 (1-222) x CA087764 (1-603)

Qy          8 LeuLeuValThrIleLeuValLeuLeu 16
              ||||||||||||||||||||||||||||
Db        227 CTCTTAGTCACCATCTTAGTCTTGCTA 201

RESULT 76
BB194492
LOCUS       BB194492                610 bp    mRNA    linear   EST 19-OCT-2001
DEFINITION  BB194492 RIKEN full-length enriched, adult male spinal cord Mus
            musculus cDNA clone A330083H15 3', mRNA sequence.
ACCESSION   BB194492
VERSION     BB194492.2  GI:16270905
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     On Jun 30, 2000 this sequence version replaced gi:8855111.
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
```

```
          Sugahara,Y. and Hayashizaki,Y.
           Computer-based methods for the mouse full-length cDNA
          encyclopedia: real-time sequence clustering for construction of a
          nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
           Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
          Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
          Hayashizaki,Y.
           Computational Analysis of Full-Length Mouse cDNAs Compared with
          Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
           Please visit our web site (http://genome.gsc.riken.go.jp/) for
          further details.
          cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
ATURES              Location/Qualifiers
   source           1. .610
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="A330083H15"
                    /sex="male"
                    /tissue_type="spinal cord"
                    /dev_stage="adult"
                    /lab_host="DH10B"
                    /clone_lib="RIKEN full-length enriched, adult male spinal
                    cord"
                    /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                    prepared and sequenced in Mouse Genome Encyclopedia
                    Project of Genome Exploration Research Group in Riken
                    Genomic Sciences Center and Genome Science Laboratory in
                    RIKEN. Division of Experimental Animal Research in Riken
                    contributed to prepare mouse tissues. 1st strand cDNA was
                    primed with a primer [5'
                    GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                    prepared by using trehalose thermo-activated reverse
                    transcriptase and subsequently enriched for full-length by
                    cap-trapper. cDNA went through one round of normalization
                    to Rot = 10.0 and subtraction to Rot = 459.0. Second
                    strand cDNA was prepared with the primer adapter of
                    sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                    3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                    modified pBluescript KS(+) after bulk excision from Lambda
                    FLC I. "
IGIN

ignment Scores:
ed. No.:              385            Length:        610
ore:                  9.00           Matches:       9
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            4.1%           Indels:        0
:                     7              Gaps:          0

-10-821-670A-33 (1-222) x BB194492 (1-610)

         29 ProThrProThrProSerProGlyMet 37
            |||||||||||||||||||||||||||||
        222 CCCACCCCCACCCCCTCTCCTGGCATG 248

SULT 77
488094
CUS       BH488094                 610 bp    DNA     linear   GSS 13-DEC-2001
FINITION  BOGBX77TR BOGB Brassica oleracea genomic clone BOGBX77, genomic
          survey sequence.
CESSION   BH488094
RSION     BH488094.1  GI:17696198
YWORDS    GSS.
URCE      Brassica oleracea
ORGANISM  Brassica oleracea
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1  (bases 1 to 610)
  AUTHORS   Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
            Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea and its
            application to gene discovery and annotation in Arabidopsis
  JOURNAL   Genome Res. 15 (4), 487-495 (2005)
   PUBMED   15805490
COMMENT     Other_GSSs: BOGBX77TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES              Location/Qualifiers
     source           1. .610
                      /organism="Brassica oleracea"
                      /mol_type="genomic DNA"
                      /strain="TO1000DH3"
                      /db_xref="taxon:3712"
                      /clone="BOGBX77"
                      /clone_lib="BOGB"
                      /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                      genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Alignment Scores:
Pred. No.:              385            Length:        610
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.1%           Indels:        0
DB:                     11             Gaps:          0

US-10-821-670A-33 (1-222) x BH488094 (1-610)

Qy        112 SerCysLeuAlaSerArgLysThrSer 120
              |||||||||||||||||||||||||||
Db        430 TCTTGTCTCGCATCCCGAAAGACGTCA 456

RESULT 78
CZ102767
LOCUS       CZ102767                 617 bp    DNA     linear   GSS 13-JAN-2005
DEFINITION  OM__Ba0111B06.f OM__Ba Oryza minuta genomic clone OM__Ba0111B06 5',
            genomic survey sequence.
ACCESSION   CZ102767
VERSION     CZ102767.1  GI:57677146
KEYWORDS    GSS.
SOURCE      Oryza minuta
  ORGANISM  Oryza minuta
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            Plate: 0111  row: B  column: 06
            Class: BAC ends.
FEATURES              Location/Qualifiers
```

```
   source          1. .617
                   /organism="Oryza minuta"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:63629"
                   /clone="OM__Ba0111B06"
                   /tissue_type="leaves"
                   /lab_host="DH10B"
                   /clone_lib="OM__Ba"
                   /note="Vector: pCUGIBAC1; Site_1: HindIII; Site_2:
                   HindIII"
IGIN

ignment Scores:
ed. No.:                389             Length:         617
ore:                    9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              4.1%            Indels:         0
:                       13              Gaps:           0

-10-821-670A-33 (1-222) x CZ102767 (1-617)

         85 ValGluAlaCysLeuProLeuGluLeu 93
            |||||||||||||||||||||||||||
        540 GTCGAAGCATGTTTGCCACTAGAGTTG 566

SULT 79
244996
CUS        CW244996                  634 bp    DNA     linear   GSS 30-OCT-2004
FINITION   104_706_11220867_148_35074_014 Sorghum methylation filtered library
           (LibID: 104) Sorghum bicolor genomic clone 11220867, genomic survey
           sequence.
CESSION    CW244996
RSION      CW244996.1  GI:54953823
(WORDS     GSS.
URCE       Sorghum bicolor (sorghum)
RGANISM    Sorghum bicolor
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Sorghum.
FERENCE    1  (bases 1 to 634)
AUTHORS    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
           Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
           McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
           Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
           Martienssen,R.A.
ITLE       Sorghum genome sequencing by methylation filtration
OURNAL     PLoS Biol. 3 (1), e13 (2005)
 PUBMED    15660154
MMENT      Contact: Bedell JA
           Orion Genomics, LLC
           4041 Forest Park Ave, St. Louis, MO 63108, USA
           Tel: 314 615 6979
           Fax: 314 615 5975
           Email: jbedell@oriongenomics.com
           Plate: 706  row: c  column: 03
           Seq primer: SWfor Forward
           Class: methylation filtered
           High quality sequence stop: 634.
ATURES                Location/Qualifiers
     source           1. .634
                      /organism="Sorghum bicolor"
                      /mol_type="genomic DNA"
                      /cultivar="ATx623"
                      /db_xref="taxon:4558"
                      /clone="11220867"
                      /clone_lib="Sorghum methylation filtered library (LibID:
                      104)"
                      /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                      prepared from purified nuclei was randomly sheared,
                      end-repaired, size fractionated to enrich for the 0.5 to 5
                      kb fraction, ligated into HincII-digested pBCSK(-) vector
                      and electroporated into E. coli cells. This is a
                      methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              400             Length:         634
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.1%            Indels:         0
DB:                     13              Gaps:           0

US-10-821-670A-33 (1-222) x CW244996 (1-634)

Qy          18 HisLeuAspHisLeuSerLeuAlaArg 26
               |||||||||||||||||||||||||||
Db         515 CATCTCGATCATCTCAGCCTCGCGCGC 541

RESULT 80
CW292734/c
LOCUS       CW292734                  653 bp    DNA     linear   GSS 31-OCT-2004
DEFINITION  104_772_11414243_116_35579_034 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 11414243, genomic survey
            sequence.
ACCESSION   CW292734
VERSION     CW292734.1  GI:55008922
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 653)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
  PUBMED    15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 772  row: p  column: 11
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 653.
FEATURES              Location/Qualifiers
     source           1. .653
                      /organism="Sorghum bicolor"
                      /mol_type="genomic DNA"
                      /cultivar="ATx623"
                      /db_xref="taxon:4558"
                      /clone="11414243"
                      /clone_lib="Sorghum methylation filtered library (LibID:
                      104)"
                      /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                      prepared from purified nuclei was randomly sheared,
                      end-repaired, size fractionated to enrich for the 0.5 to 5
                      kb fraction, ligated into HincII-digested pBCSK(-) vector
                      and electroporated into E. coli cells. This is a
                      methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              412             Length:         653
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.1%            Indels:         0
```

```
:                    13             Gaps:          0

-10-821-670A-33 (1-222) x CW292734 (1-653)

          7 LeuLeuLeuValThrIleLeuValLeu 15
            ||||||||||||||||||||||||||||
        544 TTATTACTAGTAACTATATTGGTGTTG 518

SULT 81
:44997
:US        CW244997                660 bp    DNA     linear   GSS 30-OCT-2004
FINITION   104_706_11220867_148_37594_014 Sorghum methylation filtered library
           (LibID: 104) Sorghum bicolor genomic clone 11220867, genomic survey
           sequence.
:CESSION   CW244997
RSION      CW244997.1  GI:54953824
:WORDS     GSS.
URCE       Sorghum bicolor (sorghum)
ORGANISM   Sorghum bicolor
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Sorghum.
FERENCE    1  (bases 1 to 660)
AUTHORS    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
           Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
           McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
           Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
           Martienssen,R.A.
:ITLE      Sorghum genome sequencing by methylation filtration
JOURNAL    PLoS Biol. 3 (1), e13 (2005)
 PUBMED    15660154
MMENT      Contact: Bedell JA
           Orion Genomics, LLC
           4041 Forest Park Ave, St. Louis, MO 63108, USA
           Tel: 314 615 6979
           Fax: 314 615 5975
           Email: jbedell@oriongenomics.com
           Plate: 706  row: c  column: 03
           Seq primer: SWfor Forward
           Class: methylation filtered
           High quality sequence stop: 660.
ATURES             Location/Qualifiers
   source          1. .660
                   /organism="Sorghum bicolor"
                   /mol_type="genomic DNA"
                   /cultivar="ATx623"
                   /db_xref="taxon:4558"
                   /clone="11220867"
                   /clone_lib="Sorghum methylation filtered library (LibID:
                   104)"
                   /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                   prepared from purified nuclei was randomly sheared,
                   end-repaired, size fractionated to enrich for the 0.5 to 5
                   kb fraction, ligated into HincII-digested pBCSK(-) vector
                   and electroporated into E. coli cells. This is a
                   methylation filtered library."
:GIN

:gnment Scores:
ed. No.:              416            Length:        660
ore:                  9.00           Matches:       9
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            4.1%           Indels:        0
:                     13             Gaps:          0

-10-821-670A-33 (1-222) x CW244997 (1-660)

         18 HisLeuAspHisLeuSerLeuAlaArg 26
            |||||||||||||||||||||||||||
        515 CATCTCGATCATCTCAGCCTCGCGCGC 541

SULT 82
```

```
CF809729
LOCUS       CF809729                663 bp    mRNA    linear   EST 27-OCT-2003
DEFINITION  Lr_LC1ED_30H01_SAC Lumbricus rubellus Late Cocoon Library 1
            Lumbricus rubellus cDNA clone Lr_LC1ED_30H01 5' similar to
            ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
            terrestris, mRNA sequence.
ACCESSION   CF809729
VERSION     CF809729.1  GI:37998060
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
            Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Jones,M., Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S.,
            Kille,P. and Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a cocoon
            library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK.
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            The library was prepared using protocols given by the supplier
            (Stratagene).
            PCR PRimers
            FORWARD: M13R(AGCGGATAACAATTTCACACAGGA)
            BACKWARD: T7PL(CTCACTATAGGGCGAATTGG)
            Plate: 30  row: H  column: 01
            Seq primer: SAC(GGGAACAAAAGCTGGAG)
            High quality sequence stop: 503.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Lumbricus rubellus"
                     /mol_type="mRNA"
                     /db_xref="taxon:35632"
                     /clone="Lr_LC1ED_30H01"
                     /tissue_type="Whole worm"
                     /dev_stage="Late Cocoon"
                     /clone_lib="Lumbricus rubellus Late Cocoon Library 1"
                     /note="Vector: pBluescript II SK+; The library was
                     prepared using protocols given by the supplier
                     (Stratagene)."
ORIGIN

Alignment Scores:
Pred. No.:              418            Length:        663
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.1%           Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-33 (1-222) x CF809729 (1-663)

Qy          40 CysLeuAsnHisSerGlnThrLeuLeu 48
               ||||||||||||||||||||||||||||
Db         179 TGCCTCAACCATTCGCAGACGCTATTA 205

RESULT 83
DR603821
LOCUS       DR603821                665 bp    mRNA    linear   EST 11-JUL-2005
DEFINITION  EST993949 FvG Gibberella moniliformis cDNA clone FVGAG84, mRNA
            sequence.
ACCESSION   DR603821
VERSION     DR603821.1  GI:70678469
KEYWORDS    EST.
SOURCE      Gibberella moniliformis
  ORGANISM  Gibberella moniliformis
```

```
          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
          Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
FERENCE   1  (bases 1 to 665)
AUTHORS   Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.,
          Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
          Kendra,D.F., Town,C.D. and Whitelaw,C.A.
ITLE      Comparative analysis of 87,000 expressed sequence tags from the
          fumonisin-producing fungus Fusarium verticillioides
JOURNAL   Fungal Genet. Biol. 42 (10), 848-861 (2005)
 PUBMED   16099185
MMENT     Contact: Brown, D.W.
          USDA/ARS/NCAUR
          USDA
          1815 N. University St, Peoria, IL 61604, USA
          Tel: 309 681 6230
          Fax: 309 681 6689
          Email: browndw@ncaur.usda.gov
          TIGR sequence name: FVGAG84TV
          Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
ATURES              Location/Qualifiers
   source           1. .665
                    /organism="Gibberella moniliformis"
                    /mol_type="mRNA"
                    /strain="m3125"
                    /db_xref="taxon:117187"
                    /clone="FVGAG84"
                    /tissue_type="mycelia"
                    /clone_lib="FvG"
                    /note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
                    Site_2: XhoI; anamorph: Fusarium verticillioides. Mycelia
                    was collected after growth in liquid GYAM medium for 96
                    hours. Cultures were vacuum filtered and the mycelial mats
                    were frozen in liquid nitrogen, ground to a powder, and
                    then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
                    approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
                    directionally ligated into the pBlueScript II SK(+) XR
                    vector (cDNA Synthesis Kit; Stratagene)."
IGIN

gnment Scores:
ed. No.:              420          Length:        665
ore:                  9.00         Matches:       9
cent Similarity:      100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            4.1%         Indels:        0
:                     10           Gaps:          0

-10-821-670A-33 (1-222) x DR603821 (1-665)

        13 LeuValLeuLeuAsnHisLeuAspHis 21
           |||||||||||||||||||||||||||
       425 CTTGTCCTGCTGAACCATTTGGATCAT 451

SULT 84
)08485
CUS       DR008485                671 bp    mRNA    linear   EST 18-MAY-2005
FINITION  Lr_Cu2CF_09D10 Earthworm Copper Exposure Library Lumbricus rubellus
          cDNA clone Lr_Cu2CF_09D10 similar to UniRef100_Q37546
          NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
          Score = 362 bits (928), Expect = 6e-99, mRNA sequence.
CESSION   DR008485
RSION     DR008485.1  GI:66272629
YWORDS    EST.
URCE      Lumbricus rubellus (humus earthworm)
RGANISM   Lumbricus rubellus
          Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
          Lumbricina; Lumbricidae; Lumbricus.
FERENCE   1  (bases 1 to 671)
AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
          Sturzenbaum,S., Kille,P. and Blaxter,M.
ITLE      The Lumbricus rubellus EST program - Sequences from a Copper
          exposure library
JOURNAL   Unpublished (2005)
COMMENT   Contact: Jennifer Chaseley
          BIOSI 1
          Cardiff University
          Main College, Museum Avenue, Cardiff, CF11 3TL, UK
          Tel: +44 2920876680
          Fax: +44 2920874305
          Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
          Sequencing was performed in Cardiff using the pBluescript II XR
          cDNA library (Stratagene) protocol.
          PCR PRimers
          FORWARD: M13(gttttcccagtcacgacgtt)
          BACKWARD: M13R(caggaaacagctatgaccatg)
          Plate: 09  row: D  column: 10
          Seq primer: caggaaacagctatgaccatg
          High quality sequence start: 9
          High quality sequence stop: 531.
FEATURES            Location/Qualifiers
     source         1. .671
                    /organism="Lumbricus rubellus"
                    /mol_type="mRNA"
                    /db_xref="taxon:35632"
                    /clone="Lr_Cu2CF_09D10"
                    /sex="mixed"
                    /tissue_type="whole worm"
                    /dev_stage="Adult"
                    /clone_lib="Earthworm Copper Exposure Library"
                    /note="Vector: pbluescript II SK; The library was prepared
                    using protocols given by the supplier (Clontech)."
ORIGIN

Alignment Scores:
Pred. No.:              423          Length:        671
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            4.1%         Indels:        0
DB:                     9            Gaps:          0

US-10-821-670A-33 (1-222) x DR008485 (1-671)

Qy          40 CysLeuAsnHisSerGlnThrLeuLeu 48
               |||||||||||||||||||||||||||||
Db         120 TGCCTCAACCATTCGCAGACGCTATTA 146

RESULT 85
CO408614
LOCUS       CO408614                679 bp    mRNA    linear   EST 02-JUL-2004
DEFINITION  Lr_CHECF_02E05_M13R Earthworm Head Enriched library Lumbricus
          rubellus cDNA clone Lr_CHECF_02E05 similar to NU1M_LUMTE (Q37546)
          NADH-ubiquinone oxidoreductase chain 1 (EC. Score = 365 bits (936),
          Expect = e-100, mRNA sequence.
ACCESSION   CO408614
VERSION     CO408614.1  GI:49624861
KEYWORDS    EST.
SOURCE      Lumbricus rubellus (humus earthworm)
  ORGANISM  Lumbricus rubellus
          Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
          Lumbricina; Lumbricidae; Lumbricus.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Chaseley,J., Hedley,B.A., Morgan,A.J., Sturzenbaum,S., Kille,P. and
          Blaxter,M.
  TITLE     The Lumbricus rubellus EST program - Sequences from a Head enriched
          library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Jennifer Chaseley
          BIOSI 1
          Cardiff University
          Main College, Museum Avenue, Cardiff, CF11 3TL, UK
          Tel: +44 2920876680
          Fax: +44 2920874305
          Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
          PCR PRimers
          FORWARD: gttttcccagtcacgacg
```

```
          BACKWARD: caggaaacagctatgaccatg
          Plate: 02  row: E  column: 05
          Seq primer: M13R (caggaaacagctatgaccatg)
          High quality sequence start: 4
          High quality sequence stop: 528.
ATURES              Location/Qualifiers
   source           1. .679
                    /organism="Lumbricus rubellus"
                    /mol_type="mRNA"
                    /db_xref="taxon:35632"
                    /clone="Lr_CHECF_02E05"
                    /sex="Mixed"
                    /clone_lib="Earthworm Head Enriched library"
IGIN

ignment Scores:
ed. No.:                428             Length:         679
ore:                    9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              4.1%            Indels:         0
                        8               Gaps:           0

-10-821-670A-33 (1-222) x CO408614 (1-679)

         40 CysLeuAsnHisSerGlnThrLeuLeu 48
            ||||||||||||||||||||||||||||
        117 TGCCTCAACCATTCGCAGACGCTATTA 143

SULT 86
B10266
CUS       CF810266                680 bp    mRNA    linear   EST 27-OCT-2003
FINITION  Lr_LC1ED_39A02_SAC Lumbricus rubellus Late Cocoon Library 1
          Lumbricus rubellus cDNA clone Lr_LC1ED_39A02 5' similar to
          ref|NP_008248.1|ND1_10599 NADH dehydrogenase subunit 1 - Lumbricus
          terrestris, mRNA sequence.
CESSION   CF810266
RSION     CF810266.1  GI:37998597
YWORDS    EST.
URCE      Lumbricus rubellus (humus earthworm)
ORGANISM  Lumbricus rubellus
          Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
          Lumbricina; Lumbricidae; Lumbricus.
FERENCE   1  (bases 1 to 680)
AUTHORS   Jones,M., Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S.,
          Kille,P. and Blaxter,M.
ITLE      The Lumbricus rubellus EST program - Sequences from a cocoon
          library
JOURNAL   Unpublished (2003)
MMENT     Contact: Blaxter ML
          Institute of Cell, Animal and Population Biology
          University of Edinburgh
          Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
          3JT, UK.
          Tel: +44 131 650 6760
          Fax: +44 131 670 5450
          Email: mark.blaxter@ed.ac.uk
          The library was prepared using protocols given by the supplier
          (Stratagene).
          PCR PRimers
          FORWARD: M13R(AGCGGATAACAATTTCACACAGGA)
          BACKWARD: T7PL(CTCACTATAGGGCGAATTGG)
          Plate: 39  row: A  column: 02
          Seq primer: SAC(GGGAACAAAAGCTGGAG)
          High quality sequence stop: 503.
ATURES              Location/Qualifiers
   source           1. .680
                    /organism="Lumbricus rubellus"
                    /mol_type="mRNA"
                    /db_xref="taxon:35632"
                    /clone="Lr_LC1ED_39A02"
                    /tissue_type="Whole worm"
                    /dev_stage="Late Cocoon"
                    /clone_lib="Lumbricus rubellus Late Cocoon Library 1"
                    /note="Vector: pBluescript II SK+; The library was
                    prepared using protocols given by the supplier
                    (Stratagene)."
ORIGIN

Alignment Scores:
Pred. No.:                  429             Length:         680
Score:                      9.00            Matches:        9
Percent Similarity:         100.0%          Conservative:   0
Best Local Similarity:      100.0%          Mismatches:     0
Query Match:                4.1%            Indels:         0
DB:                         5               Gaps:           0

US-10-821-670A-33 (1-222) x CF810266 (1-680)

Qy          40 CysLeuAsnHisSerGlnThrLeuLeu 48
               ||||||||||||||||||||||||||||
Db         119 TGCCTCAACCATTCGCAGACGCTATTA 145

RESULT 87
BI922485
LOCUS       BI922485                685 bp    mRNA    linear   EST 17-OCT-2001
DEFINITION  EST542389 tomato callus Lycopersicon esculentum cDNA clone
            cLEC77L21 5' end, mRNA sequence.
ACCESSION   BI922485
VERSION     BI922485.1  GI:16219646
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (Solanum lycopersicum)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 685)
  AUTHORS   Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A.,
            Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M.,
            Martin,G.B., Tanksley,S.D. and Giovannoni,J.
  TITLE     Generation of ESTs from tomato callus tissue (2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            This clone is available through the Clemson University Genomics
            Institute
            Seq primer: T3.
FEATURES                Location/Qualifiers
     source             1. .685
                        /organism="Lycopersicon esculentum"
                        /mol_type="mRNA"
                        /cultivar="TA496"
                        /db_xref="taxon:4081"
                        /clone="cLEC77L21"
                        /tissue_type="callus"
                        /dev_stage="25-40 days old"
                        /lab_host="XL1-Blue MRF'"
                        /clone_lib="tomato callus"
                        /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                        XhoI; supplier: Boyce Thompson Institute; sequencing: The
                        Institute for Genomic Research; cLEC - Cotyledons of
                        seedlings 7-10 days post-germination were excised, cut at
                        both ends and placed on MS medium with no selection. Mixed
                        callus was harvested at 25 and 40 days and included
                        undifferentiated masses. Tomato Callus EST Library"
ORIGIN

Alignment Scores:
Pred. No.:                  432             Length:         685
Score:                      9.00            Matches:        9
Percent Similarity:         100.0%          Conservative:   0
Best Local Similarity:      100.0%          Mismatches:     0
Query Match:                4.1%            Indels:         0
```

```
:                    2              Gaps:          0

-10-821-670A-33 (1-222) x BI922485 (1-685)

          3 ProProArgGlyLeuLeuLeuValThr 11
            ||||||||||||||||||||||||||||
         69 CCACCAAGAGGTTTGCTTTTAGTCACG 95

SULT 88
299956/c
CUS       BE299956                 692 bp    mRNA    linear   EST 20-JUL-2000
FINITION  600944512F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960667 5',
          mRNA sequence.
CESSION   BE299956
SION      BE299956.1  GI:9183704
WORDS     EST.
URCE      Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 692)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
MMENT     Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          Plate: LLCM54  row: g  column: 04
          High quality sequence stop: 676.
ATURES              Location/Qualifiers
   source           1. .692
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2960667"
                    /tissue_type="rhabdomyosarcoma"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_17"
                    /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                    Site_2: XhoI; cDNA made by oligo-dT priming.
                    Directionally cloned into EcoRI/XhoI sites using the
                    following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                    for average insert size 1.8kb.  Library constructed by
                    Ling Hong in the laboratory of Gerald M. Rubin (University
                    of California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."
IGIN

ignment Scores:
ed. No.:              437            Length:        692
ore:                  9.00           Matches:       9
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            4.1%           Indels:        0
:                     7              Gaps:          0

-10-821-670A-33 (1-222) x BE299956 (1-692)

         29 ProThrProThrProSerProGlyMet 37
            |||||||||||||||||||||||||||||
        451 CCGACACCAACTCCAAGTCCAGGGATG 425

SULT 89
306792
CUS       AZ306792                 705 bp    DNA     linear   GSS 29-SEP-2000
FINITION  1M0008F02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
          clone UUGC1M0008F02 F, genomic survey sequence.

ACCESSION   AZ306792
VERSION     AZ306792.1  GI:10345148
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 705)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0008  row: F  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 705.
FEATURES              Location/Qualifiers
     source           1. .705
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0008F02"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

Alignment Scores:
Pred. No.:              445            Length:        705
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.1%           Indels:        0
DB:                     11             Gaps:          0

US-10-821-670A-33 (1-222) x AZ306792 (1-705)

Qy        180 ValProGlnAsnSerSerLeuGluGlu 188
              ||||||||||||||||||||||||||||
Db        344 GTTCCCCAAAATAGCTCTTTAGAAGAG 370
```

```
SULT 90
881972
CUS       CD881972                709 bp    mRNA    linear   EST 14-JUL-2003
FINITION  F1.1104O09F010329 F1 Triticum aestivum cDNA clone F1104O09, mRNA
          sequence.
CESSION   CD881972
RSION     CD881972.1  GI:32642412
YWORDS    EST.
URCE      Triticum aestivum (bread wheat)
ORGANISM  Triticum aestivum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Pooideae; Triticeae; Triticum.
FERENCE   1  (bases 1 to 709)
AUTHORS   Genoplante.
ITLE      Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
MMENT     Contact: Genoplante
          Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.infobiogen.fr).
ATURES              Location/Qualifiers
   source           1. .709
                    /organism="Triticum aestivum"
                    /mol_type="mRNA"
                    /cultivar="recital"
                    /db_xref="taxon:4565"
                    /clone="F1104O09"
                    /tissue_type="leaf one"
                    /clone_lib="F1"
IGIN

gnment Scores:
d. No.:              447           Length:        709
ore:                 9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
st Local Similarity: 100.0%        Mismatches:    0
ery Match:           4.1%          Indels:        0
                     5             Gaps:          0

-10-821-670A-33 (1-222) x CD881972 (1-709)

          4 ProArgGlyLeuLeuLeuValThrIle 12
            ||||||||||||||||||||||||||
        317 CCTCGAGGACTGTTGTTAGTAACCATC 343

SULT 91
736229/c
CUS       CN736229                709 bp    mRNA    linear   EST 14-MAY-2005
FINITION  26RDBNT_UP_013_E01_21JAN2004_007 Brassica napus 26RDBNT Brassica
          napus cDNA 5', mRNA sequence.
CESSION   CN736229
RSION     CN736229.1  GI:65294046
YWORDS    EST.
URCE      Brassica napus (rape)
ORGANISM  Brassica napus
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
FERENCE   1  (bases 1 to 709)
AUTHORS   Xiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R.
ITLE      Gene Expression Patterns during Brassica Zygotic Embryogenesis
JOURNAL   Unpublished (2004)
MMENT     Contact: Raju Datla
          Molecular and Developmental Genetics
          National Research Council of Canada
          Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
          Saskatchewan, S7N 0W9, Canada
          Tel: 306 975 5267
          Fax: 306 975 4839
          Email: Raju.Datla@nrc-cnrc.gc.ca
          High quality sequence stop: 709.
FEATURES            Location/Qualifiers
     source         1. .709
                    /organism="Brassica napus"
                    /mol_type="mRNA"
                    /db_xref="taxon:3708"
                    /clone_lib="Brassica napus 26RDBNT"
                    /note="Vector: pDNR-LIB_CREATOR; Site_1: Sfi IA; Site_2:
                    Sfi IB; Zygotic embryos at torpedo stage from Brassica
                    napus seeds were used for the isolation of PolyA RNA and
                    in the construction of the cDNA library. Sequences have
                    been trimmed to remove vector and low quality regions
                    using LUCY sequence cleanup software (www.tigr.org)."
ORIGIN

Alignment Scores:
Pred. No.:              447           Length:        709
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     8             Gaps:          0

US-10-821-670A-33 (1-222) x CN736229 (1-709)

Qy         15 LeuLeuAsnHisLeuAspHisLeuSer 23
              |||||||||||||||||||||||||||
Db        508 CTCCTGAATCATCTTGATCACTTGTCT 482

RESULT 92
CW744074
LOCUS       CW744074                710 bp    DNA     linear   GSS 05-NOV-2004
DEFINITION  MARC_912850 CHORI-240-314A10 Bos taurus genomic clone 1H2, genomic
            survey sequence.
ACCESSION   CW744074
VERSION     CW744074.1  GI:55459493
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   Smith,T.P.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Harhay,G.P.
  TITLE     SNP discovery in cattle based on low coverage sequencing of BAC
            clones
  JOURNAL   Unpublished (2004)
COMMENT     Other_GSSs: MARC_912466
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Seq primer: GTAATACGACTCACTATAGGG
            Class: BAC subclone.
FEATURES            Location/Qualifiers
     source         1. .710
                    /organism="Bos taurus"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9913"
                    /clone="1H2"
                    /sex="Male"
                    /tissue_type="Blood"
                    /clone_lib="CHORI-240-314A10"
                    /note="Vector: pBLUESCRIPT SK-; Site_1: BamHI; Site_2:
                    BamHI; BAC DNA was digested with Sau3A.  Fragments were
```

```
                sized to 800-1200 bases and subcloned into pBLUESCRIPT
                SK-."
IGIN

ignment Scores:
ed. No.:              448           Length:        710
ore:                  9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     13            Gaps:          0

-10-821-670A-33 (1-222) x CW744074 (1-710)

       111 GlySerCysLeuAlaSerArgLysThr 119
           |||||||||||||||||||||||||||
        80 GGCTCCTGTCTAGCTAGCAGGAAGACT 106

SULT 93
715412/c
CUS       BZ715412                713 bp    DNA     linear   GSS 15-JUL-2005
FINITION  HSC 00419 LL07NC01-96 well Homo sapiens genomic clone cos34b3,
          genomic survey sequence.
CESSION   BZ715412
RSION     BZ715412.2  GI:70908397
YWORDS    GSS.
URCE      Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 713)
UTHORS    Scherer,S.W., Rommens,J.M., Tsui,L.C. and Kwasnicka,D.A.
ITLE      Gene Identification on Human Chromosome 7 (Feb 13/03)
OURNAL    Unpublished (2003)
MMENT     On Jul 15, 2005 this sequence version replaced gi:28436671.
          Contact: Scherer, S.W.; Rommens, J.M.; Tsui, L.C.
          The Human Chromosome 7 Project
          Department of Genetics, The Hospital for Sick Children
          555 University Avenue, Toronto, Ontario M5G 1X8, Canada
          Tel: 416 813 7613
          Fax: 416 813 8319
          Email: steve@genet.sickkids.on.ca
          Maps to human chromosome 7q11.23
          Seq primer: T3
          Class: cosmid ends
          High quality sequence stop: 893.
ATURES                Location/Qualifiers
   source             1. .713
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /clone="cos34b3"
                      /clone_lib="LL07NC01-96 well"
                      /note="Vector: LAWRIST 16; Site_1: BamHI; Site_2: BamHI;
                      Individual chromosomes were flow sorted from a
                      rodent/hybrid cell line  containing the single human
                      chromosome of interest."
IGIN

ignment Scores:
ed. No.:              450           Length:        713
ore:                  9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     12            Gaps:          0

-10-821-670A-33 (1-222) x BZ715412 (1-713)

        29 ProThrProThrProSerProGlyMet 37
           |||||||||||||||||||||||||||
       488 CCGACACCAACTCCAAGTCCAGGGATG 462
```

```
RESULT 94
CF934165/c
LOCUS       CF934165                731 bp    mRNA    linear   EST 17-NOV-2003
DEFINITION  TrEST-B01G07.g TrEST-B Hypocrea jecorina cDNA clone Tr-B01G07.g 5',
            mRNA sequence.
ACCESSION   CF934165
VERSION     CF934165.1  GI:38353994
KEYWORDS    EST.
SOURCE      Hypocrea jecorina (anamorph: Trichoderma reesei)
  ORGANISM  Hypocrea jecorina
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Bonaccorsi,E.D., Chambergo,F.S. and El-Dorry,H.
  TITLE     TrEST-B
  JOURNAL   Unpublished (2003)
COMMENT     Contact: El-Dorry, Hamza
            Department of Biochemistry
            Institute of Chemistry. University of Sao Paulo
            Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,
            BRASIL
            Tel: (55) 11-38183848
            Fax: (55) 11-38183848
            Email: dorry@iq.usp.br
            PCR PRimers
            FORWARD: Universal M13 forward primer
            BACKWARD: Universal M13 reverse primer
            Plate: 01  row: G  column: 07
            Seq primer: M13 reverse primer
            High quality sequence stop: 518
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .731
                      /organism="Hypocrea jecorina"
                      /mol_type="mRNA"
                      /strain="QM9414 (ATCC26921)"
                      /db_xref="taxon:51453"
                      /clone="Tr-B01G07.g"
                      /sex="Asexual"
                      /tissue_type="Mycelia"
                      /dev_stage="Mycelial culture grown from 100 mM and
                      harvested to 80 mM glicose concentrations."
                      /lab_host="E. coli DH10B cells (streptomycin resistant)"
                      /clone_lib="TrEST-B"
                      /note="Vector: pUC18; cDNA cloned into SmaI site of pUC18.
                      Average insert size: 1 kb"
ORIGIN

Alignment Scores:
Pred. No.:            461           Length:        731
Score:                9.00          Matches:       9
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          4.1%          Indels:        0
DB:                   5             Gaps:          0

US-10-821-670A-33 (1-222) x CF934165 (1-731)

Qy         27 AsnLeuProThrProThrProSerPro 35
              |||||||||||||||||||||||||||
Db        552 AACCTTCCAACTCCAACTCCAAGTCCA 526

RESULT 95
DR009499
LOCUS       DR009499                731 bp    mRNA    linear   EST 18-MAY-2005
DEFINITION  Lr_Cu2CF_36D11 Earthworm Copper Exposure Library Lumbricus rubellus
            cDNA clone Lr_Cu2CF_36D11 similar to UniRef100_Q37546
            NADH-ubiquinone oxidoreductase chain 1 - Lumbricus terrestris.
            Score = 380 bits (975), Expect = e-104, mRNA sequence.
ACCESSION   DR009499
VERSION     DR009499.1  GI:66273643
KEYWORDS    EST.
```

```
URCE      Lumbricus rubellus (humus earthworm)
ORGANISM  Lumbricus rubellus
          Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
          Lumbricina; Lumbricidae; Lumbricus.
FERENCE   1  (bases 1 to 731)
AUTHORS   Calafato,S., Chaseley,J., Hedley,B.A., Morgan,A.J., Spurgeon,D.J.,
          Sturzenbaum,S., Kille,P. and Blaxter,M.
ITLE      The Lumbricus rubellus EST program - Sequences from a Copper
          exposure library
OURNAL    Unpublished (2005)
MMENT     Contact: Jennifer Chaseley
          BIOSI 1
          Cardiff University
          Main College, Museum Avenue, Cardiff, CF11 3TL, UK
          Tel: +44 2920876680
          Fax: +44 2920874305
          Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
          Sequencing was performed in Cardiff using the pBluescript II XR
          cDNA library (Stratagene) protocol.
          PCR PRimers
          FORWARD: M13(gttttcccagtcacgacgtt)
          BACKWARD: M13R(caggaaacagctatgaccatg)
          Plate: 36  row: D  column: 11
          Seq primer: caggaaacagctatgaccatg
          High quality sequence start: 2
          High quality sequence stop: 525.
ATURES              Location/Qualifiers
   source           1. .731
                    /organism="Lumbricus rubellus"
                    /mol_type="mRNA"
                    /db_xref="taxon:35632"
                    /clone="Lr_Cu2CF_36D11"
                    /sex="mixed"
                    /tissue_type="whole worm"
                    /dev_stage="Adult"
                    /clone_lib="Earthworm Copper Exposure Library"
                    /note="Vector: pbluescript II SK; The library was prepared
                    using protocols given by the supplier (Clontech)."
IGIN

ignment Scores:
ed. No.:              461           Length:        731
ore:                  9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            4.1%          Indels:        0
:                     9             Gaps:          0

-10-821-670A-33 (1-222) x DR009499 (1-731)

         40 CysLeuAsnHisSerGlnThrLeuLeu 48
            ||||||||||||||||||||||||||||
        111 TGCCTCAACCATTCGCAGACGCTATTA 137

SULT 96
419793
US        CL419793                734 bp    DNA     linear   GSS 09-MAR-2004
FINITION  ZMMBBb0423N02f ZMMBBb (HindIII) Zea mays genomic clone
          ZMMBBb0423N02 5', genomic survey sequence.
CESSION   CL419793
RSION     CL419793.1  GI:45280509
YWORDS    GSS.
URCE      Zea mays
ORGANISM  Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
FERENCE   1  (bases 1 to 734)
AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
          Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
ITLE      Sequencing of the maize genome at PGIR (2003c)
OURNAL    Unpublished (2003)
MMENT     Contact: Bharti,A.K.
          Dr.Joachim Messing's lab
          The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
          University
          190 Frelinghuysen Road, Piscataway, NJ 08854, USA
          Tel: 732 445 3801
          Fax: 732 445 5735
          Email: bharti@waksman.rutgers.edu
          Seq primer: T7
          Class: BAC ends
          High quality sequence start: 126.
FEATURES              Location/Qualifiers
     source           1. .734
                      /organism="Zea mays"
                      /mol_type="genomic DNA"
                      /cultivar="B73"
                      /db_xref="taxon:4577"
                      /clone="ZMMBBb0423N02"
                      /lab_host="E. coli DH10B"
                      /clone_lib="ZMMBBb (HindIII)"
                      /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Alignment Scores:
Pred. No.:              463           Length:        734
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            4.1%          Indels:        0
DB:                     13            Gaps:          0

US-10-821-670A-33 (1-222) x CL419793 (1-734)

Qy          28 LeuProThrProThrProSerProGly 36
               ||||||||||||||||||||||||||||
Db         491 TTGCCAACCCCGACACCATCACCTGGG 517

RESULT 97
DR608205/c
LOCUS       DR608205                736 bp    mRNA    linear   EST 11-JUL-2005
DEFINITION  EST998333 FvG Gibberella moniliformis cDNA clone FVGCH20, mRNA
            sequence.
ACCESSION   DR608205
VERSION     DR608205.1  GI:70682853
KEYWORDS    EST.
SOURCE      Gibberella moniliformis
  ORGANISM  Gibberella moniliformis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.,
            Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
            Kendra,D.F., Town,C.D. and Whitelaw,C.A.
  TITLE     Comparative analysis of 87,000 expressed sequence tags from the
            fumonisin-producing fungus Fusarium verticillioides
  JOURNAL   Fungal Genet. Biol. 42 (10), 848-861 (2005)
  PUBMED    16099185
COMMENT     Contact: Brown, D.W.
            USDA/ARS/NCAUR
            USDA
            1815 N. University St, Peoria, IL 61604, USA
            Tel: 309 681 6230
            Fax: 309 681 6689
            Email: browndw@ncaur.usda.gov
            TIGR sequence name: FVGCH20TH
            Seq primer: AAT TAA CCC TCA CTA AAG GG.
FEATURES              Location/Qualifiers
     source           1. .736
                      /organism="Gibberella moniliformis"
                      /mol_type="mRNA"
                      /strain="m3125"
                      /db_xref="taxon:117187"
                      /clone="FVGCH20"
                      /tissue_type="mycelia"
```

/clone_lib="FvG"
/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI; Site_2: XhoI; anamorph: Fusarium verticillioides. Mycelia was collected after growth in liquid GYAM medium for 96 hours. Cultures were vacuum filtered and the mycelial mats were frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIzol. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

'GIN

gnment Scores:

d. No.:	464	Length:	736
re:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.1%	Indels:	0
	10	Gaps:	0

-10-821-670A-33 (1-222) x DR608205 (1-736)

```
Qy         13 LeuValLeuLeuAsnHisLeuAspHis 21
              |||||||||||||||||||||||||||
Db        483 CTTGTCCTGCTGAACCATTTGGATCAT 457
```

ULT 98
395353
US CG395353 750 bp DNA linear GSS 22-SEP-2003
INITION ZMMBBc0010N12r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0010N12 3', genomic survey sequence.
CESSION CG395353
SION CG395353.1 GI:34338578
WORDS GSS.
URCE Zea mays
RGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
ERENCE 1 (bases 1 to 750)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
ITLE Sequencing of the maize genome at PGIR (2003b)
OURNAL Unpublished (2003)
MMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 420.

ATURES	Location/Qualifiers
source	1. .750
	/organism="Zea mays"
	/mol_type="genomic DNA"
	/cultivar="B73"
	/db_xref="taxon:4577"
	/clone="ZMMBBc0010N12"
	/lab_host="E. coli DH10B"
	/clone_lib="ZMMBBc (EcoRI)"
	/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

IGIN

gnment Scores:

ed. No.:	473	Length:	750
re:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	4.1%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-33 (1-222) x CG395353 (1-750)

```
Qy         28 LeuProThrProThrProSerProGly 36
              ||||||||||||||||||||||||||||||
Db        179 CTGCCAACCCCGACACCATCACCTGGG 205
```

RESULT 99
CG875642
LOCUS CG875642 753 bp DNA linear GSS 26-NOV-2003
DEFINITION ZMMBBc0286L13r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0286L13 3', genomic survey sequence.
ACCESSION CG875642
VERSION CG875642.1 GI:38540698
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 753)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PGIR (2003c)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 478.

FEATURES	Location/Qualifiers
source	1. .753
	/organism="Zea mays"
	/mol_type="genomic DNA"
	/cultivar="B73"
	/db_xref="taxon:4577"
	/clone="ZMMBBc0286L13"
	/lab_host="E. coli DH10B"
	/clone_lib="ZMMBBc (EcoRI)"
	/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Alignment Scores:

Pred. No.:	475	Length:	753
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-33 (1-222) x CG875642 (1-753)

```
Qy         28 LeuProThrProThrProSerProGly 36
              ||||||||||||||||||||||||||||||
Db        313 TTACCAACCCCGACGCCATCACCTGGG 339
```

RESULT 100
AJ701803/c
LOCUS AJ701803 758 bp mRNA linear EST 28-JAN-2005
DEFINITION AJ701803 ZAAE floral spathe MPIZ-ADIS-062 cDNA Zantedeschia aethiopica cDNA clone J-5-2, mRNA sequence.
ACCESSION AJ701803
VERSION AJ701803.1 GI:58317418
KEYWORDS EST.
SOURCE Zantedeschia aethiopica
ORGANISM Zantedeschia aethiopica

```
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Aroideae;
          Zantedeschieae; Zantedeschia.
FERENCE   1  (bases 1 to 758)
AUTHORS   Piques,M.C., Werber,M., Lino-Neto,T., Barbeta,C., Tavares,R.M.,
          Weisshaar,B., Pais,M.S. and Palme,K.
TITLE     Gene expression analysis during Zantedeschia aethiopica floral
          spathe senescence and senescence-inhibition using EST sequencing
          and cDNA arrays
JOURNAL   Unpublished (2005)
MMENT     Contact: Piques MC
          Institut fuer Biologie II
          Albert-Ludwigs-Universitaet Freiburg
          Schaenzlestr. 1, D-79104 Freiburg, GERMANY.
ATURES             Location/Qualifiers
   source          1. .758
                   /organism="Zantedeschia aethiopica"
                   /mol_type="mRNA"
                   /db_xref="taxon:69721"
                   /clone="J-5-2"
                   /tissue_type="floral spathe"
                   /dev_stage="floral spathe whitening and regreening"
                   /lab_host="Escherichia coli strain TOP10"
                   /clone_lib="ZAAE floral spathe MPIZ-ADIS-062 cDNA"
                   /note="Vector: pSPORT1; cDNA synthesis was performed using
                   SuperScript system (Invitrogen) and directionally-cloned
                   (Sal I at the 5'-end and Not I at the 3'-end) into pSPORT1
                   (U12390.1) country: Portugal:Braga"
IGIN

gnment Scores:
ed. No.:              478          Length:         758
ore:                  9.00         Matches:        9
cent Similarity:      100.0%       Conservative:   0
st Local Similarity:  100.0%       Mismatches:     0
ry Match:             4.1%         Indels:         0
                      1            Gaps:           0

10-821-670A-33 (1-222) x AJ701803 (1-758)

         16 LeuAsnHisLeuAspHisLeuSerLeu 24
            |||||||||||||||||||||||||
        227 TTGAACCATTTGGACCACCTGTCTTTG 201


rch completed: June 10, 2006, 16:33:22
 time : 3104.04 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 01:43:45 ; Search time 126.554 Seconds
(without alignments)
4923.420 Million cell updates/sec

tle: US-10-821-670A-33
:fect score: 222
quence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

.oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 1403666 seqs, 935554401 residues

:d size: 1

tal number of hits satisfying chosen parameters: 2800942

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlp
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110458_27682/app_query.fasta_1
B=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rni
INMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
RANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
LIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
AXLEN=2000000000 -HOST=abss05p
SER=US10821670_@CGN_1_1_677_@runat_07062006_110458_27682 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	222	100.0	666	3	US-09-917-265A-32	Sequence 32, Appl
2	222	100.0	666	3	US-09-917-265A-34	Sequence 34, Appl
3	220	99.1	689	3	US-09-011-143-26	Sequence 26, Appl
4	220	99.1	689	3	US-09-302-495-26	Sequence 26, Appl
5	220	99.1	689	3	US-10-079-616-26	Sequence 26, Appl
6	220	99.1	1441	3	US-09-011-143-8	Sequence 8, Appli
7	220	99.1	1441	3	US-09-302-495-8	Sequence 8, Appli
8	220	99.1	1441	3	US-10-079-616-8	Sequence 8, Appli
9	197	88.7	591	3	US-09-917-265A-35	Sequence 35, Appl
c 10	197	88.7	591	3	US-09-917-265A-37	Sequence 37, Appl
11	197	88.7	1533	3	US-09-917-265A-43	Sequence 43, Appl
c 12	197	88.7	1533	3	US-09-917-265A-45	Sequence 45, Appl
13	197	88.7	1599	3	US-09-917-265A-38	Sequence 38, Appl
c 14	197	88.7	1599	3	US-09-917-265A-40	Sequence 40, Appl
15	195	87.8	591	3	US-09-011-143-9	Sequence 9, Appli
16	195	87.8	591	3	US-09-302-495-9	Sequence 9, Appli
17	195	87.8	591	3	US-10-079-616-9	Sequence 9, Appli
18	187	84.2	561	3	US-09-917-265A-101	Sequence 101, App
c 19	187	84.2	561	3	US-09-917-265A-103	Sequence 103, App
20	52	23.4	591	3	US-09-917-265A-49	Sequence 49, Appl
c 21	52	23.4	591	3	US-09-917-265A-51	Sequence 51, Appl
22	52	23.4	666	3	US-09-917-265A-46	Sequence 46, Appl
c 23	52	23.4	666	3	US-09-917-265A-48	Sequence 48, Appl
24	52	23.4	669	3	US-09-079-984A-2	Sequence 2, Appli
25	52	23.4	669	3	US-09-079-984A-12	Sequence 12, Appl
26	52	23.4	669	3	US-09-390-729-2	Sequence 2, Appli
27	52	23.4	669	3	US-09-390-729-12	Sequence 12, Appl
28	52	23.4	1455	3	US-09-917-265A-104	Sequence 104, App
c 29	52	23.4	1455	3	US-09-917-265A-106	Sequence 106, App
30	52	23.4	1533	3	US-09-917-265A-66	Sequence 66, Appl
c 31	52	23.4	1533	3	US-09-917-265A-68	Sequence 68, Appl
32	52	23.4	1599	3	US-09-917-265A-61	Sequence 61, Appl
c 33	52	23.4	1599	3	US-09-917-265A-63	Sequence 63, Appl
34	29	13.1	601	3	US-09-949-016-20385	Sequence 20385, A
35	29	13.1	601	3	US-09-949-016-87352	Sequence 87352, A
36	29	13.1	660	2	US-08-186-529-3	Sequence 3, Appli
37	29	13.1	660	2	US-08-640-386A-3	Sequence 3, Appli
38	29	13.1	721	2	US-08-184-009-199	Sequence 199, App
39	29	13.1	721	2	US-08-458-356-199	Sequence 199, App
40	29	13.1	721	3	US-08-460-736-199	Sequence 199, App
41	29	13.1	721	3	US-09-535-370-199	Sequence 199, App
42	29	13.1	721	3	US-09-663-667-199	Sequence 199, App
43	29	13.1	762	3	US-08-848-760B-21	Sequence 21, Appl
44	29	13.1	762	3	US-09-826-025-21	Sequence 21, Appl
45	29	13.1	762	5	US-09-543-679A-2890	Sequence 2890, Ap
46	29	13.1	1019	3	US-09-949-016-2462	Sequence 2462, Ap
47	29	13.1	1026	2	US-08-751-767A-1	Sequence 1, Appli
48	29	13.1	1026	3	US-09-023-655-1041	Sequence 1041, Ap
49	29	13.1	1026	3	US-09-949-016-130	Sequence 130, App
50	29	13.1	1287	3	US-09-634-368-6	Sequence 6, Appli
51	29	13.1	1316	2	US-08-684-687-3	Sequence 3, Appli
52	29	13.1	1316	3	US-09-851-520-3	Sequence 3, Appli
53	29	13.1	1364	2	US-08-265-087-3	Sequence 3, Appli
54	29	13.1	1364	2	US-08-621-493-3	Sequence 3, Appli
55	29	13.1	1364	2	US-08-965-688-3	Sequence 3, Appli
56	29	13.1	1364	3	US-09-260-173-3	Sequence 3, Appli
57	29	13.1	1395	3	US-09-924-703-5	Sequence 5, Appli
58	29	13.1	1560	2	US-08-751-767A-11	Sequence 11, Appl
59	29	13.1	1623	2	US-08-751-767A-9	Sequence 9, Appli
60	29	13.1	1645	3	US-09-310-842-2	Sequence 2, Appli
61	29	13.1	4521	5	US-09-543-679A-2893	Sequence 2893, Ap
62	29	13.1	6139	2	US-08-751-767A-7	Sequence 7, Appli
63	29	13.1	10764	3	US-09-949-016-11872	Sequence 11872, A
64	29	13.1	10765	3	US-09-949-016-14204	Sequence 14204, A
65	28	12.6	601	3	US-09-949-016-20381	Sequence 20381, A
66	28	12.6	601	3	US-09-949-016-87348	Sequence 87348, A
67	26	11.7	79	3	US-09-011-143-24	Sequence 24, Appl
68	26	11.7	79	3	US-09-302-495-24	Sequence 24, Appl
69	26	11.7	79	3	US-10-079-616-24	Sequence 24, Appl
70	23	10.4	95	3	US-09-011-143-22	Sequence 22, Appl
71	23	10.4	95	3	US-09-302-495-22	Sequence 22, Appl
72	23	10.4	95	3	US-10-079-616-22	Sequence 22, Appl
c 73	12	5.4	36	3	US-09-011-143-25	Sequence 25, Appl
c 74	12	5.4	36	3	US-09-302-495-25	Sequence 25, Appl
c 75	12	5.4	36	3	US-10-079-616-25	Sequence 25, Appl
76	11	5.0	39	3	US-09-917-265A-91	Sequence 91, Appl
77	10	4.5	39	3	US-09-079-984A-15	Sequence 15, Appl
78	10	4.5	39	3	US-09-390-729-15	Sequence 15, Appl
79	10	4.5	60	3	US-09-917-265A-83	Sequence 83, Appl
c 80	10	4.5	60	3	US-09-917-265A-84	Sequence 84, Appl

81	10	4.5	582	3	US-09-634-368-1	Sequence 1, Appli
82	10	4.5	713	2	US-08-385-335A-10	Sequence 10, Appl
83	10	4.5	1278	3	US-09-634-368-5	Sequence 5, Appli
84	10	4.5	1569	3	US-09-634-368-12	Sequence 12, Appl
85	10	4.5	2013	3	US-09-634-368-11	Sequence 11, Appl
86	10	4.5	2709	3	US-09-634-368-13	Sequence 13, Appl
87	10	4.5	6295	2	US-08-659-206A-4	Sequence 4, Appli
88	10	4.5	7287	2	US-08-659-206A-1	Sequence 1, Appli
89	9	4.1	51	3	US-09-917-265A-96	Sequence 96, Appl
90	9	4.1	2210	3	US-08-464-700-53	Sequence 53, Appl
91	9	4.1	2242	2	US-08-641-627A-37	Sequence 37, Appl
92	9	4.1	2427	2	US-08-678-039A-39	Sequence 39, Appl
93	9	4.1	2845	3	US-10-104-047-945	Sequence 945, App
94	8	3.6	25	3	US-09-396-196G-121547	Sequence 121547,
95	8	3.6	27	3	US-09-917-265A-90	Sequence 90, Appl
96	8	3.6	41	3	US-09-917-265A-92	Sequence 92, Appl
97	8	3.6	452	3	US-09-621-976-13237	Sequence 13237, A
98	8	3.6	479	3	US-09-270-767-5297	Sequence 5297, Ap
99	8	3.6	479	3	US-09-270-767-20579	Sequence 20579, A
100	8	3.6	601	3	US-09-270-767-12534	Sequence 12534, A
101	8	3.6	601	3	US-09-949-016-60737	Sequence 60737, A
102	8	3.6	601	3	US-09-949-016-60738	Sequence 60738, A
103	8	3.6	601	3	US-09-949-016-60739	Sequence 60739, A
104	8	3.6	601	3	US-09-949-016-68714	Sequence 68714, A
105	8	3.6	601	3	US-09-949-016-68715	Sequence 68715, A
106	8	3.6	601	3	US-09-949-016-68716	Sequence 68716, A
107	8	3.6	601	3	US-09-949-016-111391	Sequence 111391,
108	8	3.6	601	3	US-09-949-016-111392	Sequence 111392,
109	8	3.6	601	3	US-09-949-016-147156	Sequence 147156,
110	8	3.6	601	3	US-09-949-016-154644	Sequence 154644,
111	8	3.6	601	3	US-09-949-016-154645	Sequence 154645,
112	8	3.6	762	3	US-08-956-171E-789	Sequence 789, App
113	8	3.6	762	3	US-08-781-986A-789	Sequence 789, App
114	8	3.6	1257	2	US-08-964-631-1	Sequence 1, Appli
115	8	3.6	1257	3	US-09-210-000-1	Sequence 1, Appli
116	8	3.6	1380	3	US-09-134-000C-3234	Sequence 3234, Ap
117	8	3.6	1465	4	US-09-605-703B-525	Sequence 525, App
118	8	3.6	1532	3	US-09-270-767-12796	Sequence 12796, A
119	8	3.6	1570	4	US-09-605-703B-523	Sequence 523, App
120	8	3.6	1697	3	US-09-902-540-8882	Sequence 8882, Ap
121	8	3.6	2249	3	US-08-814-052-19	Sequence 19, Appl
122	8	3.6	2279	3	US-08-814-052-17	Sequence 17, Appl
123	8	3.6	2300	3	US-08-814-052-18	Sequence 18, Appl
124	8	3.6	2792	3	US-10-104-047-458	Sequence 458, App
125	8	3.6	2957	3	US-09-221-017B-775	Sequence 775, App
126	8	3.6	3098	3	US-10-104-047-401	Sequence 401, App
127	8	3.6	3183	2	US-08-939-218A-1	Sequence 1, Appli
128	8	3.6	3187	7	PCT-US95-06815-1	Sequence 1, Appli
129	8	3.6	3192	2	US-08-706-037-26	Sequence 26, Appl
130	8	3.6	3192	2	US-08-940-661A-1	Sequence 1, Appli
131	8	3.6	3192	2	US-09-083-485-1	Sequence 1, Appli
132	8	3.6	3192	2	US-09-005-397-26	Sequence 26, Appl
133	8	3.6	4447	3	US-09-949-016-15763	Sequence 15763, A
134	8	3.6	4623	3	US-09-949-016-15769	Sequence 15769, A
135	8	3.6	9704	3	US-09-814-951A-3	Sequence 3, Appli
136	8	3.6	9704	3	US-10-109-860B-3	Sequence 3, Appli
137	8	3.6	9905	3	US-09-949-016-16862	Sequence 16862, A
138	8	3.6	9937	3	US-09-902-540-946	Sequence 946, App
139	8	3.6	37531	3	US-09-949-002-602	Sequence 602, App
140	8	3.6	37531	3	US-09-949-002-764	Sequence 764, App
141	8	3.6	45086	3	US-09-949-016-14816	Sequence 14816, A
142	8	3.6	134890	3	US-09-949-016-15602	Sequence 15602, A
143	8	3.6	137226	3	US-09-949-016-13763	Sequence 13763, A
144	8	3.6	275110	3	US-09-949-016-12706	Sequence 12706, A
145	8	3.6	275110	3	US-09-949-016-16070	Sequence 16070, A
146	8	3.6	283538	3	US-09-949-016-13506	Sequence 13506, A
147	8	3.6	374159	3	US-09-949-016-15868	Sequence 15868, A
148	7	3.2	21	3	US-09-011-143-17	Sequence 17, Appl
149	7	3.2	21	3	US-09-011-143-18	Sequence 18, Appl
150	7	3.2	21	3	US-09-302-495-17	Sequence 17, Appl
151	7	3.2	21	3	US-09-302-495-18	Sequence 18, Appl
152	7	3.2	21	3	US-10-079-616-17	Sequence 17, Appl
153	7	3.2	21	3	US-10-079-616-18	Sequence 18, Appl
154	7	3.2	32	2	US-08-859-998-383	Sequence 383, App
155	7	3.2	32	3	US-09-225-928-383	Sequence 383, App
156	7	3.2	32	3	US-09-225-201B-383	Sequence 383, App
c 157	7	3.2	39	3	US-09-079-984A-16	Sequence 16, Appl
c 158	7	3.2	39	3	US-09-390-729-16	Sequence 16, Appl
159	7	3.2	94	2	US-08-497-134A-17	Sequence 17, Appl
c 160	7	3.2	146	3	US-09-513-999C-35664	Sequence 35664, A
161	7	3.2	153	3	US-08-651-136C-39	Sequence 39, Appl
162	7	3.2	153	3	US-09-229-911A-39	Sequence 39, Appl
163	7	3.2	153	3	US-10-007-521-39	Sequence 39, Appl
c 164	7	3.2	185	3	US-09-513-999C-14715	Sequence 14715, A
c 165	7	3.2	186	3	US-09-787-986A-8	Sequence 8, Appli
c 166	7	3.2	201	4	US-09-880-107-1316	Sequence 1316, Ap
c 167	7	3.2	210	3	US-09-107-433-2218	Sequence 2218, Ap
168	7	3.2	225	2	US-08-073-807A-7	Sequence 7, Appli
c 169	7	3.2	225	3	US-09-134-000C-1758	Sequence 1758, Ap
170	7	3.2	233	3	US-09-513-999C-35730	Sequence 35730, A
171	7	3.2	235	3	US-09-009-156-9	Sequence 9, Appli
172	7	3.2	235	3	US-09-372-154-9	Sequence 9, Appli
173	7	3.2	235	3	US-09-950-688-9	Sequence 9, Appli
174	7	3.2	245	3	US-09-513-999C-21110	Sequence 21110, A
c 175	7	3.2	256	3	US-09-313-294A-2559	Sequence 2559, Ap
176	7	3.2	270	3	US-09-248-796A-12538	Sequence 12538, A
c 177	7	3.2	271	3	US-09-313-294A-848	Sequence 848, App
c 178	7	3.2	272	3	US-09-513-999C-17321	Sequence 17321, A
179	7	3.2	277	3	US-09-313-294A-6859	Sequence 6859, Ap
180	7	3.2	291	3	US-09-270-767-28709	Sequence 28709, A
181	7	3.2	299	3	US-09-313-294A-786	Sequence 786, App
182	7	3.2	299	4	US-09-297-648-564	Sequence 564, App
183	7	3.2	301	3	US-09-270-767-2250	Sequence 2250, Ap
184	7	3.2	301	3	US-09-270-767-17532	Sequence 17532, A
c 185	7	3.2	313	3	US-09-621-976-16883	Sequence 16883, A
186	7	3.2	314	3	US-09-513-999C-22788	Sequence 22788, A
187	7	3.2	323	3	US-09-009-156-8	Sequence 8, Appli
188	7	3.2	323	3	US-09-372-154-8	Sequence 8, Appli
189	7	3.2	323	3	US-09-392-184-25	Sequence 25, Appl
190	7	3.2	323	3	US-09-950-688-8	Sequence 8, Appli
c 191	7	3.2	324	3	US-10-149-736-33	Sequence 33, Appl
192	7	3.2	326	3	US-09-673-395A-64	Sequence 64, Appl
c 193	7	3.2	332	3	US-09-513-999C-11474	Sequence 11474, A
194	7	3.2	337	3	US-09-188-930-50	Sequence 50, Appl
195	7	3.2	337	3	US-09-312-283C-50	Sequence 50, Appl
c 196	7	3.2	363	3	US-09-248-796A-1466	Sequence 1466, Ap
c 197	7	3.2	375	3	US-09-601-198-91	Sequence 91, Appl
c 198	7	3.2	376	3	US-09-149-476-201	Sequence 201, App
199	7	3.2	409	3	US-09-640-211A-1395	Sequence 1395, Ap
200	7	3.2	419	3	US-09-799-451-705	Sequence 705, App

ALIGNMENTS

```
RESULT 1
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
```

```
  LOCATION: (1)..(666)
-09-917-265A-32

ignment Scores:
ed. No.:                8.23e-219       Length:         666
ore:                    222.00          Matches:        222
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              100.0%          Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265A-32 (1-666)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

        221 AlaSer 222
            ||||||
        661 GCTTCC 666

SULT 2
-09-917-265A-34/c
Sequence 34, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

Alignment Scores:
Pred. No.:              8.23e-219       Length:         666
Score:                  222.00          Matches:        222
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265A-34 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
              ||||||
Db          6 GCTTCC 1

RESULT 3
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
```

```
  APPLICANT:  IMAMURA, Takayuki
  APPLICANT:  MAEDA, Hiroaki
  APPLICANT:  FUJIYASU, Takeshi
  APPLICANT:  IMAGAWA, Yoshitaka
  APPLICANT:  TOKIYOSHI, Sachio
  TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
  NUMBER OF SEQUENCES:  26
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  BROWDY AND NEIMARK
    STREET:  419 Seventh Street, N.W., Suite 300
    CITY:  Washington
    STATE:  D.C.
    COUNTRY:  USA
    ZIP:  20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/011,143
    FILING DATE:  04-FEB-1998
    CLASSIFICATION:  536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/JP97/01824
    FILING DATE:  29-MAY-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  JP 165249/1996
    FILING DATE:  04-JUN-1996
  ATTORNEY/AGENT INFORMATION:
    NAME:  BROWDY, Roger L.
    REGISTRATION NUMBER:  25,618
    REFERENCE/DOCKET NUMBER:  IMAMURA=1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  202-628-5197
    TELEFAX:  202-737-3528
INFORMATION FOR SEQ ID NO:  26:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  689 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
-09-011-143-26

ignment Scores:
ed. No.:              9.67e-217      Length:        689
re:                   220.00         Matches:       220
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            99.1%          Indels:        0
:                     3              Gaps:          0

-10-821-670A-33 (1-222) x US-09-011-143-26 (1-689)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy       101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy       121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy       141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy       161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy       181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy       201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

RESULT 4
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
```

```
          TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
-09-302-495-26

ignment Scores:
ed. No.:                9.67e-217       Length:         689
ore:                    220.00          Matches:        220
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              99.1%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-302-495-26 (1-689)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

SULT 5
-10-079-616-26
Sequence 26, Application US/10079616
Patent No. 6566097
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
;           STREET: 419 Seventh Street, N.W., Suite 300
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20004
;      COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/079,616
;           FILING DATE: 22-Feb-2002
;           CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/011,143
;           FILING DATE: 04-FEB-1998
;           APPLICATION NUMBER: PCT/JP97/01824
;           FILING DATE: 29-MAY-1997
;           APPLICATION NUMBER: JP 165249/1996
;           FILING DATE: 04-JUN-1996
;      ATTORNEY/AGENT INFORMATION:
;           NAME: BROWDY, Roger L.
;           REGISTRATION NUMBER: 25,618
;           REFERENCE/DOCKET NUMBER: IMAMURA=1
;      TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 202-628-5197
;           TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 26:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 689 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;      MOLECULE TYPE: cDNA
;      SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

Alignment Scores:
Pred. No.:              9.67e-217       Length:         689
Score:                  220.00          Matches:        220
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            99.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-079-616-26 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

      141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

      161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

      181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

      201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666
```

SULT 6
-09-011-143-8
Sequence 8, Application US/09011143
Patent No. 6472509
GENERAL INFORMATION:
APPLICANT: IMAMURA, Takayuki
APPLICANT: MAEDA, Hiroaki
APPLICANT: FUJIYASU, Takeshi
APPLICANT: IMAGAWA, Yoshitaka
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,143
FILING DATE: 04-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
-09-011-143-8

lgnment Scores:

ed. No.:	1.95e-216	Length:	1441
ore:	220.00	Matches:	220
rcent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.1%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-011-143-8 (1-1441)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802
```

RESULT 7
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```
        SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/302,495
        FILING DATE: 30-Apr-1999
        CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/09/011,143
        FILING DATE: 04-FEB-1998
        APPLICATION NUMBER: PCT/JP97/01824
        FILING DATE: 29-MAY-1997
        APPLICATION NUMBER: JP 165249/1996
        FILING DATE: 04-JUN-1996
      ATTORNEY/AGENT INFORMATION:
        NAME: BROWDY, Roger L.
        REGISTRATION NUMBER: 25,618
        REFERENCE/DOCKET NUMBER: IMAMURA=1
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 202-628-5197
        TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 8:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 1441 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 8:
-09-302-495-8

ignment Scores:
ed. No.:              1.95e-216      Length:         1441
ore:                  220.00         Matches:        220
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            99.1%          Indels:         0
:                     3              Gaps:           0

-10-821-670A-33 (1-222) x US-09-302-495-8 (1-1441)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy      181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy      201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

RESULT 8
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: BROWDY AND NEIMARK
;           STREET: 419 Seventh Street, N.W., Suite 300
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20004
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/079,616
;           FILING DATE: 22-Feb-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/011,143
;           FILING DATE: 04-FEB-1998
;           APPLICATION NUMBER: PCT/JP97/01824
;           FILING DATE: 29-MAY-1997
;           APPLICATION NUMBER: JP 165249/1996
;           FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: BROWDY, Roger L.
;           REGISTRATION NUMBER: 25,618
;           REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 202-628-5197
;           TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1441 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

Alignment Scores:
Pred. No.:              1.95e-216      Length:         1441
Score:                  220.00         Matches:        220
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.1%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-33 (1-222) x US-10-079-616-8 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

       21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

       41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

       61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

       81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

      101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

      121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

      141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

      161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

      181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

      201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802
```

```
ULT 9
-09-917-265A-35
equence 35, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
EQ ID NO 35
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(591)
-09-917-265A-35

ignment Scores:
ed. No.:              3.68e-193      Length:        591
ore:                  197.00         Matches:       197
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
Query Match:          88.7%          Indels:        0
DB:                   3              Gaps:          0

US-10-821-670A-33 (1-222) x US-09-917-265A-35 (1-591)

Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

RESULT 10
US-09-917-265A-37/c
; Sequence 37, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-37

Alignment Scores:
Pred. No.:            3.68e-193      Length:        591
Score:                197.00         Matches:       197
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          88.7%          Indels:        0
```

```
                    3             Gaps:          0

-10-821-670A-33 (1-222) x US-09-917-265A-37 (1-591)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

SULT 11
-09-917-265A-43
Sequence 43, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 43
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1533)
-09-917-265A-43

ignment Scores:
ed. No.:              9.12e-193      Length:        1533
ore:                  197.00         Matches:       197
rcent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            88.7%        Indels:        0
DB:                     3            Gaps:          0

US-10-821-670A-33 (1-222) x US-09-917-265A-43 (1-1533)

Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

RESULT 12
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.:              9.12e-193      Length:        1533
Score:                  197.00         Matches:       197
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
```

ery Match: 88.7% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-917-265A-45 (1-1533)

```
 26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

 46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

 66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

 86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

ULT 13
-09-917-265A-38
equence 38, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 38
LENGTH: 1599
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
-09-917-265A-38

lgnment Scores:
ed. No.: 9.5e-193 Length: 1599
re: 197.00 Matches: 197

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 88.7% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-33 (1-222) x US-09-917-265A-38 (1-1599)

```
Qy   26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy   46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy   66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy   86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy  106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy  126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy  146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy  166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy  186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy  206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
```

RESULT 14
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.: 9.5e-193 Length: 1599
Score: 197.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0

```
:st Local Similarity:  100.0%          Mismatches:     0
:ery Match:            88.7%           Indels:         0
:                      3               Gaps:           0

;-10-821-670A-33 (1-222) x US-09-917-265A-40 (1-1599)

          26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

          46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

          66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

          86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

         106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

         126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

         146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

         166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

         186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

         206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||
          51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

SULT 15
;-09-011-143-9
Sequence 9, Application US/09011143
Patent No. 6472509
 GENERAL INFORMATION:
   APPLICANT:  IMAMURA, Takayuki
   APPLICANT:  MAEDA, Hiroaki
   APPLICANT:  FUJIYASU, Takeshi
   APPLICANT:  IMAGAWA, Yoshitaka
   APPLICANT:  TOKIYOSHI, Sachio
   TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
   NUMBER OF SEQUENCES:  26
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  BROWDY AND NEIMARK
     STREET:  419 Seventh Street, N.W., Suite 300
     CITY:  Washington
     STATE:  D.C.
     COUNTRY:  USA
     ZIP:  20004
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/011,143
     FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  591 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-9

Alignment Scores:
Pred. No.:              4.18e-191       Length:         591
Score:                  195.00          Matches:        195
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            87.8%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-011-143-9 (1-591)

Qy          26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy          46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy          66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy          86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy         126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy         146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy         166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy         186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy         206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
               ||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585
```

```
SULT 16
-09-302-495-9
Sequence 9, Application US/09302495
Patent No. 6518045
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
            STREET: 419 Seventh Street, N.W., Suite 300
            CITY: Washington
            STATE: D.C.
            COUNTRY: USA
            ZIP: 20004
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/302,495
            FILING DATE: 30-Apr-1999
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: US/09/011,143
            FILING DATE: 04-FEB-1998
            APPLICATION NUMBER: PCT/JP97/01824
            FILING DATE: 29-MAY-1997
            APPLICATION NUMBER: JP 165249/1996
            FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
            NAME: BROWDY, Roger L.
            REGISTRATION NUMBER: 25,618
            REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 202-628-5197
            TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 9:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 591 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
-09-302-495-9

ignment Scores:
ed. No.:              4.18e-191      Length:        591
ore:                  195.00         Matches:       195
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            87.8%          Indels:        0
:                     3              Gaps:          0

-10-821-670A-33 (1-222) x US-09-302-495-9 (1-591)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy          86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy         126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy         146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy         166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy         186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy         206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
               ||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

RESULT 17
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
```

```
           LENGTH: 591 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
:-10-079-616-9

.ignment Scores:
'ed. No.:              4.18e-191      Length:        591
:ore:                  195.00         Matches:       195
:rcent Similarity:     100.0%         Conservative:  0
:st Local Similarity:  100.0%         Mismatches:    0
!ery Match:            87.8%          Indels:        0
::                     3              Gaps:          0

:-10-821-670A-33 (1-222) x US-10-079-616-9 (1-591)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

:SULT 18
:-09-917-265A-101
 Sequence 101, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111

;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
US-09-917-265A-101

Alignment Scores:
Pred. No.:             6.67e-183      Length:        561
Score:                 187.00         Matches:       187
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           84.2%          Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-33 (1-222) x US-09-917-265A-101 (1-561)

Qy         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        216 MetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 19
US-09-917-265A-103/c
; Sequence 103, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
```

```
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
EQ ID NO 103
  LENGTH: 561
  TYPE: DNA
  ORGANISM: Felis catus
-09-917-265A-103

ignment Scores:
ed. No.:                6.67e-183       Length:         561
re:                     187.00          Matches:        187
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               84.2%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265A-103 (1-561)

         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

        216 MetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||
         21 ATGAGCTATCTGAATGCTTCC 1

ULT 20
-09-917-265A-49
equence 49, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-09-917-265A-49

Alignment Scores:
Pred. No.:              4.2e-44         Length:         591
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265A-49 (1-591)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               ||||||||||||||||||||||||||||||||||||
Db         238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 21
US-09-917-265A-51/c
; Sequence 51, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-51

Alignment Scores:
Pred. No.:              4.2e-44         Length:         591
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265A-51 (1-591)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355
```

```
       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           ||||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 22
-09-917-265A-46
Sequence 46, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
  LENGTH: 666
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(666)
-09-917-265A-46

ignment Scores:
ed. No.:              4.7e-44        Length:        666
ore:                  52.00          Matches:       52
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            23.4%          Indels:        0
:                     3              Gaps:          0

-10-821-670A-33 (1-222) x US-09-917-265A-46 (1-666)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           ||||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 23
-09-917-265A-48/c
Sequence 48, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
  LENGTH: 666
  TYPE: DNA
  ORGANISM: Canis familiaris
-09-917-265A-48

Alignment Scores:
Pred. No.:              4.7e-44        Length:        666
Score:                  52.00          Matches:       52
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            23.4%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-33 (1-222) x US-09-917-265A-48 (1-666)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               ||||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 24
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:
;   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;   APPLICANT:  Yamada, Katsushige
;   TITLE OF INVENTION:  Canine interleukin 12, a production method
;   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;   TITLE OF INVENTION:  method using it
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Miller & Christenbury Intellectual Property
;     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;     STREET:  1600 Market Street, 39th Floor
;     CITY:  Philadelphia
;     STATE:  PA
;     COUNTRY:  USA
;     ZIP:  19103
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy Disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/079,984A
;     FILING DATE:  15-MAY-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Austin R. Miller
;     REGISTRATION NUMBER:  16,602
;     REFERENCE/DOCKET NUMBER:  1051-98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-1810
;     TELEFAX:  (215) 568-6946
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  669 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM:  Canis familiaris
;   FEATURE:
;     NAME/KEY:  Canine IL12
;     LOCATION:  1 to 666
;     IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

Alignment Scores:
Pred. No.:              4.72e-44       Length:        669
```

```
ore:                52.00          Matches:       52
cent Similarity:    100.0%         Conservative:  0
st Local Similarity: 100.0%        Mismatches:    0
ery Match:          23.4%          Indels:        0
:                   3              Gaps:          0

-10-821-670A-33 (1-222) x US-09-079-984A-2 (1-669)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
       313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 25
-09-079-984A-12
Sequence 12, Application US/09079984A
Patent No. 6231850
 GENERAL INFORMATION:
   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
   APPLICANT:  Yamada, Katsushige
   TITLE OF INVENTION:  Canine interleukin 12, a production method
   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
   TITLE OF INVENTION:  method using it
   NUMBER OF SEQUENCES:  16
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Miller & Christenbury Intellectual Property
     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
     STREET:  1600 Market Street, 39th Floor
     CITY:  Philadelphia
     STATE:  PA
     COUNTRY:  USA
     ZIP:  19103
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy Disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  WordPerfect 5.1
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/079,984A
     FILING DATE:  15-MAY-1998
   ATTORNEY/AGENT INFORMATION:
     NAME:  Austin R. Miller
     REGISTRATION NUMBER:  16,602
     REFERENCE/DOCKET NUMBER:  1051-98
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (215) 563-1810
     TELEFAX:  (215) 568-6946
 INFORMATION FOR SEQ ID NO:  12:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  669 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA to mRNA
   ORIGINAL SOURCE:
     ORGANISM:  Canis familiaris
   FEATURE:
     NAME/KEY:  Canine IL12
     LOCATION:  1 to 666
     IDENTIFICATION METHOD:  Similarity
-09-079-984A-12

ignment Scores:
ed. No.:            4.72e-44       Length:        669
ore:                52.00          Matches:       52
cent Similarity:    100.0%         Conservative:  0
```

```
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:        23.4%          Indels:        0
DB:                 3              Gaps:          0

US-10-821-670A-33 (1-222) x US-09-079-984A-12 (1-669)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 26
US-09-390-729-2
; Sequence 2, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-2

Alignment Scores:
Pred. No.:          4.72e-44       Length:        669
Score:              52.00          Matches:       52
```

rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 23.4% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-390-729-2 (1-669)

```
Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

SULT 27
-09-390-729-12
Sequence 12, Application US/09390729
Patent No. 6562334
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/390,729
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/079,984
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 666
IDENTIFICATION METHOD: Similarity
-09-390-729-12

ignment Scores:
ed. No.: 4.72e-44 Length: 669

Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 23.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-33 (1-222) x US-09-390-729-12 (1-669)

```
Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348
```

RESULT 28
US-09-917-265A-104
; Sequence 104, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(897)
US-09-917-265A-104

Alignment Scores:
Pred. No.: 9.91e-44 Length: 1455
Score: 52.00 Matches: 52
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 23.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-33 (1-222) x US-09-917-265A-104 (1-1455)

```
Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579
```

RESULT 29
US-09-917-265A-106/c
; Sequence 106, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.

APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 106
LENGTH: 1455
TYPE: DNA
ORGANISM: Canis familiaris
-09-917-265A-106

ignment Scores:

ed. No.:	9.91e-44	Length:	1455
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	23.4%	Indels:	0
:	3	Gaps:	0

-10-821-670A-33 (1-222) x US-09-917-265A-106 (1-1455)

```
Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||||
Db        912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877
```

SULT 30
-09-917-265A-66
Sequence 66, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66
LENGTH: 1533
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
-09-917-265A-66

ignment Scores:

ed. No.:	1.04e-43	Length:	1533
ore:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	23.4%	Indels:	0
:	3	Gaps:	0

-10-821-670A-33 (1-222) x US-09-917-265A-66 (1-1533)

```
Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215
```

RESULT 31
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265A-68

Alignment Scores:

Pred. No.:	1.04e-43	Length:	1533
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-917-265A-68 (1-1533)

```
Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319
```

RESULT 32
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61

LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
-09-917-265A-61

ignment Scores:
ed. No.: 1.08e-43 Length: 1599
ore: 52.00 Matches: 52
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 23.4% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-917-265A-61 (1-1599)

65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

SULT 33
-09-917-265A-63/c
Sequence 63, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
-09-917-265A-63

ignment Scores:
ed. No.: 1.08e-43 Length: 1599
ore: 52.00 Matches: 52
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 23.4% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-917-265A-63 (1-1599)

65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 34
US-09-949-016-20385
; Sequence 20385, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20385
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-20385

Alignment Scores:
Pred. No.: 1.88e-20 Length: 601
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-33 (1-222) x US-09-949-016-20385 (1-601)

Qy 184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
Db 91 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 150

Qy 204 AlaPheArgIleArgAlaValThrIle 212
Db 151 GCTTTCAGAATTCGGGCAGTGACTATT 177

RESULT 35
US-09-949-016-87352
; Sequence 87352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87352
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-87352

Alignment Scores:
Pred. No.: 1.88e-20 Length: 601
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0

```
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            13.1%         Indels:        0
:                     3             Gaps:          0

-10-821-670A-33 (1-222) x US-09-949-016-87352 (1-601)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         91 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 150

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
        151 GCTTTCAGAATTCGGGCAGTGACTATT 177

SULT 36
-08-186-529-3
Sequence 3, Application US/08186529
Patent No. 5573764
 GENERAL INFORMATION:
   APPLICANT:  Sykes, Megan
   APPLICANT:  Wolf, Stanley F.
   TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
   TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
     STREET:  87 CambridgePark Drive
     CITY:  Cambridge
     STATE:  MA
     COUNTRY:  USA
     ZIP:  02140
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/186,529
     FILING DATE:
     CLASSIFICATION:  424
   ATTORNEY/AGENT INFORMATION:
     NAME:  McDaniels, Patricia A.
     REGISTRATION NUMBER:  33,194
     REFERENCE/DOCKET NUMBER:  GI 5225
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  617-498-8401
     TELEFAX:  617-876-5851
 INFORMATION FOR SEQ ID NO:  3:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  660 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   ORIGINAL SOURCE:
     ORGANISM:  Homo sapiens
     CELL TYPE:  Lymphoblast
     CELL LINE:  RPMI 8866
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  1..660
-08-186-529-3

ignment Scores:
ed. No.:              2.05e-20       Length:        660
ore:                  29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     2              Gaps:          0

-10-821-670A-33 (1-222) x US-08-186-529-3 (1-660)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
Db      601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 37
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

Alignment Scores:
Pred. No.:            2.05e-20       Length:        660
Score:                29.00          Matches:       29
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:          13.1%          Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-33 (1-222) x US-08-640-386A-3 (1-660)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
```

```
        601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 38
-08-184-009-199
Sequence 199, Application US/08184009
Patent No. 5833975
 GENERAL INFORMATION:
   APPLICANT:  Paoletti, Enzo
   APPLICANT:  Tartaglia, James
   APPLICANT:  Cox, William I.
   TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
   NUMBER OF SEQUENCES:  217
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Curtis, Morris & Safford
     STREET:  530 Fifth Avenue
     CITY:  New York
     STATE:  NY
     COUNTRY:  USA
     ZIP:  10036
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/184,009
     FILING DATE:  19-JAN-1994
     CLASSIFICATION:  435
   ATTORNEY/AGENT INFORMATION:
     NAME:  Frommer, William S.
     REGISTRATION NUMBER:  25,506
     REFERENCE/DOCKET NUMBER:  454310-2530
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (212) 840-3333
     TELEFAX:  (212) 840-0712
     TELEX:  425066CURTMS
  INFORMATION FOR SEQ ID NO:  199:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  721 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-08-184-009-199

ignment Scores:
ed. No.:                2.23e-20        Length:         721
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-33 (1-222) x US-08-184-009-199 (1-721)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

SULT 39
-08-458-356-199
Sequence 199, Application US/08458356
Patent No. 5942235
 GENERAL INFORMATION:
   APPLICANT:  Paoletti, Enzo
   APPLICANT:  Tartaglia, James
   APPLICANT:  Cox, William I.
   TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
   NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-199

Alignment Scores:
Pred. No.:                2.23e-20        Length:         721
Score:                    29.00           Matches:        29
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              13.1%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-33 (1-222) x US-08-458-356-199 (1-721)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 40
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/460,736
     FILING DATE:  02-JUN-1995
     CLASSIFICATION:  514
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  US 08/184,009
     FILING DATE:  19-JAN-1994
   ATTORNEY/AGENT INFORMATION:
     NAME:  Frommer, William S.
     REGISTRATION NUMBER:  25,506
     REFERENCE/DOCKET NUMBER:  454310-2530
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (212) 840-3333
     TELEFAX:  (212) 840-0712
     TELEX:  425066CURTMS
 INFORMATION FOR SEQ ID NO:  199:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  721 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-08-460-736-199

ignment Scores:
ed. No.:                2.23e-20        Length:         721
ore:                    29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-08-460-736-199 (1-721)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

SULT 41
-09-535-370-199
Sequence 199, Application US/09535370
Patent No. 6537594
  GENERAL INFORMATION:
       APPLICANT: Paoletti, Enzo
                  Tartaglia, James
                  Cox, William I.
       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
       NUMBER OF SEQUENCES: 217
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: Curtis, Morris & Safford
            STREET: 530 Fifth Avenue
            CITY: New York
            STATE: NY
            COUNTRY: USA
            ZIP: 10036
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.25
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/535,370
            FILING DATE: 24-Mar-2000
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/460,736
;           FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;           NAME: Frommer, William S.
;           REGISTRATION NUMBER: 25,506
;           REFERENCE/DOCKET NUMBER: 454310-2530
;      TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 840-3333
;           TELEFAX: (212) 840-0712
;           TELEX: 425066CURTMS
;  INFORMATION FOR SEQ ID NO: 199:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 721 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;      MOLECULE TYPE: cDNA
;      SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-535-370-199

Alignment Scores:
Pred. No.:              2.23e-20        Length:         721
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-535-370-199 (1-721)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

RESULT 42
US-09-663-667-199
; Sequence 199, Application US/09663667
; Patent No. 6780407
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,667
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/184,009
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
```

```
          TELEX: 425066CURTMS
  INFORMATION FOR SEQ ID NO: 199:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 721 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 199:
-09-663-667-199

ignment Scores:
ed. No.:                2.23e-20        Length:         721
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-663-667-199 (1-721)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

SULT 43
-08-848-760B-21
Sequence 21, Application US/08848760B
Patent No. 6248721
  GENERAL INFORMATION:
       APPLICANT: Chang, Lung-Ji
       TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
       NUMBER OF SEQUENCES: 33
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
            STREET: 2421 N.W. 41st Street, Suite A-1
            CITY: Gainesville
            STATE: Florida
            COUNTRY: United States of America
            ZIP: 32606
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/08/848,760B
            FILING DATE: 25-Jan-2001
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/838,702
            FILING DATE: 09-APR-1997
       ATTORNEY/AGENT INFORMATION:
            NAME: PACE, DORAN R.
            REGISTRATION NUMBER: 38,261
            REFERENCE/DOCKET NUMBER: CNG-100C1
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: (352) 375-8100
            TELEFAX: (352) 372-5800
  INFORMATION FOR SEQ ID NO: 21:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 762 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: double
            TOPOLOGY: linear
       MOLECULE TYPE: other nucleic acid
            DESCRIPTION: /desc = "DNA"
       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
-08-848-760B-21

Alignment Scores:
Pred. No.:              2.35e-20        Length:         762
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-08-848-760B-21 (1-762)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
Db      703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 44
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. 6730512
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

Alignment Scores:
Pred. No.:              2.35e-20        Length:         762
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-826-025-21 (1-762)
```

```
        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||||
        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 45
-09-543-679A-2890
Sequence 2890, Application US/09543679A
Patent No. 7034007
  GENERAL INFORMATION:
       APPLICANT: NYCE, Jonathan W.
       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
                           OF AIRWAY DISORDERS ASSOCIATED WITH
                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
       NUMBER OF SEQUENCES: 3111
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
            STREET: 7 Clarke Drive
            CITY: Cranbury
            STATE: NJ
            COUNTRY: USA
            ZIP: 08512
       COMPUTER READABLE FORM:
            MEDIUM TYPE: CD-R
            COMPUTER: IBM Compatible
            OPERATING SYSTEM: DOS
            SOFTWARE: N/A
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/543,679A
            FILING DATE: 13-Apr-2000
            CLASSIFICATION: UNKNOWN
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 60/127,958
            FILING DATE: 1998-08-03
       ATTORNEY/AGENT INFORMATION:
            NAME: Amzel, Viviana
            REGISTRATION NUMBER: 30,930
            REFERENCE/DOCKET NUMBER: EPI-0067191b
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 609-409-3035
            TELEFAX: 413-254-9245
            TELEX: <Unknown>
  INFORMATION FOR SEQ ID NO: 2890:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 762 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       SEQUENCE DESCRIPTION: SEQ ID NO: 2890:
-09-543-679A-2890

ignment Scores:
ed. No.:                2.35e-20        Length:         762
ore:                    29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       5               Gaps:           0

-10-821-670A-33 (1-222) x US-09-543-679A-2890 (1-762)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||||
        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 46
US-09-949-016-2462
; Sequence 2462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2462
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2462

Alignment Scores:
Pred. No.:              3.11e-20        Length:         1019
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-949-016-2462 (1-1019)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 762

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||||
Db        763 GCTTTCAGAATTCGGGCAGTGACTATT 789

RESULT 47
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
```

```
    REFERENCE/DOCKET NUMBER:  117-221
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  7038164091
    TELEFAX:  7038164100
 INFORMATION FOR SEQ ID NO:  1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1026 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  170..826
:-08-751-767A-1

ignment Scores:
:ed. No.:              3.13e-20      Length:        1026
'ore:                  29.00         Matches:       29
rcent Similarity:      100.0%        Conservative:  0
st Local Similarity:   100.0%        Mismatches:    0
:ery Match:            13.1%         Indels:        0
:                      2             Gaps:          0

-10-821-670A-33 (1-222) x US-08-751-767A-1 (1-1026)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

SULT 48
-09-023-655-1041
Sequence 1041, Application US/09023655
Patent No. 6607879
 GENERAL INFORMATION:
   APPLICANT:  Cocks, Benjamin G.
   APPLICANT:  Susan G. Stuart
   APPLICANT:  Jeffrey J. Seilhamer
   TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
   TITLE OF INVENTION:  EXPRESSION
   NUMBER OF SEQUENCES:  1508
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
     STREET:  3174 PORTER DRIVE
     CITY:  PALO ALTO
     STATE:  CALIFORNIA
     COUNTRY:  USA
     ZIP:  94304
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/023,655
     FILING DATE:  HEREWITH
     CLASSIFICATION:
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:
     FILING DATE:
     CLASSIFICATION:
   ATTORNEY/AGENT INFORMATION:
     NAME:  Zeller, Karen J.
     REGISTRATION NUMBER:  37,071
     REFERENCE/DOCKET NUMBER:  PA-0001 US
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (650) 855-0555
     TELEFAX:  (650) 845-4166
 INFORMATION FOR SEQ ID NO:  1041:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g180623
US-09-023-655-1041

Alignment Scores:
Pred. No.:              3.13e-20      Length:        1026
Score:                  29.00         Matches:       29
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            13.1%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-33 (1-222) x US-09-023-655-1041 (1-1026)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 49
US-09-949-016-130
; Sequence 130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-130

Alignment Scores:
Pred. No.:              3.13e-20      Length:        1026
Score:                  29.00         Matches:       29
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            13.1%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-33 (1-222) x US-09-949-016-130 (1-1026)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 50
US-09-634-368-6
```

```
Sequence 6, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
 APPLICANT:  Gillies, Stephen
 APPLICANT:  Lo, Kin Ming
 TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
 FILE REFERENCE:  LEX-010
 CURRENT APPLICATION NUMBER: US/09/634,368
 CURRENT FILING DATE:  2000-08-09
 PRIOR APPLICATION NUMBER:  60/147,924
 PRIOR FILING DATE:  1999-08-09
 NUMBER OF SEQ ID NOS:  32
 SOFTWARE:  PatentIn Ver. 2.0
SEQ ID NO 6
  LENGTH: 1287
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
  OTHER INFORMATION: fusion protein coding sequence
 09-634-368-6

ignment Scores:
ed. No.:                3.88e-20        Length:         1287
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-634-368-6 (1-1287)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
       1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254

SULT 51
-08-684-687-3
Sequence 3, Application US/08684687
Patent No. 5830451
 GENERAL INFORMATION:
   APPLICANT:  KIEFF, ELLIOTT D.
   APPLICANT:  DEVERGNE, ODILE
   TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
   TITLE OF INVENTION:  THEREFOR
   NUMBER OF SEQUENCES:  8
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
     STREET:  600 ATLANTIC AVENUE
     CITY:  BOSTON
     STATE:  MA
     COUNTRY:  USA
     ZIP:  02210
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/684,687
     FILING DATE:
     CLASSIFICATION:  514
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  60/005,092
     FILING DATE:  11-OCT-1995
   ATTORNEY/AGENT INFORMATION:
     NAME:  GATES, EDWARD R.
     REGISTRATION NUMBER:  31,616
     REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  102..863
US-08-684-687-3

Alignment Scores:
Pred. No.:              3.96e-20        Length:         1316
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x US-08-684-687-3 (1-1316)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db        804 GCTTTCAGAATTCGGGCAGTGACTATT 830

RESULT 52
US-09-851-520-3
; Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

Alignment Scores:
Pred. No.:              3.96e-20        Length:         1316
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-851-520-3 (1-1316)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

Qy        204 AlaPheArgIleArgAlaValThrIle 212
```

```
              ||||||||||||||||||||||||||||
        804 GCTTTCAGAATTCGGGCAGTGACTATT 830

SULT 53
-08-265-087-3
Sequence 3, Application US/08265087
Patent No. 5571515
 GENERAL INFORMATION:
   APPLICANT:  Scott, Phillip
   APPLICANT:  Trinchieri, Giorgio
   TITLE OF INVENTION:  Compositions and Methods for Use of
   TITLE OF INVENTION:  IL-12 as an Adjuvant
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Howson and Howson
     STREET:  Spring House Corporate Center, PO Box 457
     CITY:  Spring House
     STATE:  Pennsylvania
     COUNTRY:  USA
     ZIP:  19477
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/265,087
     FILING DATE:
     CLASSIFICATION:  424
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  US 08/229,282
     FILING DATE:  18-APR-1994
   ATTORNEY/AGENT INFORMATION:
     NAME:  Bak, Mary E.
     REGISTRATION NUMBER:  31,215
     REFERENCE/DOCKET NUMBER:  WST51AUSA
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  215-540-9206
     TELEFAX:  215-540-5818
 INFORMATION FOR SEQ ID NO:  3:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1364 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  unknown
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  101..859
-08-265-087-3

ignment Scores:
ed. No.:                4.1e-20        Length:         1364
ore:                    29.00          Matches:        29
rcent Similarity:       100.0%         Conservative:   0
st Local Similarity:    100.0%         Mismatches:     0
ery Match:              13.1%          Indels:         0
:                       2              Gaps:           0

-10-821-670A-33 (1-222) x US-08-265-087-3 (1-1364)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        803 GCTTTCAGAATTCGGGCAGTGACTATT 829

SULT 54
-08-621-493-3
Sequence 3, Application US/08621493
Patent No. 5723127

;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

Alignment Scores:
Pred. No.:                4.1e-20        Length:         1364
Score:                    29.00          Matches:        29
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              13.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-33 (1-222) x US-08-621-493-3 (1-1364)

Qy          184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

Qy          204 AlaPheArgIleArgAlaValThrIle 212
                |||||||||||||||||||||||||
Db          803 GCTTTCAGAATTCGGGCAGTGACTATT 829

RESULT 55
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
```

```
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Howson and Howson
     STREET:  Spring House Corporate Center, PO Box 457
     CITY:  Spring House
     STATE:  Pennsylvania
     COUNTRY:  USA
     ZIP:  19477
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/965,688
     FILING DATE:
     CLASSIFICATION:
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  08/621,493
     FILING DATE:  25-MAR-1996
     APPLICATION NUMBER:  08/265,087
     FILING DATE:  17-JUN-1994
     APPLICATION NUMBER:  US 08/229,282
     FILING DATE:  18-APR-1994
   ATTORNEY/AGENT INFORMATION:
     NAME:  Bak, Mary E.
     REGISTRATION NUMBER:  31,215
     REFERENCE/DOCKET NUMBER:  WST51AUSA
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  215-540-9206
     TELEFAX:  215-540-5818
 INFORMATION FOR SEQ ID NO:  3:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1364 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  unknown
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  101..859
-08-965-688-3

ignment Scores:
ed. No.:              4.1e-20       Length:        1364
ore:                  29.00         Matches:       29
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            13.1%         Indels:        0
:                     2             Gaps:          0

-10-821-670A-33 (1-222) x US-08-965-688-3 (1-1364)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        803 GCTTTCAGAATTCGGGCAGTGACTATT 829

SULT 56
-09-260-173-3
Sequence 3, Application US/09260173
Patent No. 6168923
  GENERAL INFORMATION:
       APPLICANT: Scott, Phillip
                  Trinchieri, Giorgio
       TITLE OF INVENTION: Compositions and Methods for Use of
                           IL-12 as an Adjuvant
       NUMBER OF SEQUENCES: 4
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: Howson and Howson
            STREET: Spring House Corporate Center, PO Box 457
            CITY: Spring House
            STATE: Pennsylvania
            COUNTRY: USA
            ZIP: 19477
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.25
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/260,173
            FILING DATE: 01-Mar-1999
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/965,688
            FILING DATE: <Unknown>
            APPLICATION NUMBER: 08/265,087
            FILING DATE: 17-JUN-1994
            APPLICATION NUMBER: US 08/229,282
            FILING DATE: 18-APR-1994
       ATTORNEY/AGENT INFORMATION:
            NAME: Bak, Mary E.
            REGISTRATION NUMBER: 31,215
            REFERENCE/DOCKET NUMBER: WST51AUSA
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 215-540-9206
            TELEFAX: 215-540-5818
  INFORMATION FOR SEQ ID NO: 3:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 1364 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: double
            TOPOLOGY: unknown
       MOLECULE TYPE: cDNA
       FEATURE:
            NAME/KEY:  CDS
            LOCATION:  101..859
       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

Alignment Scores:
Pred. No.:            4.1e-20       Length:        1364
Score:                29.00         Matches:       29
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          13.1%         Indels:        0
DB:                   3             Gaps:          0

US-10-821-670A-33 (1-222) x US-09-260-173-3 (1-1364)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 802

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db        803 GCTTTCAGAATTCGGGCAGTGACTATT 829

RESULT 57
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
```

```
 FILE REFERENCE: 01142.0142.0100
 CURRENT APPLICATION NUMBER: US/09/924,703
 CURRENT FILING DATE:  2001-08-09
 PRIOR APPLICATION NUMBER: 09/325,958
 PRIOR FILING DATE: 1999-06-04
 PRIOR APPLICATION NUMBER: 08/858,000
 PRIOR FILING DATE: 1997-05-16
 PRIOR APPLICATION NUMBER: 08/403,013
 PRIOR FILING DATE: 1995-03-13
 PRIOR APPLICATION NUMBER: 07/584,941
 PRIOR FILING DATE: 1990-09-18
 PRIOR APPLICATION NUMBER: 07/307,817
 PRIOR FILING DATE: 1989-02-07
 PRIOR APPLICATION NUMBER: 07/269,945
 PRIOR FILING DATE: 1988-11-10
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
  LENGTH: 1395
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
  OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
  NAME/KEY: CDS
  LOCATION: (114)..(872)
-09-924-703-5

ignment Scores:
ed. No.:                4.19e-20        Length:         1395
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-924-703-5 (1-1395)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        756 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 815

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        816 GCTTTCAGAATTCGGGCAGTGACTATT 842

SULT 58
-08-751-767A-11
Sequence 11, Application US/08751767A
Patent No. 5994104
 GENERAL INFORMATION:
   APPLICANT:  ANDERSON, ROBERT J.
   APPLICANT:  GRANT, HUGH
   APPLICANT:  MACDONALD, IAN D.
   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
   NUMBER OF SEQUENCES:  80
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  NIXON & VANDERHYE P.C.
     STREET:  1100 NORTH GLEBE ROAD
     CITY:  ARLINGTON
     STATE:  VA
     COUNTRY:  USA
     ZIP:  22201
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/751,767A
     FILING DATE:  08-NOV-1996
     CLASSIFICATION:  536
   ATTORNEY/AGENT INFORMATION:
     NAME:  SADOFF, B.J.
     REGISTRATION NUMBER:  36,663
     REFERENCE/DOCKET NUMBER:  117-221
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  7038164091
     TELEFAX:  7038164100
 INFORMATION FOR SEQ ID NO:  11:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1560 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  1..1557
US-08-751-767A-11

Alignment Scores:
Pred. No.:              4.66e-20        Length:         1560
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x US-08-751-767A-11 (1-1560)

Qy       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1500

Qy       204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      1501 GCTTTCAGAATTCGGGCAGTGACTATT 1527

RESULT 59
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
```

```
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  1..1620
-08-751-767A-9

ignment Scores:
ed. No.:                4.84e-20        Length:         1623
ore:                    29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               13.1%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-33 (1-222) x US-08-751-767A-9 (1-1623)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1504 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1563

       204 AlaPheArgIleArgAlaValThrIle 212
           |||||||||||||||||||||||||||
      1564 GCTTTCAGAATTCGGGCAGTGACTATT 1590

3ULT 60
-09-310-842-2
Sequence 2, Application US/09310842A
Patent No. 6451593
GENERAL INFORMATION:
 APPLICANT: Wittig, Prof. Burghardt
 APPLICANT: Junghans, Claas
 TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
 TITLE OF INVENTION: Therapy
 FILE REFERENCE: XI 597/99
 CURRENT APPLICATION NUMBER: US/09/310,842A
 CURRENT FILING DATE: 1999-05-12
 EARLIER APPLICATION NUMBER: DE 196 48 625.4
 EARLIER FILING DATE: 1996-11-13
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
  LENGTH: 1645
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  NAME/KEY: gene
  LOCATION: (1)..(1645)
  OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
  OTHER INFORMATION: Dumbbell
  FEATURE:
  NAME/KEY: misc_binding
  LOCATION: (1)..(2)
  OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
  OTHER INFORMATION: position 1 to 2  can be modified with amino or caroxy
  OTHER INFORMATION: features
  FEATURE:
  NAME/KEY: misc_binding
  LOCATION: (1644)..(1645)
  OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1644
  OTHER INFORMATION: to 1645  can be modified with amino or caroxy features
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
  OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
-09-310-842-2

ignment Scores:
ed. No.:                4.9e-20         Length:         1645
ore:                    29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               13.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-310-842-2 (1-1645)

Qy          184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1275 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1334

Qy          204 AlaPheArgIleArgAlaValThrIle 212
                |||||||||||||||||||||||||||
Db         1335 GCTTTCAGAATTCGGGCAGTGACTATT 1361

RESULT 61
US-09-543-679A-2893
; Sequence 2893, Application US/09543679A
; Patent No. 7034007
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2893:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4521 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2893:
US-09-543-679A-2893

Alignment Scores:
Pred. No.:              1.29e-19        Length:         4521
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-543-679A-2893 (1-4521)

Qy          184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702
```

```
       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
       703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 62
-08-751-767A-7
Sequence 7, Application US/08751767A
Patent No. 5994104
 GENERAL INFORMATION:
   APPLICANT:  ANDERSON, ROBERT J.
   APPLICANT:  GRANT, HUGH
   APPLICANT:  MACDONALD, IAN D.
   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
   NUMBER OF SEQUENCES:  80
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  NIXON & VANDERHYE P.C.
     STREET:  1100 NORTH GLEBE ROAD
     CITY:  ARLINGTON
     STATE:  VA
     COUNTRY:  USA
     ZIP:  22201
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/751,767A
     FILING DATE:  08-NOV-1996
     CLASSIFICATION:  536
   ATTORNEY/AGENT INFORMATION:
     NAME:  SADOFF, B.J.
     REGISTRATION NUMBER:  36,663
     REFERENCE/DOCKET NUMBER:  117-221
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  7038164091
     TELEFAX:  7038164100
 INFORMATION FOR SEQ ID NO:  7:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  6139 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  both
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  3222..4841
-08-751-767A-7

ignment Scores:
ed. No.:                1.72e-19        Length:         6139
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-33 (1-222) x US-08-751-767A-7 (1-6139)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      4725 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 4784

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
      4785 GCTTTCAGAATTCGGGCAGTGACTATT 4811

SULT 63
-09-949-016-11872
Sequence 11872, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11872
;   LENGTH: 10764
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11872

Alignment Scores:
Pred. No.:              2.94e-19        Length:         10764
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-949-016-11872 (1-10764)

Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8448 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 8507

Qy         204 AlaPheArgIleArgAlaValThrIle 212
               ||||||||||||||||||||||||||
Db        8508 GCTTTCAGAATTCGGGCAGTGACTATT 8534

RESULT 64
US-09-949-016-14204
; Sequence 14204, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14204
;   LENGTH: 10765
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14204

Alignment Scores:
Pred. No.:              2.94e-19        Length:         10765
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-949-016-14204 (1-10765)

Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
```

```
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     8448 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 8507

      204 AlaPheArgIleArgAlaValThrIle 212
          |||||||||||||||||||||||||||
     8508 GCTTTCAGAATTCGGGCAGTGACTATT 8534
```

SULT 65
-09-949-016-20381
Sequence 20381, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20381
LENGTH: 601
TYPE: DNA
ORGANISM: Human
-09-949-016-20381

ignment Scores:

ed. No.:	2e-19	Length:	601
ore:	28.00	Matches:	28
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ry Match:	12.6%	Indels:	0
:	3	Gaps:	0

-10-821-670A-33 (1-222) x US-09-949-016-20381 (1-601)

```
       67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      135 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 194

       87 AlaCysLeuProLeuGluLeuThr 94
          |||||||||||||||||||||||
      195 GCCTGTTTACCATTGGAATTAACC 218
```

SULT 66
-09-949-016-87348
Sequence 87348, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 87348
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-87348

Alignment Scores:

Pred. No.:	2e-19	Length:	601
Score:	28.00	Matches:	28
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	12.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-949-016-87348 (1-601)

```
Qy         67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 TGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAG 194

Qy         87 AlaCysLeuProLeuGluLeuThr 94
              |||||||||||||||||||||||
Db        195 GCCTGTTTACCATTGGAATTAACC 218
```

RESULT 67
US-09-011-143-24
; Sequence 24, Application US/09011143
; Patent No. 6472509
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: FUJIYASU, Takeshi
; APPLICANT: IMAGAWA, Yoshitaka
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,143
; FILING DATE: 04-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/01824
; FILING DATE: 29-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: IMAMURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-011-143-24

Alignment Scores:

Pred. No.:	3.29e-18	Length:	79
Score:	26.00	Matches:	26

```
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            11.7%           Indels:        0
:                     3               Gaps:          0

-10-821-670A-33 (1-222) x US-09-011-143-24 (1-79)

         75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 94
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

         95 MetAsnGluSerCysLeu 100
            ||||||||||||||||||
         62 ATGAATGAGAGTTGCCTG 79

SULT 68
-09-302-495-24
Sequence 24, Application US/09302495
Patent No. 6518045
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
            STREET: 419 Seventh Street, N.W., Suite 300
            CITY: Washington
            STATE: D.C.
            COUNTRY: USA
            ZIP: 20004
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/302,495
            FILING DATE: 30-Apr-1999
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: US/09/011,143
            FILING DATE: 04-FEB-1998
            APPLICATION NUMBER: PCT/JP97/01824
            FILING DATE: 29-MAY-1997
            APPLICATION NUMBER: JP 165249/1996
            FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
            NAME: BROWDY, Roger L.
            REGISTRATION NUMBER: 25,618
            REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 202-628-5197
            TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 24:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 79 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
-09-302-495-24

ignment Scores:
ed. No.:              3.29e-18        Length:        79
ore:                  26.00           Matches:       26
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            11.7%           Indels:        0
```

```
DB:                   3               Gaps:          0

US-10-821-670A-33 (1-222) x US-09-302-495-24 (1-79)

Qy         75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

Qy         95 MetAsnGluSerCysLeu 100
              ||||||||||||||||||
Db         62 ATGAATGAGAGTTGCCTG 79

RESULT 69
US-10-079-616-24
; Sequence 24, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 79 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-079-616-24

Alignment Scores:
Pred. No.:            3.29e-18        Length:        79
Score:                26.00           Matches:       26
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          11.7%           Indels:        0
DB:                   3               Gaps:          0

US-10-821-670A-33 (1-222) x US-10-079-616-24 (1-79)
```

```
        75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 94
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         2 GAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACC 61

        95 MetAsnGluSerCysLeu 100
           |||||||||||||||||
        62 ATGAATGAGAGTTGCCTG 79

3ULT 70
-09-011-143-22
3equence 22, Application US/09011143
?atent No. 6472509
 GENERAL INFORMATION:
   APPLICANT:  IMAMURA, Takayuki
   APPLICANT:  MAEDA, Hiroaki
   APPLICANT:  FUJIYASU, Takeshi
   APPLICANT:  IMAGAWA, Yoshitaka
   APPLICANT:  TOKIYOSHI, Sachio
   TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
   NUMBER OF SEQUENCES:  26
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  BROWDY AND NEIMARK
     STREET:  419 Seventh Street, N.W., Suite 300
     CITY:  Washington
     STATE:  D.C.
     COUNTRY:  USA
     ZIP:  20004
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/011,143
     FILING DATE:  04-FEB-1998
     CLASSIFICATION:  536
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  PCT/JP97/01824
     FILING DATE:  29-MAY-1997
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  JP 165249/1996
     FILING DATE:  04-JUN-1996
   ATTORNEY/AGENT INFORMATION:
     NAME:  BROWDY, Roger L.
     REGISTRATION NUMBER:  25,618
     REFERENCE/DOCKET NUMBER:  IMAMURA=1
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  202-628-5197
     TELEFAX:  202-737-3528
 INFORMATION FOR SEQ ID NO:  22:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  95 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-09-011-143-22

ıgnment Scores:
ɜd. No.:              4.76e-15       Length:         95
›re:                  23.00          Matches:        23
:cent Similarity:     100.0%         Conservative:   0
ɜt Local Similarity:  100.0%         Mismatches:     0
ɜry Match:            10.4%          Indels:         0
:                     3              Gaps:           0

-10-821-670A-33 (1-222) x US-09-011-143-22 (1-95)

         1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        27 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 86

Qy          21 HisLeuSer 23
               |||||||||
Db          87 CACCTCAGT 95

RESULT 71
US-09-302-495-22
; Sequence 22, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 22:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 95 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-302-495-22

Alignment Scores:
Pred. No.:              4.76e-15       Length:         95
Score:                  23.00          Matches:        23
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            10.4%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-33 (1-222) x US-09-302-495-22 (1-95)

Qy           1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          27 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 86

Qy          21 HisLeuSer 23
               |||||||||
Db          87 CACCTCAGT 95
```

```
SULT 72
-10-079-616-22
Sequence 22, Application US/10079616
Patent No. 6566097
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
            STREET: 419 Seventh Street, N.W., Suite 300
            CITY: Washington
            STATE: D.C.
            COUNTRY: USA
            ZIP: 20004
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/10/079,616
            FILING DATE: 22-Feb-2002
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 09/011,143
            FILING DATE: 04-FEB-1998
            APPLICATION NUMBER: PCT/JP97/01824
            FILING DATE: 29-MAY-1997
            APPLICATION NUMBER: JP 165249/1996
            FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
            NAME: BROWDY, Roger L.
            REGISTRATION NUMBER: 25,618
            REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 202-628-5197
            TELEFAX: 202-737-3528
   INFORMATION FOR SEQ ID NO: 22:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 95 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 22:
-10-079-616-22

ignment Scores:
ed. No.:                4.76e-15        Length:         95
ore:                    23.00           Matches:        23
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              10.4%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-10-079-616-22 (1-95)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         27 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 86

          21 HisLeuSer 23
             |||||||||
         87 CACCTCAGT 95

SULT 73
-09-011-143-25/c
; Sequence 25, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-25

Alignment Scores:
Pred. No.:                0.000384        Length:         36
Score:                    12.00           Matches:        12
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              5.4%            Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-011-143-25 (1-36)

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 152
              ||||||||||||||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

RESULT 74
US-09-302-495-25/c
; Sequence 25, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
```

```
      NUMBER OF SEQUENCES: 26
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: BROWDY AND NEIMARK
           STREET: 419 Seventh Street, N.W., Suite 300
           CITY: Washington
           STATE: D.C.
           COUNTRY: USA
           ZIP: 20004
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/302,495
           FILING DATE: 30-Apr-1999
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: US/09/011,143
           FILING DATE: 04-FEB-1998
           APPLICATION NUMBER: PCT/JP97/01824
           FILING DATE: 29-MAY-1997
           APPLICATION NUMBER: JP 165249/1996
           FILING DATE: 04-JUN-1996
      ATTORNEY/AGENT INFORMATION:
           NAME: BROWDY, Roger L.
           REGISTRATION NUMBER: 25,618
           REFERENCE/DOCKET NUMBER: IMAMURA=1
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: 202-628-5197
           TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 25:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 36 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 25:
-09-302-495-25

ıgnment Scores:
ed. No.:              0.000384      Length:         36
ore:                  12.00         Matches:        12
cent Similarity:      100.0%        Conservative:   0
t Local Similarity:   100.0%        Mismatches:     0
ery Match:            5.4%          Indels:         0
:                     3             Gaps:           0

-10-821-670A-33 (1-222) x US-09-302-495-25 (1-36)

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 152
            ||||||||||||||||||||||||||||||||||||
         36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

3ULT 75
-10-079-616-25/c
Sequence 25, Application US/10079616
Patent No. 6566097
  GENERAL INFORMATION:
      APPLICANT: IMAMURA, Takayuki
                 MAEDA, Hiroaki
                 FUJIYASU, Takeshi
                 IMAGAWA, Yoshitaka
                 TOKIYOSHI, Sachio
      TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
      NUMBER OF SEQUENCES: 26
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: BROWDY AND NEIMARK
           STREET: 419 Seventh Street, N.W., Suite 300
           CITY: Washington
           STATE: D.C.
           COUNTRY: USA
           ZIP: 20004
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/10/079,616
           FILING DATE: 22-Feb-2002
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 09/011,143
           FILING DATE: 04-FEB-1998
           APPLICATION NUMBER: PCT/JP97/01824
           FILING DATE: 29-MAY-1997
           APPLICATION NUMBER: JP 165249/1996
           FILING DATE: 04-JUN-1996
      ATTORNEY/AGENT INFORMATION:
           NAME: BROWDY, Roger L.
           REGISTRATION NUMBER: 25,618
           REFERENCE/DOCKET NUMBER: IMAMURA=1
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: 202-628-5197
           TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 25:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 36 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-079-616-25

Alignment Scores:
Pred. No.:              0.000384      Length:         36
Score:                  12.00         Matches:        12
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            5.4%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-33 (1-222) x US-10-079-616-25 (1-36)

Qy         141 PheLysAlaMetAsnAlaLysLeuLeuMetAspPro 152
               ||||||||||||||||||||||||||||||||||||
Db          36 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCT 1

RESULT 76
US-09-917-265A-91
; Sequence 91, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-91

Alignment Scores:
```

ed. No.: 0.00441 Length: 39
ore: 11.00 Matches: 11
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 5.0% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-917-265A-91 (1-39)

35 ProGlyMetPheGlnCysLeuAsnHisSerGln 45
7 CCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 39

SULT 77
-09-079-984A-15
Sequence 15, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other DNA; synthetic DNA
-09-079-984A-15

ignment Scores:
ed. No.: 0.0471 Length: 39
ore: 10.00 Matches: 10
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 4.5% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-079-984A-15 (1-39)

1 MetCysProProArgGlyLeuLeuLeuVal 10
10 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTG 39

SULT 78
-09-390-729-15
Sequence 15, Application US/09390729

; Patent No. 6562334
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/390,729
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/079,984
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other DNA; synthetic DNA
US-09-390-729-15

Alignment Scores:
Pred. No.: 0.0471 Length: 39
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-33 (1-222) x US-09-390-729-15 (1-39)

Qy 1 MetCysProProArgGlyLeuLeuLeuVal 10
Db 10 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTG 39

RESULT 79
US-09-917-265A-83
; Sequence 83, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2

```
SEQ ID NO 83
  LENGTH: 60
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
-09-917-265A-83

ignment Scores:
ed. No.:                0.071          Length:         60
ore:                    10.00          Matches:        10
cent Similarity:        100.0%         Conservative:   0
t Local Similarity:     100.0%         Mismatches:     0
ry Match:               4.5%           Indels:         0
:                       3              Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265A-83 (1-60)

        26 ArgAsnLeuProThrProThrProSerPro 35
           |||||||||||||||||||||||||||||||
        29 AGAAACTTGCCAACCCCTACTCCATCCCCG 58

SULT 80
-09-917-265A-84/c
Sequence 84, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 84
  LENGTH: 60
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
-09-917-265A-84

ignment Scores:
ed. No.:                0.071          Length:         60
ore:                    10.00          Matches:        10
cent Similarity:        100.0%         Conservative:   0
t Local Similarity:     100.0%         Mismatches:     0
ry Match:               4.5%           Indels:         0
:                       3              Gaps:           0

 10-821-670A-33 (1-222) x US-09-917-265A-84 (1-60)

        26 ArgAsnLeuProThrProThrProSerPro 35
           |||||||||||||||||||||||||||||||
        32 AGAAACTTGCCAACCCCTACTCCATCCCCG 3

SULT 81
-09-634-368-1
Sequence 1, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
 APPLICANT:  Gillies, Stephen
 APPLICANT:  Lo, Kin Ming
 TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
 FILE REFERENCE:  LEX-010
 CURRENT APPLICATION NUMBER: US/09/634,368
 CURRENT FILING DATE:  2000-08-09
 PRIOR APPLICATION NUMBER:  60/147,924
 PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine p35
;   OTHER INFORMATION: coding sequence for mature protein
US-09-634-368-1

Alignment Scores:
Pred. No.:              0.619          Length:         582
Score:                  10.00          Matches:        10
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            4.5%           Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-33 (1-222) x US-09-634-368-1 (1-582)

Qy        129 SerIleTyrGluAspLeuLysMetTyrGln 138
              |||||||||||||||||||||||||||||||
Db        298 AGCATCTATGAGGACTTGAAGATGTACCAG 327

RESULT 82
US-08-385-335A-10
; Sequence 10, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  713 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-385-335A-10

Alignment Scores:
Pred. No.:              0.752          Length:         713
Score:                  10.00          Matches:        10
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            4.5%           Indels:         0
DB:                     2              Gaps:           0
```

-10-821-670A-33 (1-222) x US-08-385-335A-10 (1-713)

```
        129 SerIleTyrGluAspLeuLysMetTyrGln 138
            ||||||||||||||||||||||||||||||
        410 AGCATCTATGAGGACTTGAAGATGTACCAG 439
```

SULT 83
-09-634-368-5
Sequence 5, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/09/634,368
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1278
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: Fc-p35 fusion protein coding sequence
-09-634-368-5

ignment Scores:

ed. No.:	1.31	Length:	1278
ore:	10.00	Matches:	10
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	4.5%	Indels:	0
:	3	Gaps:	0

-10-821-670A-33 (1-222) x US-09-634-368-5 (1-1278)

```
        129 SerIleTyrGluAspLeuLysMetTyrGln 138
            ||||||||||||||||||||||||||||||
        994 AGCATCTATGAGGACTTGAAGATGTACCAG 1023
```

SULT 84
-09-634-368-12
Sequence 12, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/09/634,368
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 1569
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
-09-634-368-12

ignment Scores:

ed. No.:	1.59	Length:	1569
ore:	10.00	Matches:	10
rcent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.5%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-634-368-12 (1-1569)

```
Qy        129 SerIleTyrGluAspLeuLysMetTyrGln 138
              ||||||||||||||||||||||||||||||
Db        298 AGCATCTATGAGGACTTGAAGATGTACCAG 327
```

RESULT 85
US-09-634-368-11
; Sequence 11, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/09/634,368
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-09-634-368-11

Alignment Scores:

Pred. No.:	2.02	Length:	2013
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.5%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-634-368-11 (1-2013)

```
Qy        129 SerIleTyrGluAspLeuLysMetTyrGln 138
              ||||||||||||||||||||||||||||||
Db        298 AGCATCTATGAGGACTTGAAGATGTACCAG 327
```

RESULT 86
US-09-634-368-13
; Sequence 13, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/09/634,368
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
; OTHER INFORMATION: sequence
US-09-634-368-13

```
ignment Scores:
ed. No.:                2.68            Length:         2709
ore:                    10.00           Matches:        10
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              4.5%            Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-634-368-13 (1-2709)

        129 SerIleTyrGluAspLeuLysMetTyrGln 138
            ||||||||||||||||||||||||||||||
        994 AGCATCTATGAGGACTTGAAGATGTACCAG 1023

SULT 87
-08-659-206A-4
Sequence 4, Application US/08659206A
Patent No. 5922685
 GENERAL INFORMATION:
   APPLICANT:  Rakhmilevich, Alexander
   TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
   NUMBER OF SEQUENCES:  6
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Quarles & Brady
     STREET:  1 South Pinckney Street
     CITY:  Madison
     STATE:  WI
     COUNTRY:  US
     ZIP:  53703
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/659,206A
     FILING DATE:
     CLASSIFICATION:  435
   ATTORNEY/AGENT INFORMATION:
     NAME:  Seay, Nicholas J
     REGISTRATION NUMBER:  27386
     REFERENCE/DOCKET NUMBER:  110229.91144
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  608-251-5000
     TELEFAX:  608-251-9166
 INFORMATION FOR SEQ ID NO:  4:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  6295 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  circular
   MOLECULE TYPE:  other nucleic acid
     DESCRIPTION:  /desc = "plasmid pWRG3196"
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  join(955..1260, 1334..1675)
     OTHER INFORMATION:  /product= "p35 gene product"
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  2377..3384
     OTHER INFORMATION:  /product= "p40 gene product"
-08-659-206A-4

ignment Scores:
ed. No.:                5.99            Length:         6295
ore:                    10.00           Matches:        10
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              4.5%            Indels:         0
:                       2               Gaps:           0

-10-821-670A-33 (1-222) x US-08-659-206A-4 (1-6295)

Qy        129 SerIleTyrGluAspLeuLysMetTyrGln 138
              ||||||||||||||||||||||||||||||
Db       1391 AGCATCTATGAGGACTTGAAGATGTACCAG 1420

RESULT 88
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Plasmid DNA"
;    IMMEDIATE SOURCE:
;      CLONE:  pWRG3169
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..628
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  629..810
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(953..1258, 1332..1673)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1797..2024
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1
```

```
ignment Scores:
ed. No.:                6.89          Length:          7287
ore:                    10.00         Matches:         10
rcent Similarity:       100.0%        Conservative:    0
st Local Similarity:    100.0%        Mismatches:      0
ery Match:              4.5%          Indels:          0
:                       2             Gaps:            0

-10-821-670A-33 (1-222) x US-08-659-206A-1 (1-7287)

        129 SerIleTyrGluAspLeuLysMetTyrGln 138
            ||||||||||||||||||||||||||||||
       1389 AGCATCTATGAGGACTTGAAGATGTACCAG 1418

SULT 89
-09-917-265A-96/c
Sequence 96, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 96
  LENGTH: 51
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
-09-917-265A-96

ignment Scores:
ed. No.:                0.649         Length:          51
ore:                    9.00          Matches:         9
rcent Similarity:       100.0%        Conservative:    0
st Local Similarity:    100.0%        Mismatches:      0
ery Match:              4.1%          Indels:          0
:                       3             Gaps:            0

-10-821-670A-33 (1-222) x US-09-917-265A-96 (1-51)

        212 IleAsnArgMetMetSerTyrLeuAsn 220
            |||||||||||||||||||||||||||
         49 ATCAATAGAATGATGTCCTACTTGAAC 23

SULT 90
-08-464-700-53/c
Sequence 53, Application US/08464700
Patent No. 6232458
 GENERAL INFORMATION:
   APPLICANT:  WEISS, ANTHONY S
   APPLICANT:  MARTIN, STEPHEN L
   TITLE OF INVENTION:  SYNTHETIC POLYNUCLEOTIDES
   NUMBER OF SEQUENCES:  54
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Howson and Howson
     STREET:  Spring House Corporate Cntr, PO Box 457
     CITY:  Spring House
     STATE:  Pennsylvania
     COUNTRY:  USA
     ZIP:  19477
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,700
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PL6520
;      FILING DATE:  22-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PL9661
;      FILING DATE:  28-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU93/00655
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  GHC3USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2210 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-464-700-53

Alignment Scores:
Pred. No.:              23.6          Length:          2210
Score:                  9.00          Matches:         9
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            4.1%          Indels:          0
DB:                     3             Gaps:            0

US-10-821-670A-33 (1-222) x US-08-464-700-53 (1-2210)

Qy          29 ProThrProThrProSerProGlyMet 37
               |||||||||||||||||||||||||||
Db        1603 CCGACACCAACTCCAAGTCCAGGGATG 1577

RESULT 91
US-08-641-627A-37/c
; Sequence 37, Application US/08641627A
; Patent No. 5726040
;  GENERAL INFORMATION:
;    APPLICANT:  Ensley PhD, Burt D.
;    APPLICANT:  Ludmer, Matthew
;    TITLE OF INVENTION:  Cosmetic Compositions Including
;    TITLE OF INVENTION:  Tropoelastin Isomorphs
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Choate, Hall & Stewart
;      STREET:  53 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  usa
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/641,627A
;      FILING DATE:  02-MAY-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jarrell Ph.D., Brenda H.
```

```
     REGISTRATION NUMBER:  39,223
     REFERENCE/DOCKET NUMBER:  0062912-0001
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (617) 248-5000
     TELEFAX:  (617) 248-4000
 INFORMATION FOR SEQ ID NO:  37:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  2242 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  both
     TOPOLOGY:  both
   MOLECULE TYPE:  cDNA
   ORIGINAL SOURCE:
     STRAIN:  tropoelastin cDNA (cHE-3)
-08-641-627A-37

ignment Scores:
ed. No.:                23.9          Length:        2242
ore:                    9.00          Matches:       9
cent Similarity:        100.0%        Conservative:  0
st Local Similarity:    100.0%        Mismatches:    0
ery Match:              4.1%          Indels:        0
:                       2             Gaps:          0

-10-821-670A-33 (1-222) x US-08-641-627A-37 (1-2242)

         29 ProThrProThrProSerProGlyMet 37
            |||||||||||||||||||||||||||
       1740 CCGACACCAACTCCAAGTCCAGGGATG 1714

SULT 92
-08-678-039A-39/c
Sequence 39, Application US/08678039A
Patent No. 5858662
 GENERAL INFORMATION:
   APPLICANT:  Keating, Mark T.
   APPLICANT:  Morris, Colleen A.
   TITLE OF INVENTION:  Diagnosis of Williams Syndrome and
   TITLE OF INVENTION:  Williams Syndrome Cognitive Profile by Analysis of the
   TITLE OF INVENTION:  Presence or Absence of a LIM-Kinase Gene
   NUMBER OF SEQUENCES:  42
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Rothwell, Figg, Ernst & Kurz, P.C.
     STREET:  555 Thirteenth Street, N.W., Suite 701 East
     STREET:  Tower
     CITY:  Washington
     STATE:  DC
     COUNTRY:  U.S.A.
     ZIP:  20004
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/678,039A
     FILING DATE:  10-JUL-1996
     CLASSIFICATION:  435
   ATTORNEY/AGENT INFORMATION:
     NAME:  Saxe, Stephen A.
     REGISTRATION NUMBER:  38,609
     REFERENCE/DOCKET NUMBER:  2323-120A
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  202-624-1589
     TELEFAX:  202-783-6031
 INFORMATION FOR SEQ ID NO:  39:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  2427 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  49..2424
US-08-678-039A-39

Alignment Scores:
Pred. No.:                25.8          Length:        2427
Score:                    9.00          Matches:       9
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              4.1%          Indels:        0
DB:                       2             Gaps:          0

US-10-821-670A-33 (1-222) x US-08-678-039A-39 (1-2427)

Qy         29 ProThrProThrProSerProGlyMet 37
              |||||||||||||||||||||||||||
Db       1826 CCGACACCAACTCCAAGTCCAGGGATG 1800

RESULT 93
US-10-104-047-945/c
; Sequence 945, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 6943241el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 945
;    LENGTH: 2845
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-104-047-945

Alignment Scores:
Pred. No.:                30            Length:        2845
Score:                    9.00          Matches:       9
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              4.1%          Indels:        0
DB:                       3             Gaps:          0

US-10-821-670A-33 (1-222) x US-10-104-047-945 (1-2845)

Qy         29 ProThrProThrProSerProGlyMet 37
              |||||||||||||||||||||||||||
Db       1420 CCGACACCAACTCCAAGTCCAGGGATG 1394

RESULT 94
US-09-396-196G-121547
; Sequence 121547, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
SEQ ID NO 121547
  LENGTH: 25
  TYPE: DNA
  ORGANISM: mus musculus
-09-396-196G-121547

ignment Scores:
ed. No.:                3.51          Length:         25
ore:                    8.00          Matches:        8
rcent Similarity:       100.0%        Conservative:   0
st Local Similarity:    100.0%        Mismatches:     0
ery Match:              3.6%          Indels:         0
:                       3             Gaps:           0

-10-821-670A-33 (1-222) x US-09-396-196G-121547 (1-25)

        197 LysLeuCysIleLeuLeuHisAla 204
            |||||||||||||||||||||||||
          1 AAGCTCTGCATCCTGCTTCACGCC 24

SULT 95
-09-917-265A-90/c
Sequence 90, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 90
  LENGTH: 27
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
-09-917-265A-90

ignment Scores:
ed. No.:                3.77          Length:         27
ore:                    8.00          Matches:        8
rcent Similarity:       100.0%        Conservative:   0
st Local Similarity:    100.0%        Mismatches:     0
ery Match:              3.6%          Indels:         0
:                       3             Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265A-90 (1-27)

        215 MetMetSerTyrLeuAsnAlaSer 222
            |||||||||||||||||||||||||
         27 ATGATGAGCTATCTGAATGCTTCC 4

SULT 96
-09-917-265A-92/c
Sequence 92, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 92
  LENGTH: 41
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
US-09-917-265A-92

Alignment Scores:
Pred. No.:              5.62          Length:         41
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            3.6%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265A-92 (1-41)

Qy          215 MetMetSerTyrLeuAsnAlaSer 222
                |||||||||||||||||||||||||
Db           41 ATGATGAGCTATCTGAATGCTTCC 18

RESULT 97
US-09-621-976-13237/c
; Sequence 13237, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 13237
;   LENGTH: 452
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-13237

Alignment Scores:
Pred. No.:              55.4          Length:         452
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            3.6%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-33 (1-222) x US-09-621-976-13237 (1-452)

Qy           28 LeuProThrProThrProSerPro 35
                |||||||||||||||||||||||||
Db          148 CTCCCCACTCCTACCCCCTCACCA 125

RESULT 98
US-09-270-767-5297
; Sequence 5297, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5297
;   LENGTH: 479
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
```

-09-270-767-5297

Ignment Scores:
ed. No.: 58.5 Length: 479
ore: 8.00 Matches: 8
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 3.6% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-270-767-5297 (1-479)

```
          7 LeuLeuLeuValThrIleLeuVal 14
            |||||||||||||||||||||||||
        103 CTGCTCCTGGTCACGATCCTGGTC 126
```

SULT 99
-09-270-767-20579
Sequence 20579, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20579
LENGTH: 479
TYPE: DNA
ORGANISM: Drosophila melanogaster
-09-270-767-20579

Ignment Scores:
ed. No.: 58.5 Length: 479
ore: 8.00 Matches: 8
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 3.6% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-270-767-20579 (1-479)

```
          7 LeuLeuLeuValThrIleLeuVal 14
            |||||||||||||||||||||||||
        103 CTGCTCCTGGTCACGATCCTGGTC 126
```

SULT 100
-09-270-767-12534/c
Sequence 12534, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12534
LENGTH: 601
TYPE: DNA
ORGANISM: Drosophila melanogaster
-09-270-767-12534

Ignment Scores:
ed. No.: 72.6 Length: 601
ore: 8.00 Matches: 8
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 3.6% Indels: 0
: 3 Gaps: 0

US-10-821-670A-33 (1-222) x US-09-270-767-12534 (1-601)

```
Qy          9 LeuValThrIleLeuValLeuLeu 16
              ||||||||||||||||||||||||
Db        324 CTCGTCACGATACTCGTACTCCTT 301
```

Search completed: June 10, 2006, 04:48:25
Job time : 155.554 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 11, 2006, 22:10:55 ; Search time 1072.1 Seconds
(without alignments)
3816.589 Million cell updates/sec

tle: US-10-821-670A-33
rfect score: 222
quence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 18892170 seqs, 6143817638 residues

rd size: 1

tal number of hits satisfying chosen parameters: 37767822

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110503_27781/app_query.fasta_1
B=Published_Applications_NA_Main -QFMT=fastap
UFFIX=oligo.p2n.200scores.rnpbm -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
NITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
OCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
ORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
SER=US10821670_@CGN_1_1_4932_@runat_07062006_110503_27781 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	222	100.0	666	3	US-09-917-265-32	Sequence 32, Appl
c 2	222	100.0	666	3	US-09-917-265-34	Sequence 34, Appl
3	222	100.0	666	9	US-10-821-670-32	Sequence 32, Appl
c 4	222	100.0	666	9	US-10-821-670-34	Sequence 34, Appl
5	220	99.1	689	6	US-10-079-616-26	Sequence 26, Appl
6	220	99.1	1441	6	US-10-079-616-8	Sequence 8, Appli
7	197	88.7	591	3	US-09-917-265-35	Sequence 35, Appl
c 8	197	88.7	591	3	US-09-917-265-37	Sequence 37, Appl
9	197	88.7	591	9	US-10-821-670-35	Sequence 35, Appl
c 10	197	88.7	591	9	US-10-821-670-37	Sequence 37, Appl
11	197	88.7	1533	3	US-09-917-265-43	Sequence 43, Appl
c 12	197	88.7	1533	3	US-09-917-265-45	Sequence 45, Appl
13	197	88.7	1533	9	US-10-821-670-43	Sequence 43, Appl
c 14	197	88.7	1533	9	US-10-821-670-45	Sequence 45, Appl
15	197	88.7	1599	3	US-09-917-265-38	Sequence 38, Appl
c 16	197	88.7	1599	3	US-09-917-265-40	Sequence 40, Appl
17	197	88.7	1599	9	US-10-821-670-38	Sequence 38, Appl
c 18	197	88.7	1599	9	US-10-821-670-40	Sequence 40, Appl
19	195	87.8	591	6	US-10-079-616-9	Sequence 9, Appli
20	187	84.2	561	3	US-09-917-265-101	Sequence 101, App
c 21	187	84.2	561	3	US-09-917-265-103	Sequence 103, App
22	187	84.2	561	9	US-10-821-670-101	Sequence 101, App
c 23	187	84.2	561	9	US-10-821-670-103	Sequence 103, App
24	65	29.3	669	7	US-10-041-672C-2	Sequence 2, Appli
25	52	23.4	591	3	US-09-917-265-49	Sequence 49, Appl
c 26	52	23.4	591	3	US-09-917-265-51	Sequence 51, Appl
27	52	23.4	591	9	US-10-821-670-49	Sequence 49, Appl
c 28	52	23.4	591	9	US-10-821-670-51	Sequence 51, Appl
29	52	23.4	666	3	US-09-917-265-46	Sequence 46, Appl
c 30	52	23.4	666	3	US-09-917-265-48	Sequence 48, Appl
31	52	23.4	666	9	US-10-821-670-46	Sequence 46, Appl
c 32	52	23.4	666	9	US-10-821-670-48	Sequence 48, Appl
33	52	23.4	1455	3	US-09-917-265-104	Sequence 104, App
c 34	52	23.4	1455	3	US-09-917-265-106	Sequence 106, App
35	52	23.4	1455	9	US-10-821-670-104	Sequence 104, App
c 36	52	23.4	1455	9	US-10-821-670-106	Sequence 106, App
37	52	23.4	1533	3	US-09-917-265-66	Sequence 66, Appl
c 38	52	23.4	1533	3	US-09-917-265-68	Sequence 68, Appl
39	52	23.4	1533	9	US-10-821-670-66	Sequence 66, Appl
c 40	52	23.4	1533	9	US-10-821-670-68	Sequence 68, Appl
41	52	23.4	1599	3	US-09-917-265-61	Sequence 61, Appl
c 42	52	23.4	1599	3	US-09-917-265-63	Sequence 63, Appl
43	52	23.4	1599	9	US-10-821-670-61	Sequence 61, Appl
c 44	52	23.4	1599	9	US-10-821-670-63	Sequence 63, Appl
45	29	13.1	201	8	US-10-741-601-946	Sequence 946, App
46	29	13.1	201	8	US-10-741-601-947	Sequence 947, App
47	29	13.1	201	8	US-10-741-601-951	Sequence 951, App
48	29	13.1	201	8	US-10-741-601-955	Sequence 955, App
49	29	13.1	201	8	US-10-741-601-957	Sequence 957, App
50	29	13.1	201	8	US-10-741-601-960	Sequence 960, App
51	29	13.1	201	8	US-10-741-601-7417	Sequence 7417, Ap
52	29	13.1	201	8	US-10-741-601-7418	Sequence 7418, Ap
53	29	13.1	201	8	US-10-741-601-7431	Sequence 7431, Ap
c 54	29	13.1	201	8	US-10-741-601-11370	Sequence 11370, A
c 55	29	13.1	201	8	US-10-741-601-11372	Sequence 11372, A
c 56	29	13.1	201	8	US-10-741-601-11417	Sequence 11417, A
57	29	13.1	201	9	US-10-741-600-3487	Sequence 3487, Ap
58	29	13.1	201	9	US-10-741-600-3488	Sequence 3488, Ap
59	29	13.1	201	9	US-10-741-600-3492	Sequence 3492, Ap
60	29	13.1	201	9	US-10-741-600-3496	Sequence 3496, Ap
61	29	13.1	201	9	US-10-741-600-3498	Sequence 3498, Ap
62	29	13.1	201	9	US-10-741-600-3501	Sequence 3501, Ap
63	29	13.1	201	9	US-10-741-600-20963	Sequence 20963, A
64	29	13.1	201	9	US-10-741-600-20964	Sequence 20964, A
65	29	13.1	201	9	US-10-741-600-20992	Sequence 20992, A
c 66	29	13.1	201	9	US-10-741-600-28831	Sequence 28831, A
c 67	29	13.1	201	9	US-10-741-600-28833	Sequence 28833, A
c 68	29	13.1	201	9	US-10-741-600-28877	Sequence 28877, A
69	29	13.1	201	10	US-10-995-561-1976	Sequence 1976, Ap
70	29	13.1	201	10	US-10-995-561-1977	Sequence 1977, Ap
71	29	13.1	201	10	US-10-995-561-1981	Sequence 1981, Ap
72	29	13.1	201	10	US-10-995-561-1986	Sequence 1986, Ap
73	29	13.1	201	10	US-10-995-561-1988	Sequence 1988, Ap
74	29	13.1	201	10	US-10-995-561-1991	Sequence 1991, Ap

75	29	13.1	201	10	US-10-995-561-18302	Sequence 18302, A
76	29	13.1	201	10	US-10-995-561-18303	Sequence 18303, A
77	29	13.1	201	10	US-10-995-561-18335	Sequence 18335, A
78	29	13.1	201	10	US-10-995-561-26362	Sequence 26362, A
79	29	13.1	201	10	US-10-995-561-26545	Sequence 26545, A
80	29	13.1	201	10	US-10-995-561-26548	Sequence 26548, A
81	29	13.1	201	10	US-10-995-561-73346	Sequence 73346, A
82	29	13.1	201	10	US-10-995-561-73349	Sequence 73349, A
83	29	13.1	201	10	US-10-995-561-73383	Sequence 73383, A
84	29	13.1	660	3	US-09-754-014-6	Sequence 6, Appli
85	29	13.1	660	3	US-09-754-014-7	Sequence 7, Appli
86	29	13.1	660	3	US-09-754-014-8	Sequence 8, Appli
87	29	13.1	660	3	US-09-836-866-4	Sequence 4, Appli
88	29	13.1	721	7	US-10-267-384-199	Sequence 199, App
89	29	13.1	762	3	US-09-826-025-21	Sequence 21, Appl
90	29	13.1	762	9	US-10-785-577-21	Sequence 21, Appl
91	29	13.1	762	9	US-10-688-845-57	Sequence 57, Appl
92	29	13.1	811	7	US-10-373-456-19	Sequence 19, Appl
93	29	13.1	856	7	US-10-349-507-4	Sequence 4, Appli
94	29	13.1	856	7	US-10-267-565-4	Sequence 4, Appli
95	29	13.1	868	7	US-10-373-456-17	Sequence 17, Appl
96	29	13.1	1026	6	US-10-172-399-5	Sequence 5, Appli
97	29	13.1	1026	8	US-10-641-643-1041	Sequence 1041, Ap
98	29	13.1	1287	8	US-10-603-064-6	Sequence 6, Appli
99	29	13.1	1316	9	US-10-476-960-3	Sequence 3, Appli
100	29	13.1	1316	15	US-11-089-191-3	Sequence 3, Appli
101	29	13.1	1395	3	US-09-924-703-5	Sequence 5, Appli
102	29	13.1	1395	8	US-10-358-395-5	Sequence 5, Appli
103	29	13.1	1444	7	US-10-429-802-43	Sequence 43, Appl
104	29	13.1	1444	7	US-10-430-503-34	Sequence 34, Appl
105	29	13.1	1494	8	US-10-322-696-131	Sequence 131, App
106	29	13.1	1526	8	US-10-322-696-185	Sequence 185, App
107	29	13.1	1532	8	US-10-741-601-29	Sequence 29, Appl
108	29	13.1	1532	9	US-10-741-600-51	Sequence 51, Appl
109	29	13.1	1532	10	US-10-995-561-38	Sequence 38, Appl
110	29	13.1	1607	8	US-10-741-601-28	Sequence 28, Appl
111	29	13.1	1607	9	US-10-741-600-50	Sequence 50, Appl
112	29	13.1	1607	10	US-10-995-561-37	Sequence 37, Appl
113	29	13.1	1645	6	US-10-228-811-2	Sequence 2, Appli
114	29	13.1	1828	7	US-10-373-456-2	Sequence 2, Appli
115	29	13.1	2390	10	US-10-528-644A-53	Sequence 53, Appl
116	29	13.1	2466	7	US-10-373-456-1	Sequence 1, Appli
117	29	13.1	5686	7	US-10-136-837-1	Sequence 1, Appli
118	29	13.1	8578	3	US-09-828-825-1	Sequence 1, Appli
119	29	13.1	8578	3	US-09-828-825-3	Sequence 3, Appli
120	29	13.1	8608	3	US-09-828-825-7	Sequence 7, Appli
121	29	13.1	8623	3	US-09-828-825-5	Sequence 5, Appli
122	29	13.1	8629	3	US-09-828-825-15	Sequence 15, Appl
123	29	13.1	8638	3	US-09-828-825-9	Sequence 9, Appli
124	29	13.1	8644	3	US-09-828-825-13	Sequence 13, Appl
125	29	13.1	8659	3	US-09-828-825-11	Sequence 11, Appl
126	29	13.1	11453	10	US-10-511-237-3	Sequence 3, Appli
127	29	13.1	11569	10	US-10-511-237-1	Sequence 1, Appli
128	29	13.1	19277	8	US-10-741-601-5620	Sequence 5620, Ap
129	29	13.1	19277	9	US-10-741-600-17576	Sequence 17576, A
130	29	13.1	19277	10	US-10-995-561-13214	Sequence 13214, A
131	29	13.1	27277	8	US-10-322-696-130	Sequence 130, App
132	29	13.1	29618	8	US-10-741-601-5750	Sequence 5750, Ap
133	29	13.1	29618	9	US-10-741-600-17908	Sequence 17908, A
134	29	13.1	29618	10	US-10-995-561-13444	Sequence 13444, A
135	29	13.1	61916	8	US-10-741-601-5631	Sequence 5631, Ap
136	29	13.1	61916	9	US-10-741-600-17621	Sequence 17621, A
137	29	13.1	305312	10	US-10-995-561-13236	Sequence 13236, A
138	26	11.7	79	6	US-10-079-616-24	Sequence 24, Appl
139	23	10.4	71	7	US-10-041-672C-8	Sequence 8, Appli
140	23	10.4	95	6	US-10-079-616-22	Sequence 22, Appl
141	20	9.0	201	8	US-10-741-601-943	Sequence 943, App
142	20	9.0	201	8	US-10-741-601-952	Sequence 952, App
143	20	9.0	201	8	US-10-741-601-7415	Sequence 7415, Ap
144	20	9.0	201	8	US-10-741-601-11410	Sequence 11410, A
145	20	9.0	201	9	US-10-741-600-3484	Sequence 3484, Ap
146	20	9.0	201	9	US-10-741-600-3493	Sequence 3493, Ap
147	20	9.0	201	9	US-10-741-600-20983	Sequence 20983, A
c 148	20	9.0	201	9	US-10-741-600-28870	Sequence 28870, A
149	20	9.0	201	10	US-10-995-561-1973	Sequence 1973, Ap
150	20	9.0	201	10	US-10-995-561-1983	Sequence 1983, Ap
151	20	9.0	201	10	US-10-995-561-18326	Sequence 18326, A
c 152	20	9.0	201	10	US-10-995-561-26586	Sequence 26586, A
c 153	20	9.0	201	10	US-10-995-561-73379	Sequence 73379, A
c 154	18	8.1	76	7	US-10-041-672C-6	Sequence 6, Appli
c 155	18	8.1	76	7	US-10-041-672C-9	Sequence 9, Appli
156	13	5.9	60	3	US-09-908-975-12410	Sequence 12410, A
157	13	5.9	201	10	US-10-995-561-1982	Sequence 1982, Ap
158	13	5.9	201	10	US-10-995-561-18376	Sequence 18376, A
c 159	13	5.9	201	10	US-10-995-561-26316	Sequence 26316, A
c 160	13	5.9	201	10	US-10-995-561-73335	Sequence 73335, A
c 161	12	5.4	36	6	US-10-079-616-25	Sequence 25, Appl
162	11	5.0	39	3	US-09-917-265-91	Sequence 91, Appl
163	11	5.0	39	9	US-10-821-670-91	Sequence 91, Appl
164	10	4.5	60	3	US-09-917-265-83	Sequence 83, Appl
c 165	10	4.5	60	3	US-09-917-265-84	Sequence 84, Appl
166	10	4.5	60	9	US-10-821-670-83	Sequence 83, Appl
c 167	10	4.5	60	9	US-10-821-670-84	Sequence 84, Appl
168	10	4.5	582	8	US-10-603-064-1	Sequence 1, Appli
169	10	4.5	600	16	US-11-136-527-4750	Sequence 4750, Ap
170	10	4.5	793	16	US-11-136-527-654	Sequence 654, App
171	10	4.5	1231	8	US-10-322-696-128	Sequence 128, App
172	10	4.5	1265	6	US-10-172-399-1	Sequence 1, Appli
173	10	4.5	1278	8	US-10-603-064-5	Sequence 5, Appli
174	10	4.5	1569	8	US-10-603-064-12	Sequence 12, Appl
175	10	4.5	2013	8	US-10-603-064-11	Sequence 11, Appl
176	10	4.5	2709	8	US-10-603-064-13	Sequence 13, Appl
177	10	4.5	5966	7	US-10-136-837-3	Sequence 3, Appli
178	10	4.5	11458	10	US-10-511-237-2	Sequence 2, Appli
179	10	4.5	27125	8	US-10-322-696-127	Sequence 127, App
c 180	9	4.1	51	3	US-09-917-265-96	Sequence 96, Appl
c 181	9	4.1	51	9	US-10-821-670-96	Sequence 96, Appl
c 182	9	4.1	190	10	US-10-287-436A-942	Sequence 942, App
183	9	4.1	201	8	US-10-741-601-7429	Sequence 7429, Ap
c 184	9	4.1	201	8	US-10-741-601-11308	Sequence 11308, A
c 185	9	4.1	201	9	US-10-741-600-5983	Sequence 5983, Ap
c 186	9	4.1	201	9	US-10-741-600-5985	Sequence 5985, Ap
c 187	9	4.1	201	9	US-10-741-600-5992	Sequence 5992, Ap
c 188	9	4.1	201	9	US-10-741-600-6000	Sequence 6000, Ap
c 189	9	4.1	201	9	US-10-741-600-6002	Sequence 6002, Ap
c 190	9	4.1	201	9	US-10-741-600-6009	Sequence 6009, Ap
191	9	4.1	201	9	US-10-741-600-20990	Sequence 20990, A
c 192	9	4.1	201	9	US-10-741-600-27751	Sequence 27751, A
c 193	9	4.1	201	9	US-10-741-600-27778	Sequence 27778, A
c 194	9	4.1	201	9	US-10-741-600-28770	Sequence 28770, A
c 195	9	4.1	201	10	US-10-995-561-3430	Sequence 3430, Ap
c 196	9	4.1	201	10	US-10-995-561-3435	Sequence 3435, Ap
c 197	9	4.1	201	10	US-10-995-561-3440	Sequence 3440, Ap
c 198	9	4.1	201	10	US-10-995-561-3451	Sequence 3451, Ap
c 199	9	4.1	201	10	US-10-995-561-3456	Sequence 3456, Ap
c 200	9	4.1	201	10	US-10-995-561-3461	Sequence 3461, Ap

ALIGNMENTS

RESULT 1
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32

LENGTH: 666
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(666)
OTHER INFORMATION:
-09-917-265-32

ignment Scores:

ed. No.:	1.92e-220	Length:	666
ore:	222.00	Matches:	222
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	100.0%	Indels:	0
:	3	Gaps:	0

-10-821-670A-33 (1-222) x US-09-917-265-32 (1-666)

```
          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

        221 AlaSer 222
            ||||||
        661 GCTTCC 666
```

SULT 2
-09-917-265-34/c
Sequence 34, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.

; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-34

Alignment Scores:

Pred. No.:	1.92e-220	Length:	666
Score:	222.00	Matches:	222
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-917-265-34 (1-666)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
              ||||||
Db          6 GCTTCC 1
```

```
SULT 3
 10-821-670-32
Sequence 32, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
  LENGTH: 666
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(666)
-10-821-670-32

ignment Scores:
ed. No.:              1.92e-220      Length:        666
ore:                  222.00         Matches:       222
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            100.0%         Indels:        0
:                     9              Gaps:          0

-10-821-670A-33 (1-222) x US-10-821-670-32 (1-666)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy      201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy      221 AlaSer 222
            ||||||
Db      661 GCTTCC 666

RESULT 4
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

Alignment Scores:
Pred. No.:              1.92e-220      Length:        666
Score:                  222.00         Matches:       222
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-33 (1-222) x US-10-821-670-34 (1-666)

Qy        1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy       21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy       41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy       61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy       81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy      101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy      121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy      141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187
```

```
       161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

       181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

       201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

       221 AlaSer 222
           ||||||
         6 GCTTCC 1

SULT 5
-10-079-616-26
Sequence 26, Application US/10079616
Publication No. US20020107366A1
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
            STREET: 419 Seventh Street, N.W., Suite 300
            CITY: Washington
            STATE: D.C.
            COUNTRY: USA
            ZIP: 20004
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/10/079,616
            FILING DATE: 22-Feb-2002
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 09/011,143
            FILING DATE: 04-FEB-1998
            APPLICATION NUMBER: PCT/JP97/01824
            FILING DATE: 29-MAY-1997
            APPLICATION NUMBER: JP 165249/1996
            FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
            NAME: BROWDY, Roger L.
            REGISTRATION NUMBER: 25,618
            REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 202-628-5197
            TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 26:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 689 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
-10-079-616-26

ignment Scores:
ed. No.:              2.39e-218      Length:        689
ore:                  220.00         Matches:       220
rcent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            99.1%        Indels:        0
DB:                     6            Gaps:          0

US-10-821-670A-33 (1-222) x US-10-079-616-26 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

RESULT 6
US-10-079-616-8
; Sequence 8, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
        SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/10/079,616
        FILING DATE: 22-Feb-2002
        CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 09/011,143
        FILING DATE: 04-FEB-1998
        APPLICATION NUMBER: PCT/JP97/01824
        FILING DATE: 29-MAY-1997
        APPLICATION NUMBER: JP 165249/1996
        FILING DATE: 04-JUN-1996
      ATTORNEY/AGENT INFORMATION:
        NAME: BROWDY, Roger L.
        REGISTRATION NUMBER: 25,618
        REFERENCE/DOCKET NUMBER: IMAMURA=1
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 202-628-5197
        TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 8:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 1441 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 8:
-10-079-616-8

ıgnment Scores:
ed. No.:              4.79e-218      Length:         1441
ore:                  220.00         Matches:        220
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            99.1%          Indels:         0
:                     6              Gaps:           0

 10-821-670A-33 (1-222) x US-10-079-616-8 (1-1441)

          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy      181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy      201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

RESULT 7
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-35

Alignment Scores:
Pred. No.:              1.77e-194      Length:         591
Score:                  197.00         Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            88.7%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-35 (1-591)

Qy       26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy       46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy       66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy       86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy      106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy      126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy      146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
```

```
        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

```
SULT 8
-09-917-265-37/c
Sequence 37, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Felis catus
-09-917-265-37

ignment Scores:
ed. No.:              1.77e-194      Length:         591
ore:                  197.00         Matches:        197
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            88.7%          Indels:         0
:                     3              Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265-37 (1-591)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy      186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy      206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-10-821-670-35
; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-10-821-670-35

Alignment Scores:
Pred. No.:              1.77e-194      Length:         591
Score:                  197.00         Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            88.7%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-35 (1-591)

Qy       26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy       46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy       66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy       86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy      106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy      126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy      146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
```

```
        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

ULT 10
-10-821-670-37/c
equence 37, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 37
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Felis catus
-10-821-670-37

ignment Scores:
ed. No.:              1.77e-194      Length:         591
ore:                  197.00         Matches:        197
cent Similarity:      100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            88.7%          Indels:         0
:                     9              Gaps:           0

-10-821-670A-33 (1-222) x US-10-821-670-37 (1-591)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy      186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy      206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 11
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:
Pred. No.:              4.36e-194      Length:         1533
Score:                  197.00         Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            88.7%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-43 (1-1533)

Qy       26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy       46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy       66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy       86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy      106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy      126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy      146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362
```

```
       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||
      1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

SULT 12
-09-917-265-45/c
Sequence 45, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 1533
TYPE: DNA
ORGANISM: Felis catus
-09-917-265-45

ignment Scores:

ed. No.:	4.36e-194	Length:	1533
ore:	197.00	Matches:	197
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	88.7%	Indels:	0
:	3	Gaps:	0

-10-821-670A-33 (1-222) x US-09-917-265-45 (1-1533)

```
        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy     186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy     206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 13
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-10-821-670-43

Alignment Scores:

Pred. No.:	4.36e-194	Length:	1533
Score:	197.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	88.7%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-821-670-43 (1-1533)

```
Qy      26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy      46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy      66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy      86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy     106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy     126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy     146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362
```

```
        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

SULT 14
-10-821-670-45/c
Sequence 45, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 45
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Felis catus
-10-821-670-45

gnment Scores:
ed. No.:              4.36e-194      Length:          1533
ore:                  197.00         Matches:         197
cent Similarity:      100.0%         Conservative:    0
st Local Similarity:  100.0%         Mismatches:      0
ry Match:             88.7%          Indels:          0
:                     9              Gaps:            0

 10-821-670A-33 (1-222) x US-10-821-670-45 (1-1533)

         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

         46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy      166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy      186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy      206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 15
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.:              4.53e-194      Length:          1599
Score:                  197.00         Matches:         197
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            88.7%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-33 (1-222) x US-09-917-265-38 (1-1599)

Qy       26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy       46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy       66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy       86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy      106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy      126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy      146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
      1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||
      1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

SULT 16
-09-917-265-40/c
Sequence 40, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 40
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Felis catus
-09-917-265-40

ignment Scores:
ed. No.:              4.53e-194      Length:          1599
ore:                  197.00         Matches:         197
rcent Similarity:     100.0%         Conservative:    0
st Local Similarity:  100.0%         Mismatches:      0
ery Match:            88.7%          Indels:          0
:                     3              Gaps:            0

-10-821-670A-33 (1-222) x US-09-917-265-40 (1-1599)

        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy         166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy         186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy         206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 17
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:
Pred. No.:              4.53e-194      Length:          1599
Score:                  197.00         Matches:         197
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            88.7%          Indels:          0
DB:                     9              Gaps:            0

US-10-821-670A-33 (1-222) x US-10-821-670-38 (1-1599)

Qy          26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy          46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy          66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy          86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy         126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy         146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
      1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||
      1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

SULT 18
-10-821-670-40/c
Sequence 40, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Felis catus
-10-821-670-40

lgnment Scores:
ed. No.:              4.53e-194      Length:         1599
ore:                  197.00         Matches:        197
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            88.7%          Indels:         0
:                     9              Gaps:           0

-10-821-670A-33 (1-222) x US-10-821-670-40 (1-1599)

        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy         166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy         186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy         206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 19
US-10-079-616-9
; Sequence 9, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

Alignment Scores:
Pred. No.:              2.13e-192      Length:         591
Score:                  195.00         Matches:        195
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            87.8%          Indels:         0
DB:                     6              Gaps:           0
```

```
-10-821-670A-33 (1-222) x US-10-079-616-9 (1-591)

        26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

        46 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

        66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

        86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

       106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

       126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

       146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

       166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

       186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

       206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
           ||||||||||||||||||||||||||||||||||||||||||||
       541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 585

SULT 20
-09-917-265-101
Sequence 101, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 101
  LENGTH: 561
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(561)
  OTHER INFORMATION:
-09-917-265-101

ignment Scores:
ed. No.:              4.29e-184      Length:          561
ore:                  187.00         Matches:         187
rcent Similarity:     100.0%         Conservative:    0
st Local Similarity:  100.0%         Mismatches:      0
ery Match:            84.2%          Indels:          0
```

```
DB:                    3              Gaps:          0

US-10-821-670A-33 (1-222) x US-09-917-265-101 (1-561)

Qy         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        216 MetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 21
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-103

Alignment Scores:
Pred. No.:              4.29e-184      Length:          561
Score:                  187.00         Matches:         187
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            84.2%          Indels:          0
DB:                     3              Gaps:            0
```

```
10-821-670A-33 (1-222) x US-09-917-265-103 (1-561)

     36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

     56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

     76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

     96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

    116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

    136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

    156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

    176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

    196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

    216 MetSerTyrLeuAsnAlaSer 222
        ||||||||||||||||||||||
     21 ATGAGCTATCTGAATGCTTCC 1

ULT 22
10-821-670-101
equence 101, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 101
  LENGTH: 561
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(561)
-10-821-670-101

ignment Scores:
ed. No.:              4.29e-184      Length:          561
ore:                  187.00         Matches:         187
cent Similarity:      100.0%         Conservative:    0
st Local Similarity:  100.0%         Mismatches:      0
ery Match:            84.2%          Indels:          0
DB:                   9              Gaps:            0

US-10-821-670A-33 (1-222) x US-10-821-670-101 (1-561)

Qy         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        216 MetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 23
US-10-821-670-103/c
; Sequence 103, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-103

Alignment Scores:
Pred. No.:              4.29e-184      Length:          561
Score:                  187.00         Matches:         187
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            84.2%          Indels:          0
DB:                     9              Gaps:            0
```

```
-10-821-670A-33 (1-222) x US-10-821-670-103 (1-561)

         36 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 55
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

        216 MetSerTyrLeuAsnAlaSer 222
            ||||||||||||||||||||||
         21 ATGAGCTATCTGAATGCTTCC 1

SULT 24
-10-041-672C-2
Sequence 2, Application US/10041672C
Publication No. US20030157059A1
GENERAL INFORMATION:
 APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
 APPLICANT:  Universitat Zurich
 TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
 FILE REFERENCE: NHL-NP-36
 CURRENT APPLICATION NUMBER: US/10/041,672C
 CURRENT FILING DATE:  2002-01-08
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
  LENGTH: 669
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: feline IL-12 p35
-10-041-672C-2

ignment Scores:
ed. No.:              4.53e-57      Length:        669
ore:                  65.00         Matches:       65
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            29.3%         Indels:        0
:                     7             Gaps:          0

-10-821-670A-33 (1-222) x US-10-041-672C-2 (1-669)
```

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyr 65
              |||||||||||||||
Db        181 ACTCTAGAATTTTAC 195

RESULT 25
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-49

Alignment Scores:
Pred. No.:              1.36e-43      Length:        591
Score:                  52.00         Matches:       52
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            23.4%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-33 (1-222) x US-09-917-265-49 (1-591)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||||||||||||||||||||||
Db        238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 26
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERI
;  FILE REFERENCE: IM-5
```

```
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
EQ ID NO 51
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Canis familiaris
-09-917-265-51

gnment Scores:
d. No.:                1.36e-43       Length:         591
re:                    52.00          Matches:        52
cent Similarity:       100.0%         Conservative:   0
t Local Similarity:    100.0%         Mismatches:     0
ry Match:              23.4%          Indels:         0
                       3              Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265-51 (1-591)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

ULT 27
-10-821-670-49
equence 49, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
EQ ID NO 49
  LENGTH: 591
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(591)
-10-821-670-49

gnment Scores:
d. No.:                1.36e-43       Length:         591
re:                    52.00          Matches:        52
 cent Similarity:      100.0%         Conservative:   0
t Local Similarity:    100.0%         Mismatches:     0
ry Match:              23.4%          Indels:         0
                       9              Gaps:           0

 10-821-670A-33 (1-222) x US-10-821-670-49 (1-591)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       118 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 177

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 237

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         238 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 273

RESULT 28
US-10-821-670-51/c
; Sequence 51, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-51

Alignment Scores:
Pred. No.:                1.36e-43       Length:         591
Score:                    52.00          Matches:        52
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              23.4%          Indels:         0
DB:                       9              Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-51 (1-591)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 29
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
```

```
  LOCATION: (1)..(666)
  OTHER INFORMATION:
-09-917-265-46

ignment Scores:
ed. No.:              1.52e-43      Length:         666
ore:                  52.00         Matches:        52
rcent Similarity:     100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            23.4%         Indels:         0
:                     3             Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265-46 (1-666)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

SULT 30
-09-917-265-48/c
Sequence 48, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
  LENGTH: 666
  TYPE: DNA
  ORGANISM: Canis familiaris
-09-917-265-48

ignment Scores:
ed. No.:              1.52e-43      Length:         666
ore:                  52.00         Matches:        52
rcent Similarity:     100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            23.4%         Indels:         0
:                     3             Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265-48 (1-666)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 31
-10-821-670-46
Sequence 46, Application US/10821670
Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-46

Alignment Scores:
Pred. No.:              1.52e-43      Length:         666
Score:                  52.00         Matches:        52
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.4%         Indels:         0
DB:                     9             Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-46 (1-666)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 252

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 312

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db        313 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 348

RESULT 32
US-10-821-670-48/c
; Sequence 48, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-48

Alignment Scores:
Pred. No.:              1.52e-43      Length:         666
Score:                  52.00         Matches:        52
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.4%         Indels:         0
DB:                     9             Gaps:           0
```

```
10-821-670A-33 (1-222) x US-10-821-670-48 (1-666)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
       354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 33
-09-917-265-104
Sequence 104, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
  LENGTH: 1455
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (232)..(897)
  OTHER INFORMATION:
 09-917-265-104

gnment Scores:
d. No.:                3.18e-43       Length:         1455
re:                    52.00          Matches:        52
cent Similarity:       100.0%         Conservative:   0
t Local Similarity:    100.0%         Mismatches:     0
ry Match:              23.4%          Indels:         0
:                      3              Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265-104 (1-1455)

        65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

        85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543

       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           |||||||||||||||||||||||||||||||||||
       544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

SULT 34
-09-917-265-106/c
Sequence 106, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 106
  LENGTH: 1455
  TYPE: DNA
  ORGANISM: Canis familiaris
US-09-917-265-106

Alignment Scores:
Pred. No.:                3.18e-43       Length:         1455
Score:                    52.00          Matches:        52
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              23.4%          Indels:         0
DB:                       3              Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-106 (1-1455)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              |||||||||||||||||||||||||||||||||||
Db         912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

RESULT 35
US-10-821-670-104
; Sequence 104, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-10-821-670-104

Alignment Scores:
Pred. No.:                3.18e-43       Length:         1455
Score:                    52.00          Matches:        52
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              23.4%          Indels:         0
DB:                       9              Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-104 (1-1455)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 483

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 543
```

```
       105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
           ||||||||||||||||||||||||||||||
       544 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 579

SULT 36
-10-821-670-106/c
Sequence 106, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 106
  LENGTH: 1455
  TYPE: DNA
  ORGANISM: Canis familiaris
-10-821-670-106

ignment Scores:
ed. No.:              3.18e-43      Length:         1455
ore:                  52.00         Matches:        52
cent Similarity:      100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            23.4%         Indels:         0
:                     9             Gaps:           0

-10-821-670A-33 (1-222) x US-10-821-670-106 (1-1455)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1032 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 973

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        972 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 913

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            ||||||||||||||||||||||||||||||||||||
        912 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 877

SULT 37
-09-917-265-66
Sequence 66, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1533)
  OTHER INFORMATION:
-09-917-265-66

Alignment Scores:
Pred. No.:              3.34e-43      Length:         1533
Score:                  52.00         Matches:        52
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.4%         Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-66 (1-1533)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215

RESULT 38
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

Alignment Scores:
Pred. No.:              3.34e-43      Length:         1533
Score:                  52.00         Matches:        52
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            23.4%         Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-68 (1-1533)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 39
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
```

TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66
LENGTH: 1533
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
10-821-670-66

gnment Scores:

d. No.:	3.34e-43	Length:	1533
re:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	23.4%	Indels:	0
	9	Gaps:	0

10-821-670A-33 (1-222) x US-10-821-670-66 (1-1533)

```
  65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

  85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

 105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
     ||||||||||||||||||||||||||||||||||||
1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1215
```

SULT 40
10-821-670-68/c
Sequence 68, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 68
LENGTH: 1533
TYPE: DNA
ORGANISM: Canis familiaris
10-821-670-68

gnment Scores:

d. No.:	3.34e-43	Length:	1533
re:	52.00	Matches:	52
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	23.4%	Indels:	0
	9	Gaps:	0

10-821-670A-33 (1-222) x US-10-821-670-68 (1-1533)

```
  65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy   85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy  105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
     ||||||||||||||||||||||||||||||||||||
Db  354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319
```

RESULT 41
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:

Pred. No.:	3.48e-43	Length:	1599
Score:	52.00	Matches:	52
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	23.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-917-265-61 (1-1599)

```
Qy   65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy   85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy  105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
        ||||||||||||||||||||||||||||||||||||
Db 1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281
```

RESULT 42
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1

```
SEQ ID NO 63
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Canis familiaris
-09-917-265-63

ignment Scores:
ed. No.:                3.48e-43        Length:         1599
ore:                    52.00           Matches:        52
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              23.4%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-917-265-63 (1-1599)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

SULT 43
-10-821-670-61
Sequence 61, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 61
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1599)
-10-821-670-61

ignment Scores:
ed. No.:                3.48e-43        Length:         1599
ore:                    52.00           Matches:        52
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              23.4%           Indels:         0
:                       9               Gaps:           0

-10-821-670A-33 (1-222) x US-10-821-670-61 (1-1599)

         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
            |||||||||||||||||||||||||||||||||||
       Db      1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 1281

RESULT 44
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;    LENGTH: 1599
;    TYPE: DNA
;    ORGANISM: Canis familiaris
US-10-821-670-63

Alignment Scores:
Pred. No.:              3.48e-43        Length:         1599
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            23.4%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-63 (1-1599)

Qy          65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy          85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy         105 IleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               |||||||||||||||||||||||||||||||||||
Db         354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCT 319

RESULT 45
US-10-741-601-946
; Sequence 946, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 946
;    LENGTH: 201
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-741-601-946

Alignment Scores:
Pred. No.:              4.2e-20         Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     8               Gaps:           0
```

```
10-821-670A-33 (1-222) x US-10-741-601-946 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

       204 AlaPheArgIleArgAlaValThrIle 212
           |||||||||||||||||||||||||||
        64 GCTTTCAGAATTCGGGCAGTGACTATT 90

SULT 46
-10-741-601-947
Sequence 947, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001500
 CURRENT APPLICATION NUMBER: US/10/741,601
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 26415
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 947
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-947

lgnment Scores:
ed. No.:              4.2e-20       Length:         201
ore:                  29.00         Matches:        29
cent Similarity:      100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ry Match:             13.1%         Indels:         0
:                     8             Gaps:           0

10-821-670A-33 (1-222) x US-10-741-601-947 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

       204 AlaPheArgIleArgAlaValThrIle 212
           |||||||||||||||||||||||||||
        72 GCTTTCAGAATTCGGGCAGTGACTATT 98

SULT 47
-10-741-601-951
Sequence 951, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001500
 CURRENT APPLICATION NUMBER: US/10/741,601
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 26415
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 951
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-951

lgnment Scores:
ed. No.:              4.2e-20       Length:         201
ore:                  29.00         Matches:        29
cent Similarity:      100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ry Match:             13.1%         Indels:         0
:                     8             Gaps:           0

US-10-821-670A-33 (1-222) x US-10-741-601-951 (1-201)

Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy         204 AlaPheArgIleArgAlaValThrIle 212
               |||||||||||||||||||||||||||
Db         173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 48
US-10-741-601-955
; Sequence 955, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-955

Alignment Scores:
Pred. No.:              4.2e-20       Length:         201
Score:                  29.00         Matches:        29
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            13.1%         Indels:         0
DB:                     8             Gaps:           0

US-10-821-670A-33 (1-222) x US-10-741-601-955 (1-201)

Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy         204 AlaPheArgIleArgAlaValThrIle 212
               |||||||||||||||||||||||||||
Db          64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 49
US-10-741-601-957
; Sequence 957, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 957
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-957

Alignment Scores:
Pred. No.:              4.2e-20       Length:         201
Score:                  29.00         Matches:        29
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            13.1%         Indels:         0
```

```
:                    8              Gaps:          0

-10-821-670A-33 (1-222) x US-10-741-601-957 (1-201)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
         72 GCTTTCAGAATTCGGGCAGTGACTATT 98

SULT 50
-10-741-601-960
Sequence 960, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001500
 CURRENT APPLICATION NUMBER: US/10/741,601
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 26415
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 960
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-960

ignment Scores:
ed. No.:              4.2e-20        Length:        201
ore:                  29.00          Matches:       29
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     8              Gaps:          0

-10-821-670A-33 (1-222) x US-10-741-601-960 (1-201)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

SULT 51
-10-741-601-7417
Sequence 7417, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001500
 CURRENT APPLICATION NUMBER: US/10/741,601
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 26415
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7417
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-7417

ignment Scores:
ed. No.:              4.2e-20        Length:        201
ore:                  29.00          Matches:       29
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
Query Match:          13.1%          Indels:        0
DB:                   8              Gaps:          0

US-10-821-670A-33 (1-222) x US-10-741-601-7417 (1-201)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db       64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 52
US-10-741-601-7418
; Sequence 7418, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7418
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7418

Alignment Scores:
Pred. No.:            4.2e-20        Length:        201
Score:                29.00          Matches:       29
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          13.1%          Indels:        0
DB:                   8              Gaps:          0

US-10-821-670A-33 (1-222) x US-10-741-601-7418 (1-201)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db       72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 53
US-10-741-601-7431
; Sequence 7431, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7431
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7431

Alignment Scores:
Pred. No.:            4.2e-20        Length:        201
Score:                29.00          Matches:       29
Percent Similarity:   100.0%         Conservative:  0
```

```
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            13.1%           Indels:        0
:                     8               Gaps:          0

-10-821-670A-33 (1-222) x US-10-741-601-7431 (1-201)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

SULT 54
10-741-601-11370/c
equence 11370, Application US/10741601
ublication No. US20040166519A1
ENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE:  2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 11370
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-11370

ignment Scores:
ed. No.:              4.2e-20         Length:        201
ore:                  29.00           Matches:       29
cent Similarity:      100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            13.1%           Indels:        0
:                     8               Gaps:          0

-10-821-670A-33 (1-222) x US-10-741-601-11370 (1-201)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        138 GCTTTCAGAATTCGGGCAGTGACTATT 112

SULT 55
-10-741-601-11372/c
equence 11372, Application US/10741601
ublication No. US20040166519A1
ENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE:  2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 11372
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-601-11372

ignment Scores:
ed. No.:              4.2e-20         Length:        201
ore:                  29.00           Matches:       29
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          13.1%           Indels:        0
DB:                   8               Gaps:          0

US-10-821-670A-33 (1-222) x US-10-741-601-11372 (1-201)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      130 GCTTTCAGAATTCGGGCAGTGACTATT 104

RESULT 56
US-10-741-601-11417/c
; Sequence 11417, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11417
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11417

Alignment Scores:
Pred. No.:            4.2e-20         Length:        201
Score:                29.00           Matches:       29
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          13.1%           Indels:        0
DB:                   8               Gaps:          0

US-10-821-670A-33 (1-222) x US-10-741-601-11417 (1-201)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db       29 GCTTTCAGAATTCGGGCAGTGACTATT 3

RESULT 57
US-10-741-600-3487
; Sequence 3487, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3487
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3487

Alignment Scores:
Pred. No.:            4.2e-20         Length:        201
```

```
ore:                    29.00          Matches:       29
rcent Similarity:       100.0%         Conservative:  0
st Local Similarity:    100.0%         Mismatches:    0
ery Match:              13.1%          Indels:        0
:                       9              Gaps:          0

-10-821-670A-33 (1-222) x US-10-741-600-3487 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
        64 GCTTTCAGAATTCGGGCAGTGACTATT 90

SULT 58
-10-741-600-3488
Sequence 3488, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3488
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-600-3488

ignment Scores:
ed. No.:                4.2e-20        Length:        201
ore:                    29.00          Matches:       29
rcent Similarity:       100.0%         Conservative:  0
st Local Similarity:    100.0%         Mismatches:    0
ery Match:              13.1%          Indels:        0
:                       9              Gaps:          0

-10-821-670A-33 (1-222) x US-10-741-600-3488 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
        72 GCTTTCAGAATTCGGGCAGTGACTATT 98

SULT 59
-10-741-600-3492
Sequence 3492, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3492
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-741-600-3492

ignment Scores:
```

```
Pred. No.:              4.2e-20        Length:        201
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-33 (1-222) x US-10-741-600-3492 (1-201)

Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy         204 AlaPheArgIleArgAlaValThrIle 212
               ||||||||||||||||||||||||||
Db         173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 60
US-10-741-600-3496
; Sequence 3496, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3496
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3496

Alignment Scores:
Pred. No.:              4.2e-20        Length:        201
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-33 (1-222) x US-10-741-600-3496 (1-201)

Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy         204 AlaPheArgIleArgAlaValThrIle 212
               ||||||||||||||||||||||||||
Db          64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 61
US-10-741-600-3498
; Sequence 3498, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3498
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3498
```

```
gnment Scores:
d. No.:                 4.2e-20         Length:         201
re:                     29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               13.1%           Indels:         0
                        9               Gaps:           0

-10-821-670A-33 (1-222) x US-10-741-600-3498 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
        72 GCTTTCAGAATTCGGGCAGTGACTATT 98

SULT 62
-10-741-600-3501
Sequence 3501, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3501
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
 10-741-600-3501

gnment Scores:
d. No.:                 4.2e-20         Length:         201
re:                     29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               13.1%           Indels:         0
                        9               Gaps:           0

-10-821-670A-33 (1-222) x US-10-741-600-3501 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
       173 GCTTTCAGAATTCGGGCAGTGACTATT 199

SULT 63
-10-741-600-20963
Sequence 20963, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE:  2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20963
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
 10-741-600-20963

Alignment Scores:
Pred. No.:              4.2e-20         Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-741-600-20963 (1-201)

Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy         204 AlaPheArgIleArgAlaValThrIle 212
               ||||||||||||||||||||||||||||
Db          64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 64
US-10-741-600-20964
; Sequence 20964, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20964
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20964

Alignment Scores:
Pred. No.:              4.2e-20         Length:         201
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-741-600-20964 (1-201)

Qy         184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy         204 AlaPheArgIleArgAlaValThrIle 212
               ||||||||||||||||||||||||||||
Db          72 GCTTTCAGAATTCGGGCAGTGACTATT 98

RESULT 65
US-10-741-600-20992
; Sequence 20992, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20992
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

-10-741-600-20992

ignment Scores:
ed. No.: 4.2e-20 Length: 201
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 9 Gaps: 0

-10-821-670A-33 (1-222) x US-10-741-600-20992 (1-201)

```
       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
       173 GCTTTCAGAATTCGGGCAGTGACTATT 199
```

SULT 66
-10-741-600-28831/c
Sequence 28831, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28831
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
-10-741-600-28831

ignment Scores:
ed. No.: 4.2e-20 Length: 201
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 9 Gaps: 0

-10-821-670A-33 (1-222) x US-10-741-600-28831 (1-201)

```
       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
       138 GCTTTCAGAATTCGGGCAGTGACTATT 112
```

SULT 67
-10-741-600-28833/c
Sequence 28833, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28833
LENGTH: 201
TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-28833

Alignment Scores:
Pred. No.: 4.2e-20 Length: 201
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 9 Gaps: 0

US-10-821-670A-33 (1-222) x US-10-741-600-28833 (1-201)

```
Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||||
Db        130 GCTTTCAGAATTCGGGCAGTGACTATT 104
```

RESULT 68
US-10-741-600-28877/c
; Sequence 28877, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28877
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-28877

Alignment Scores:
Pred. No.: 4.2e-20 Length: 201
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 9 Gaps: 0

US-10-821-670A-33 (1-222) x US-10-741-600-28877 (1-201)

```
Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||||
Db         29 GCTTTCAGAATTCGGGCAGTGACTATT 3
```

RESULT 69
US-10-995-561-1976
; Sequence 1976, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1976

```
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-1976

ignment Scores:
ed. No.:              4.2e-20        Length:        201
re:                   29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ry Match:             13.1%          Indels:        0
                      10             Gaps:          0

-10-821-670A-33 (1-222) x US-10-995-561-1976 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
        64 GCTTTCAGAATTCGGGCAGTGACTATT 90

SULT 70
-10-995-561-1977
equence 1977, Application US/10995561
ublication No. US20050272054A1
ENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 1977
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-1977

ignment Scores:
ed. No.:              4.2e-20        Length:        201
re:                   29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ry Match:             13.1%          Indels:        0
                      10             Gaps:          0

-10-821-670A-33 (1-222) x US-10-995-561-1977 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
        72 GCTTTCAGAATTCGGGCAGTGACTATT 98

SULT 71
-10-995-561-1981
equence 1981, Application US/10995561
ublication No. US20050272054A1
ENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1981
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1981

Alignment Scores:
Pred. No.:            4.2e-20        Length:        201
Score:                29.00          Matches:       29
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          13.1%          Indels:        0
DB:                   10             Gaps:          0

US-10-821-670A-33 (1-222) x US-10-995-561-1981 (1-201)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        173 GCTTTCAGAATTCGGGCAGTGACTATT 199

RESULT 72
US-10-995-561-1986
; Sequence 1986, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1986
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1986

Alignment Scores:
Pred. No.:            4.2e-20        Length:        201
Score:                29.00          Matches:       29
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          13.1%          Indels:        0
DB:                   10             Gaps:          0

US-10-821-670A-33 (1-222) x US-10-995-561-1986 (1-201)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90

RESULT 73
US-10-995-561-1988
; Sequence 1988, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
```

FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1988
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
-10-995-561-1988

ignment Scores:

ed. No.:	4.2e-20	Length:	201
ore:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
:	10	Gaps:	0

-10-821-670A-33 (1-222) x US-10-995-561-1988 (1-201)

```
       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
        72 GCTTTCAGAATTCGGGCAGTGACTATT 98
```

SULT 74
-10-995-561-1991
Sequence 1991, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1991
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
-10-995-561-1991

ignment Scores:

ed. No.:	4.2e-20	Length:	201
ore:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
:	10	Gaps:	0

-10-821-670A-33 (1-222) x US-10-995-561-1991 (1-201)

```
       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||||
       173 GCTTTCAGAATTCGGGCAGTGACTATT 199
```

SULT 75
-10-995-561-18302
Sequence 18302, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18302
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-18302

Alignment Scores:

Pred. No.:	4.2e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	13.1%	Indels:	0
DB:	10	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-995-561-18302 (1-201)

```
Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 63

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||||
Db         64 GCTTTCAGAATTCGGGCAGTGACTATT 90
```

RESULT 76
US-10-995-561-18303
; Sequence 18303, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18303
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-18303

Alignment Scores:

Pred. No.:	4.2e-20	Length:	201
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	13.1%	Indels:	0
DB:	10	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-995-561-18303 (1-201)

```
Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 71

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||||
Db         72 GCTTTCAGAATTCGGGCAGTGACTATT 98
```

RESULT 77
US-10-995-561-18335
; Sequence 18335, Application US/10995561

```
ublication No. US20050272054A1
ENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 18335
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-18335

ignment Scores:
ed. No.:              4.2e-20        Length:        201
ore:                  29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     10             Gaps:          0

-10-821-670A-33 (1-222) x US-10-995-561-18335 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       113 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 172

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
       173 GCTTTCAGAATTCGGGCAGTGACTATT 199

ULT 78
10-995-561-26362/c
equence 26362, Application US/10995561
ublication No. US20050272054A1
ENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 26362
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-26362

ignment Scores:
ed. No.:              4.2e-20        Length:        201
ore:                  29.00          Matches:       29
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            13.1%          Indels:        0
:                     10             Gaps:          0

-10-821-670A-33 (1-222) x US-10-995-561-26362 (1-201)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

       204 AlaPheArgIleArgAlaValThrIle 212
           ||||||||||||||||||||||||||
        29 GCTTTCAGAATTCGGGCAGTGACTATT 3
```

```
RESULT 79
US-10-995-561-26545/c
; Sequence 26545, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26545
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26545

Alignment Scores:
Pred. No.:              4.2e-20        Length:        201
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     10             Gaps:          0

US-10-821-670A-33 (1-222) x US-10-995-561-26545 (1-201)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              ||||||||||||||||||||||||||
Db        138 GCTTTCAGAATTCGGGCAGTGACTATT 112

RESULT 80
US-10-995-561-26548/c
; Sequence 26548, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26548
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26548

Alignment Scores:
Pred. No.:              4.2e-20        Length:        201
Score:                  29.00          Matches:       29
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            13.1%          Indels:        0
DB:                     10             Gaps:          0

US-10-821-670A-33 (1-222) x US-10-995-561-26548 (1-201)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

Qy        204 AlaPheArgIleArgAlaValThrIle 212
```

```
          ||||||||||||||||||||||||||
      130 GCTTTCAGAATTCGGGCAGTGACTATT 104

SULT 81
-10-995-561-73346/c
Sequence 73346, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73346
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-73346

ignment Scores:
ed. No.:              4.2e-20       Length:         201
ore:                  29.00         Matches:        29
rcent Similarity:     100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            13.1%         Indels:         0
:                     10            Gaps:           0

-10-821-670A-33 (1-222) x US-10-995-561-73346 (1-201)

      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      198 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 139

      204 AlaPheArgIleArgAlaValThrIle 212
          |||||||||||||||||||||||||||
      138 GCTTTCAGAATTCGGGCAGTGACTATT 112

SULT 82
-10-995-561-73349/c
Sequence 73349, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION:  DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE:  2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73349
  LENGTH: 201
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-995-561-73349

ignment Scores:
ed. No.:              4.2e-20       Length:         201
ore:                  29.00         Matches:        29
rcent Similarity:     100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            13.1%         Indels:         0
:                     10            Gaps:           0

-10-821-670A-33 (1-222) x US-10-995-561-73349 (1-201)

      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        190 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 131

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||||
Db        130 GCTTTCAGAATTCGGGCAGTGACTATT 104

RESULT 83
US-10-995-561-73383/c
; Sequence 73383, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73383
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73383

Alignment Scores:
Pred. No.:              4.2e-20       Length:         201
Score:                  29.00         Matches:        29
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            13.1%         Indels:         0
DB:                     10            Gaps:           0

US-10-821-670A-33 (1-222) x US-10-995-561-73383 (1-201)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 30

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||||
Db         29 GCTTTCAGAATTCGGGCAGTGACTATT 3

RESULT 84
US-09-754-014-6
; Sequence 6, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
```

```
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/948,958
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Berkman, Charles S.
           REGISTRATION NUMBER: 38,077
           REFERENCE/DOCKET NUMBER: 226/284
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 6:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 660 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 6:
09-754-014-6

ignment Scores:
d. No.:                1.29e-19       Length:        660
re:                    29.00          Matches:       29
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              13.1%          Indels:        0
:                      3              Gaps:          0

-10-821-670A-33 (1-222) x US-09-754-014-6 (1-660)

       184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

       204 AlaPheArgIleArgAlaValThrIle 212
           |||||||||||||||||||||||||
       601 GCTTTCAGAATTCGGGCAGTGACTATT 627

SULT 85
-09-754-014-7
Sequence 7, Application US/09754014
Patent No. US20020119940A1
  GENERAL INFORMATION:
      APPLICANT: Jeff No. US20020119940A1dstrom
                 Bruce Freimark
                 Deepa Deshpande
      TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                          AND USES
      NUMBER OF SEQUENCES: 12
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Lyon & Lyon
           STREET: 633 West Fifth Street
                   Suite 4700
           CITY: Los Angeles
           STATE: California
           COUNTRY: U.S.A.
           ZIP: 90071-2066
      COMPUTER READABLE FORM:
           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                        storage
           COMPUTER: IBM Compatible
           OPERATING SYSTEM: IBM P.C. DOS 5.0
           SOFTWARE: FastSEQ for Windows 2.0
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/754,014
           FILING DATE: 03-Jan-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/948,958
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Berkman, Charles S.
           REGISTRATION NUMBER: 38,077
           REFERENCE/DOCKET NUMBER: 226/284
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 7:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 660 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-754-014-7

Alignment Scores:
Pred. No.:                1.29e-19       Length:        660
Score:                    29.00          Matches:       29
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              13.1%          Indels:        0
DB:                       3              Gaps:          0

US-10-821-670A-33 (1-222) x US-09-754-014-7 (1-660)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||
Db        601 GCCTTCCGCATCCGCGCCGTGACCATC 627

RESULT 86
US-09-754-014-8
; Sequence 8, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 8:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
-09-754-014-8

ignment Scores:
ed. No.: 1.29e-19 Length: 660
ore: 29.00 Matches: 29
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 13.1% Indels: 0
: 3 Gaps: 0

-10-821-670A-33 (1-222) x US-09-754-014-8 (1-660)

184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 AGCAGCCTGGAGGAGCCCGACTTCTACAAGACCAAGATCAAGCTGTGCATCCTGCTGCAC 600

204 AlaPheArgIleArgAlaValThrIle 212
|||||||||||||||||||||||||||
601 GCCTTCCGCATCCGGGCCGTGACCATC 627

SULT 87
-09-836-866-4
Sequence 4, Application US/09836866
Patent No. US20020123473A1
GENERAL INFORMATION:
APPLICANT: No. US20020123473A1dstrom, Jeff
Freimark, Bruce
Deshpande, Deepa
TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
DELIVERY SYTEMS AND USES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,866
FILING DATE: 16-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/949,160
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 226/285
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-836-866-4

Alignment Scores:
Pred. No.: 1.29e-19 Length: 660
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-33 (1-222) x US-09-836-866-4 (1-660)

Qy 184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 600

Qy 204 AlaPheArgIleArgAlaValThrIle 212
|||||||||||||||||||||||||||
Db 601 GCTTTCAGAATTCGGGCAGTGACTATT 627

RESULT 88
US-10-267-384-199
; Sequence 199, Application US/10267384
; Publication No. US20030198623A1
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; Tartaglia, James
; Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,384
; FILING DATE: 09-Oct-2002
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 199:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-10-267-384-199

Alignment Scores:
Pred. No.: 1.4e-19 Length: 721
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.1% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-33 (1-222) x US-10-267-384-199 (1-721)

```
        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        602 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 661

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
        662 GCTTTCAGAATTCGGGCAGTGACTATT 688

SULT 89
-09-826-025-21
Sequence 21, Application US/09826025
Patent No. US20020162123A1
  GENERAL INFORMATION:
       APPLICANT: Chang, Lung-Ji
       TITLE OF INVENTION: Combination Immunogene Therapy
       NUMBER OF SEQUENCES: 25
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: Medlen & Carroll, LLP
            STREET: 220 Montgomery Street, Suite 2200
            CITY: San Francisco
            STATE: California
            COUNTRY: United States of America
            ZIP: 94104
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/826,025
            FILING DATE: 04-Apr-2001
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/838,702
            FILING DATE: <Unknown>
       ATTORNEY/AGENT INFORMATION:
            NAME: Ingolia, Diane E.
            REGISTRATION NUMBER: 40,027
            REFERENCE/DOCKET NUMBER: CHANG-02687
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: (415) 705-8410
            TELEFAX: (415) 397-8338
  INFORMATION FOR SEQ ID NO: 21:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 762 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: double
            TOPOLOGY: linear
       MOLECULE TYPE: other nucleic acid
            DESCRIPTION: /desc = "DNA"
       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
-09-826-025-21

ignment Scores:
ed. No.:                1.48e-19        Length:         762
re:                     29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-33 (1-222) x US-09-826-025-21 (1-762)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||||
        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 90
```

```
US-10-785-577-21
; Sequence 21, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/785,577
;             FILING DATE: 23-Feb-2004
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/838,702
;             FILING DATE: 9-Apr-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-785-577-21

Alignment Scores:
Pred. No.:              1.48e-19        Length:         762
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-785-577-21 (1-762)

Qy        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

Qy        204 AlaPheArgIleArgAlaValThrIle 212
              |||||||||||||||||||||||||||
Db        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

RESULT 91
US-10-688-845-57
; Sequence 57, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
;  APPLICANT: Lotze, Michael T
;  APPLICANT:  Tahara, Hideaki
;  TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
;  FILE REFERENCE: UPT-004
;  CURRENT APPLICATION NUMBER: US/10/688,845
;  CURRENT FILING DATE:  2003-10-15
```

```
 PRIOR APPLICATION NUMBER: 60/418,865
 PRIOR FILING DATE: 2002-10-15
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
  LENGTH: 762
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-688-845-57

ignment Scores:
ed. No.:                1.48e-19        Length:         762
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       9               Gaps:           0

-10-821-670A-33 (1-222) x US-10-688-845-57 (1-762)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        643 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 702

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        703 GCTTTCAGAATTCGGGCAGTGACTATT 729

SULT 92
-10-373-456-19
Sequence 19, Application US/10373456
Publication No. US20040009146A1
GENERAL INFORMATION:
 APPLICANT: Podhajcer, Osvaldo
 TITLE OF INVENTION: Anti-Tumor Vaccine and Method
 FILE REFERENCE: 1423P-US/101141-14
 CURRENT APPLICATION NUMBER: US/10/373,456
 CURRENT FILING DATE:  2003-02-25
 PRIOR APPLICATION NUMBER: US 60/359,836
 PRIOR FILING DATE: 2002-02-26
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
  LENGTH: 811
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-373-456-19

ignment Scores:
ed. No.:                1.57e-19        Length:         811
ore:                    29.00           Matches:        29
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              13.1%           Indels:         0
:                       7               Gaps:           0

-10-821-670A-33 (1-222) x US-10-373-456-19 (1-811)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        489 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 548

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        549 GCTTTCAGAATTCGGGCAGTGACTATT 575

SULT 93
-10-349-507-4
Sequence 4, Application US/10349507
Publication No. US20030199002A1
GENERAL INFORMATION:
 APPLICANT: Hekimi , Siegfried
 APPLICANT:  Jiang , Ning
;  APPLICANT:  Benard, Claire
;  APPLICANT:  Kebir , Hania
;  APPLICANT:  McCright, Brenton
;  APPLICANT:  Lakowski , Bernard
;  TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
;  FILE REFERENCE: 11202-006-999
;  CURRENT APPLICATION NUMBER: US/10/349,507
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 10/312,187
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: PCT/CA01/00913
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: 60/213,174
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/254,932
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;    LENGTH: 856
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (170)...(826)
US-10-349-507-4

Alignment Scores:
Pred. No.:              1.65e-19        Length:         856
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-349-507-4 (1-856)

Qy          184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy          204 AlaPheArgIleArgAlaValThrIle 212
                ||||||||||||||||||||||||||
Db          770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 94
US-10-267-565-4
; Sequence 4, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
;  APPLICANT: Gately, Maurice
;  APPLICANT:  Gubler, Ulrich
;  APPLICANT:  Hulmes, Jeffery
;  APPLICANT:  Podlaski, Frank
;  APPLICANT:  Stern, Alvin
;  TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
;  TITLE OF INVENTION:  LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES THERETO
;  FILE REFERENCE: 11126-005
;  CURRENT APPLICATION NUMBER: US/10/267,565
;  CURRENT FILING DATE:  2003-01-23
;  PRIOR APPLICATION NUMBER: 09/401,839
;  PRIOR FILING DATE: 1999-09-22
;  PRIOR APPLICATION NUMBER: 08/459,151
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 08/205,011
;  PRIOR FILING DATE: 1994-03-02
;  PRIOR APPLICATION NUMBER: 07/857,023
;  PRIOR FILING DATE: 1992-03-24
;  PRIOR APPLICATION NUMBER: 07/572,284
;  PRIOR FILING DATE: 1990-08-27
;  PRIOR APPLICATION NUMBER: 07/520,935
;  PRIOR FILING DATE: 1990-05-09
```

```
 PRIOR APPLICATION NUMBER: 07/455,708
 PRIOR FILING DATE: 1989-12-22
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: FastSEQ for Windows Version 3.0
EQ ID NO 4
  LENGTH: 856
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (170)...(826)
-10-267-565-4

ignment Scores:
ed. No.:                1.65e-19        Length:         856
re:                     29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               13.1%           Indels:         0
                        7               Gaps:           0

 10-821-670A-33 (1-222) x US-10-267-565-4 (1-856)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        770 GCTTTCAGAATTCGGGCAGTGACTATT 796

SULT 95
-10-373-456-17
Sequence 17, Application US/10373456
Publication No. US20040009146A1
GENERAL INFORMATION:
 APPLICANT: Podhajcer, Osvaldo
 TITLE OF INVENTION: Anti-Tumor Vaccine and Method
 FILE REFERENCE: 1423P-US/101141-14
 CURRENT APPLICATION NUMBER: US/10/373,456
 CURRENT FILING DATE:  2003-02-25
 PRIOR APPLICATION NUMBER: US 60/359,836
 PRIOR FILING DATE: 2002-02-26
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.1
EQ ID NO 17
  LENGTH: 868
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-373-456-17

ignment Scores:
ed. No.:                1.67e-19        Length:         868
re:                     29.00           Matches:        29
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               13.1%           Indels:         0
                        7               Gaps:           0

 10-821-670A-33 (1-222) x US-10-373-456-17 (1-868)

        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        552 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 611

        204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
        612 GCTTTCAGAATTCGGGCAGTGACTATT 638

SULT 96
-10-172-399-5
Sequence 5, Application US/10172399
Publication No. US20030045495A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTHE
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)..(829)
US-10-172-399-5

Alignment Scores:
Pred. No.:              1.96e-19        Length:         1026
Score:                  29.00           Matches:        29
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.1%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-172-399-5 (1-1026)

Qy      184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

Qy      204 AlaPheArgIleArgAlaValThrIle 212
            ||||||||||||||||||||||||||
Db      770 GCTTTCAGAATTCGGGCAGTGACTATT 796

RESULT 97
US-10-641-643-1041
; Sequence 1041, Application US/10641643
; Publication No. US20040077003A1
;   GENERAL INFORMATION:
;        APPLICANT: Cocks, Benjamin G.
;                   Susan G. Stuart
;                   Jeffrey J. Seilhamer
;        TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;                            GENE EXPRESSION
;        NUMBER OF SEQUENCES: 1508
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;             STREET: 3174 PORTER DRIVE
;             CITY: PALO ALTO
;             STATE: CALIFORNIA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/641,643
;             FILING DATE: 14-Aug-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Zeller, Karen J.
;             REGISTRATION NUMBER: 37,071
;             REFERENCE/DOCKET NUMBER: PA-0001 US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650) 855-0555
```

TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1041:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g180623
SEQUENCE DESCRIPTION: SEQ ID NO: 1041 :
-10-641-643-1041

ignment Scores:

ed. No.:	1.96e-19	Length:	1026
ore:	29.00	Matches:	29
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
:	8	Gaps:	0

-10-821-670A-33 (1-222) x US-10-641-643-1041 (1-1026)

184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
710 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 769

204 AlaPheArgIleArgAlaValThrIle 212
770 GCTTTCAGAATTCGGGCAGTGACTATT 796

SULT 98
-10-603-064-6
Sequence 6, Application US/10603064
Publication No. US20040072299A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/10/603,064
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/634,368
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1287
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
OTHER INFORMATION: fusion protein coding sequence
-10-603-064-6

ignment Scores:

ed. No.:	2.43e-19	Length:	1287
ore:	29.00	Matches:	29
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
:	8	Gaps:	0

-10-821-670A-33 (1-222) x US-10-603-064-6 (1-1287)

184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
1168 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1227

204 AlaPheArgIleArgAlaValThrIle 212

Db 1228 GCTTTCAGAATTCGGGCAGTGACTATT 1254

RESULT 99
US-10-476-960-3
; Sequence 3, Application US/10476960
; Publication No. US20040248828A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
; FILE REFERENCE: RTSP-0392
; CURRENT APPLICATION NUMBER: US/10/476,960
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 09/851,520
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 1316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (102)...(863)
US-10-476-960-3

Alignment Scores:

Pred. No.:	2.48e-19	Length:	1316
Score:	29.00	Matches:	29
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	13.1%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-476-960-3 (1-1316)

Qy 184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
Db 744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

Qy 204 AlaPheArgIleArgAlaValThrIle 212
Db 804 GCTTTCAGAATTCGGGCAGTGACTATT 830

RESULT 100
US-11-089-191-3
; Sequence 3, Application US/11089191
; Publication No. US20050261228A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Susan Gregory
; APPLICANT: Ronnie C. Hanecak
; APPLICANT: Kevin P. Anderson
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Vickie Brown-Driver
; APPLICANT: David J. Ecker
; APPLICANT: Timothy Vickers
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Eric G. Marcusson
; APPLICANT: Nicholas M. Dean
; APPLICANT: Sanjay Bhanot
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
; FILE REFERENCE: BNDL-0021US.P1
; CURRENT APPLICATION NUMBER: US/11/089,191
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/476,960
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: PCT/US02/13871
; PRIOR FILING DATE: 2002-05-01

PRIOR APPLICATION NUMBER: 09/851,520
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: 10/67,236
PRIOR FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: 10/038,335
PRIOR FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: 09/299,058
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 08/403,888
PRIOR FILING DATE: 1995-06-12
PRIOR APPLICATION NUMBER: PCT/US93/09297
PRIOR FILING DATE: 1993-09-29
PRIOR APPLICATION NUMBER: 07/954,185
PRIOR FILING DATE: 1992-09-29
PRIOR APPLICATION NUMBER: 10/515,546
PRIOR FILING DATE: 2004-11-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 1316
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (102)...(863)
-11-089-191-3

ignment Scores:

ed. No.:	2.48e-19	Length:	1316
ore:	29.00	Matches:	29
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	13.1%	Indels:	0
	15	Gaps:	0

-10-821-670A-33 (1-222) x US-11-089-191-3 (1-1316)

```
        184 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        744 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 803

        204 AlaPheArgIleArgAlaValThrIle 212
            |||||||||||||||||||||||||
        804 GCTTTCAGAATTCGGGCAGTGACTATT 830
```

arch completed: June 12, 2006, 17:15:28
time : 1080.1 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 02:09:37 ; Search time 15.1299 Seconds
(without alignments)
2793.504 Million cell updates/sec

tle: US-10-821-670A-33
:fect score: 222
quence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 253354 seqs, 63461778 residues

:d size: 1

tal number of hits satisfying chosen parameters: 506227

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110508_27905/app_query.fasta_1
B=Published_Applications_NA_New -QFMT=fastap
UFFIX=oligo.p2n.200scores.rnpbn -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
NITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
OCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
ORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
SER=US10821670_@CGN_1_1_62_@runat_07062006_110508_27905 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	9	4.1	2984	7	US-11-293-697-34	Sequence 34, Appl
2	8	3.6	528	6	US-10-322-836-19	Sequence 19, Appl
3	8	3.6	879	6	US-10-322-836-17	Sequence 17, Appl
4	8	3.6	1017	6	US-10-322-836-15	Sequence 15, Appl
5	8	3.6	1248	6	US-10-322-836-27	Sequence 27, Appl
6	8	3.6	1254	6	US-10-471-571A-1475	Sequence 1475, Ap
7	8	3.6	1293	6	US-10-322-836-5	Sequence 5, Appli
8	8	3.6	1317	6	US-10-322-836-41	Sequence 41, Appl
9	8	3.6	1455	6	US-10-322-836-39	Sequence 39, Appl
10	8	3.6	1599	6	US-10-322-836-25	Sequence 25, Appl
11	8	3.6	1644	6	US-10-322-836-3	Sequence 3, Appli
12	8	3.6	1737	6	US-10-322-836-23	Sequence 23, Appl
13	8	3.6	1782	6	US-10-322-836-1	Sequence 1, Appli
14	8	3.6	2021	6	US-10-953-349-4560	Sequence 4560, Ap
15	8	3.6	2037	6	US-10-322-836-45	Sequence 45, Appl
16	8	3.6	2082	6	US-10-322-836-33	Sequence 33, Appl
17	8	3.6	2175	6	US-10-322-836-43	Sequence 43, Appl
18	8	3.6	2220	6	US-10-322-836-31	Sequence 31, Appl
19	8	3.6	3791	6	US-10-530-792A-1	Sequence 1, Appli
20	8	3.6	6663	7	US-11-217-529-3234	Sequence 3234, Ap
21	7	3.2	331	6	US-10-488-619-837	Sequence 837, App
c 22	7	3.2	399	6	US-10-148-883-27	Sequence 27, Appl
c 23	7	3.2	582	6	US-10-953-349-25251	Sequence 25251, A
24	7	3.2	660	7	US-11-217-529-81369	Sequence 81369, A
c 25	7	3.2	704	6	US-10-488-619-2648	Sequence 2648, Ap
26	7	3.2	759	6	US-10-471-571A-717	Sequence 717, App
27	7	3.2	894	7	US-11-217-529-1263	Sequence 1263, Ap
28	7	3.2	903	7	US-11-264-737-102	Sequence 102, App
29	7	3.2	906	6	US-10-953-349-4834	Sequence 4834, Ap
30	7	3.2	912	7	US-11-217-529-4191	Sequence 4191, Ap
31	7	3.2	915	6	US-10-953-349-36136	Sequence 36136, A
32	7	3.2	921	7	US-11-217-529-5460	Sequence 5460, Ap
33	7	3.2	932	6	US-10-953-349-38906	Sequence 38906, A
34	7	3.2	953	7	US-11-311-754-5	Sequence 5, Appli
c 35	7	3.2	955	6	US-10-488-619-3026	Sequence 3026, Ap
36	7	3.2	979	6	US-10-953-349-12779	Sequence 12779, A
c 37	7	3.2	994	6	US-10-953-349-28356	Sequence 28356, A
c 38	7	3.2	997	6	US-10-560-723-79	Sequence 79, Appl
39	7	3.2	1056	6	US-10-953-349-26293	Sequence 26293, A
40	7	3.2	1062	6	US-10-953-349-39566	Sequence 39566, A
41	7	3.2	1131	7	US-11-217-529-76797	Sequence 76797, A
42	7	3.2	1133	6	US-10-953-349-26634	Sequence 26634, A
43	7	3.2	1193	6	US-10-953-349-16752	Sequence 16752, A
c 44	7	3.2	1202	6	US-10-953-349-17414	Sequence 17414, A
c 45	7	3.2	1236	7	US-11-217-529-1292	Sequence 1292, Ap
c 46	7	3.2	1257	7	US-11-217-529-80501	Sequence 80501, A
c 47	7	3.2	1313	6	US-10-953-349-24555	Sequence 24555, A
c 48	7	3.2	1454	6	US-10-953-349-35965	Sequence 35965, A
49	7	3.2	1481	6	US-10-953-349-32584	Sequence 32584, A
50	7	3.2	1483	6	US-10-953-349-36433	Sequence 36433, A
51	7	3.2	1495	7	US-11-264-784-73	Sequence 73, Appl
52	7	3.2	1495	7	US-11-264-737-114	Sequence 114, App
53	7	3.2	1495	7	US-11-265-761-86	Sequence 86, Appl
54	7	3.2	1504	6	US-10-953-349-33213	Sequence 33213, A
c 55	7	3.2	1538	6	US-10-953-349-17700	Sequence 17700, A
c 56	7	3.2	1575	6	US-10-953-349-21291	Sequence 21291, A
c 57	7	3.2	1660	6	US-10-953-349-24275	Sequence 24275, A
58	7	3.2	1674	7	US-11-217-529-78924	Sequence 78924, A
59	7	3.2	1699	6	US-10-953-349-16452	Sequence 16452, A
60	7	3.2	1703	6	US-10-953-349-6606	Sequence 6606, Ap
c 61	7	3.2	1716	7	US-11-313-556-3	Sequence 3, Appli
62	7	3.2	1750	6	US-10-953-349-34792	Sequence 34792, A
c 63	7	3.2	1761	7	US-11-217-529-174380	Sequence 174380,
c 64	7	3.2	1804	7	US-11-251-465-7	Sequence 7, Appli
65	7	3.2	1831	7	US-11-311-754-27	Sequence 27, Appl
66	7	3.2	1868	6	US-10-505-928-693	Sequence 693, App
c 67	7	3.2	1914	6	US-10-953-349-11252	Sequence 11252, A
68	7	3.2	1933	7	US-11-293-697-275	Sequence 275, App
69	7	3.2	1977	6	US-10-953-349-1534	Sequence 1534, Ap
c 70	7	3.2	2036	7	US-11-293-697-1094	Sequence 1094, Ap
c 71	7	3.2	2037	7	US-11-217-529-77609	Sequence 77609, A
72	7	3.2	2126	7	US-11-293-697-1972	Sequence 1972, Ap
73	7	3.2	2152	7	US-11-293-697-374	Sequence 374, App
74	7	3.2	2241	7	US-11-217-529-2489	Sequence 2489, Ap
75	7	3.2	2275	7	US-11-293-697-507	Sequence 507, App
c 76	7	3.2	2315	6	US-10-511-937-649	Sequence 649, App
77	7	3.2	2558	7	US-11-293-697-1101	Sequence 1101, Ap
78	7	3.2	2651	6	US-10-196-749-135	Sequence 135, App
79	7	3.2	2651	7	US-11-101-316-23	Sequence 23, Appl
80	7	3.2	2662	7	US-11-293-697-753	Sequence 753, App
81	7	3.2	2688	7	US-11-293-697-2253	Sequence 2253, Ap
c 82	7	3.2	2692	6	US-10-511-937-551	Sequence 551, App

83	7	3.2	2792	7	US-11-293-697-1902	Sequence 1902, Ap
84	7	3.2	2805	7	US-11-217-529-82539	Sequence 82539, A
85	7	3.2	2905	7	US-11-293-697-74	Sequence 74, Appl
86	7	3.2	3138	7	US-11-312-958-55	Sequence 55, Appl
87	7	3.2	3294	7	US-11-293-697-1397	Sequence 1397, Ap
88	7	3.2	3558	6	US-10-505-928-814	Sequence 814, App
89	7	3.2	4295	7	US-11-293-697-799	Sequence 799, App
90	7	3.2	7422	7	US-11-217-529-1506	Sequence 1506, Ap
91	7	3.2	7758	6	US-10-505-928-236	Sequence 236, App
92	7	3.2	10660	7	US-11-264-737-165	Sequence 165, App
93	6	2.7	18	7	US-11-293-697-5328	Sequence 5328, Ap
94	6	2.7	22	7	US-11-266-409-9	Sequence 9, Appli
95	6	2.7	25	7	US-11-217-529-36402	Sequence 36402, A
96	6	2.7	25	7	US-11-217-529-43879	Sequence 43879, A
97	6	2.7	25	7	US-11-217-529-47657	Sequence 47657, A
98	6	2.7	25	7	US-11-217-529-53284	Sequence 53284, A
99	6	2.7	25	7	US-11-217-529-84821	Sequence 84821, A
100	6	2.7	25	7	US-11-217-529-87245	Sequence 87245, A
101	6	2.7	25	7	US-11-217-529-88955	Sequence 88955, A
102	6	2.7	25	7	US-11-217-529-99892	Sequence 99892, A
103	6	2.7	25	7	US-11-217-529-99912	Sequence 99912, A
104	6	2.7	25	7	US-11-217-529-109690	Sequence 109690,
105	6	2.7	25	7	US-11-217-529-117218	Sequence 117218,
106	6	2.7	25	7	US-11-217-529-118788	Sequence 118788,
107	6	2.7	25	7	US-11-217-529-122537	Sequence 122537,
108	6	2.7	25	7	US-11-217-529-122772	Sequence 122772,
109	6	2.7	25	7	US-11-217-529-148883	Sequence 148883,
110	6	2.7	25	7	US-11-217-529-157319	Sequence 157319,
111	6	2.7	25	7	US-11-217-529-162336	Sequence 162336,
112	6	2.7	25	7	US-11-217-529-162342	Sequence 162342,
113	6	2.7	25	7	US-11-217-529-184372	Sequence 184372,
114	6	2.7	44	7	US-11-333-672-16	Sequence 16, Appl
115	6	2.7	50	6	US-10-511-937-285	Sequence 285, App
116	6	2.7	51	6	US-10-511-937-2729	Sequence 2729, Ap
117	6	2.7	51	7	US-11-143-642-246	Sequence 246, App
118	6	2.7	51	7	US-11-245-248-1157	Sequence 1157, Ap
119	6	2.7	69	7	US-11-296-092-22	Sequence 22, Appl
120	6	2.7	84	6	US-10-525-817-154	Sequence 154, App
121	6	2.7	84	6	US-10-525-817-155	Sequence 155, App
122	6	2.7	84	6	US-10-525-817-156	Sequence 156, App
123	6	2.7	84	6	US-10-525-817-157	Sequence 157, App
124	6	2.7	93	7	US-11-217-529-6033	Sequence 6033, Ap
125	6	2.7	114	6	US-10-471-571A-5635	Sequence 5635, Ap
126	6	2.7	162	7	US-11-217-529-81244	Sequence 81244, A
127	6	2.7	182	6	US-10-473-173-401	Sequence 401, App
128	6	2.7	205	6	US-10-148-883-21	Sequence 21, Appl
129	6	2.7	213	6	US-10-471-571A-4689	Sequence 4689, Ap
130	6	2.7	231	7	US-11-217-529-174474	Sequence 174474,
131	6	2.7	260	6	US-10-511-937-2898	Sequence 2898, Ap
132	6	2.7	273	7	US-11-217-529-3952	Sequence 3952, Ap
133	6	2.7	276	7	US-11-217-529-166542	Sequence 166542,
134	6	2.7	303	7	US-11-217-529-5007	Sequence 5007, Ap
135	6	2.7	303	7	US-11-217-529-5166	Sequence 5166, Ap
136	6	2.7	303	7	US-11-217-529-80985	Sequence 80985, A
137	6	2.7	303	7	US-11-217-529-81183	Sequence 81183, A
138	6	2.7	303	7	US-11-217-529-174171	Sequence 174171,
139	6	2.7	310	7	US-11-301-554-610	Sequence 610, App
140	6	2.7	327	7	US-11-217-529-4461	Sequence 4461, Ap
141	6	2.7	330	7	US-11-217-529-75521	Sequence 75521, A
142	6	2.7	336	7	US-11-217-529-78565	Sequence 78565, A
143	6	2.7	336	7	US-11-254-679-18	Sequence 18, Appl
144	6	2.7	345	6	US-10-511-937-623	Sequence 623, App
145	6	2.7	351	7	US-11-254-679-20	Sequence 20, Appl
146	6	2.7	362	7	US-11-301-554-1167	Sequence 1167, Ap
147	6	2.7	369	6	US-10-499-266-11	Sequence 11, Appl
148	6	2.7	375	6	US-10-473-173-423	Sequence 423, App
149	6	2.7	389	6	US-10-953-349-18005	Sequence 18005, A
150	6	2.7	389	7	US-11-301-554-417	Sequence 417, App
151	6	2.7	389	7	US-11-301-554-900	Sequence 900, App
152	6	2.7	390	6	US-10-488-619-2081	Sequence 2081, Ap
153	6	2.7	398	7	US-11-242-317-27	Sequence 27, Appl
154	6	2.7	400	6	US-10-488-619-2364	Sequence 2364, Ap
155	6	2.7	416	6	US-10-488-619-91	Sequence 91, Appl
c 156	6	2.7	421	6	US-10-488-619-316	Sequence 316, App
157	6	2.7	422	6	US-10-511-937-617	Sequence 617, App
158	6	2.7	423	7	US-11-301-554-573	Sequence 573, App
c 159	6	2.7	426	7	US-11-301-554-913	Sequence 913, App
c 160	6	2.7	437	6	US-10-560-723-109	Sequence 109, App
161	6	2.7	438	6	US-10-488-619-826	Sequence 826, App
162	6	2.7	438	6	US-10-488-619-2365	Sequence 2365, Ap
163	6	2.7	443	6	US-10-953-349-13876	Sequence 13876, A
164	6	2.7	447	7	US-11-217-529-77000	Sequence 77000, A
c 165	6	2.7	455	6	US-10-488-619-107	Sequence 107, App
166	6	2.7	463	6	US-10-488-619-2614	Sequence 2614, Ap
167	6	2.7	470	6	US-10-488-619-338	Sequence 338, App
168	6	2.7	474	6	US-10-473-173-278	Sequence 278, App
c 169	6	2.7	474	7	US-11-217-529-3714	Sequence 3714, Ap
c 170	6	2.7	477	6	US-10-148-883-20	Sequence 20, Appl
171	6	2.7	480	7	US-11-301-554-1170	Sequence 1170, Ap
c 172	6	2.7	480	7	US-11-297-957-5	Sequence 5, Appli
173	6	2.7	500	7	US-11-136-524-87	Sequence 87, Appl
c 174	6	2.7	504	7	US-11-217-529-173856	Sequence 173856,
c 175	6	2.7	508	7	US-11-296-092-18	Sequence 18, Appl
c 176	6	2.7	508	7	US-11-296-092-19	Sequence 19, Appl
177	6	2.7	511	6	US-10-511-937-2900	Sequence 2900, Ap
178	6	2.7	511	6	US-10-953-349-38082	Sequence 38082, A
179	6	2.7	517	6	US-10-473-173-459	Sequence 459, App
c 180	6	2.7	517	6	US-10-473-173-459	Sequence 459, App
181	6	2.7	520	6	US-10-953-349-29838	Sequence 29838, A
c 182	6	2.7	522	6	US-10-488-619-1461	Sequence 1461, Ap
183	6	2.7	526	7	US-11-301-554-1473	Sequence 1473, Ap
184	6	2.7	529	6	US-10-953-349-30756	Sequence 30756, A
c 185	6	2.7	534	7	US-11-217-529-78894	Sequence 78894, A
c 186	6	2.7	536	6	US-10-953-349-10529	Sequence 10529, A
187	6	2.7	536	6	US-10-953-349-13039	Sequence 13039, A
188	6	2.7	540	6	US-10-471-571A-5055	Sequence 5055, Ap
c 189	6	2.7	540	7	US-11-301-554-14	Sequence 14, Appl
c 190	6	2.7	540	7	US-11-217-529-76012	Sequence 76012, A
c 191	6	2.7	552	7	US-11-217-529-4706	Sequence 4706, Ap
c 192	6	2.7	557	6	US-10-953-349-5665	Sequence 5665, Ap
c 193	6	2.7	558	7	US-11-217-529-82089	Sequence 82089, A
194	6	2.7	561	7	US-11-301-554-72	Sequence 72, Appl
c 195	6	2.7	564	7	US-11-301-554-729	Sequence 729, App
c 196	6	2.7	564	7	US-11-217-529-174198	Sequence 174198,
c 197	6	2.7	565	6	US-10-953-349-9446	Sequence 9446, Ap
c 198	6	2.7	571	6	US-10-488-619-1362	Sequence 1362, Ap
c 199	6	2.7	579	6	US-10-560-723-169	Sequence 169, App
c 200	6	2.7	588	7	US-11-217-529-4641	Sequence 4641, Ap

ALIGNMENTS

```
RESULT 1
US-11-293-697-34/c
; Sequence 34, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 2984
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-34

Alignment Scores:
Pred. No.:              7.54          Length:          2984
Score:                  9.00          Matches:         9
Percent Similarity:     100.0%        Conservative:    0
```

```
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            4.1%            Indels:        0
:                     7               Gaps:          0

-10-821-670A-33 (1-222) x US-11-293-697-34 (1-2984)

        29 ProThrProThrProSerProGlyMet 37
           |||||||||||||||||||||||||||
      1505 CCGACACCAACTCCAAGTCCAGGGATG 1479

SULT 2
-10-322-836-19
Sequence 19, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
 APPLICANT: Turner, Alexander C., Jr.
 APPLICANT:  Zambrowicz, Brian
 APPLICANT:  Nehls, Michael
 APPLICANT:  Freidrich, Glenn A.
 APPLICANT:  Sands, Arthur T.
 TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
 TITLE OF INVENTION:  ENCODED THEREBY
 FILE REFERENCE: 8535-0037-999
 CURRENT APPLICATION NUMBER: US/10/322,836
 CURRENT FILING DATE:  2002-12-18
 PRIOR APPLICATION NUMBER: US/09/579,114
 PRIOR FILING DATE: 2000-05-25
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
  LENGTH: 528
  TYPE: DNA
  ORGANISM: Homo sapien
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)...(525)
-10-322-836-19

ignment Scores:
ed. No.:              14.9            Length:        528
ore:                  8.00            Matches:       8
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            3.6%            Indels:        0
:                     6               Gaps:          0

-10-821-670A-33 (1-222) x US-10-322-836-19 (1-528)

        56 GlnLysAlaArgGlnThrLeuGlu 63
           |||||||||||||||||||||||
        61 CAAAAAGCCAGGCAGACCCTGGAG 84

SULT 3
-10-322-836-17
Sequence 17, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
 APPLICANT: Turner, Alexander C., Jr.
 APPLICANT:  Zambrowicz, Brian
 APPLICANT:  Nehls, Michael
 APPLICANT:  Freidrich, Glenn A.
 APPLICANT:  Sands, Arthur T.
 TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
 TITLE OF INVENTION:  ENCODED THEREBY
 FILE REFERENCE: 8535-0037-999
 CURRENT APPLICATION NUMBER: US/10/322,836
 CURRENT FILING DATE:  2002-12-18
 PRIOR APPLICATION NUMBER: US/09/579,114
 PRIOR FILING DATE: 2000-05-25
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
  LENGTH: 879
;  TYPE: DNA
;  ORGANISM: Homo sapien
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(876)
US-10-322-836-17

Alignment Scores:
Pred. No.:            24.1            Length:        879
Score:                8.00            Matches:       8
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          3.6%            Indels:        0
DB:                   6               Gaps:          0

US-10-821-670A-33 (1-222) x US-10-322-836-17 (1-879)

Qy         56 GlnLysAlaArgGlnThrLeuGlu 63
              |||||||||||||||||||||||
Db         61 CAAAAAGCCAGGCAGACCCTGGAG 84

RESULT 4
US-10-322-836-15
; Sequence 15, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 1017
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1014)
US-10-322-836-15

Alignment Scores:
Pred. No.:            27.7            Length:        1017
Score:                8.00            Matches:       8
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          3.6%            Indels:        0
DB:                   6               Gaps:          0

US-10-821-670A-33 (1-222) x US-10-322-836-15 (1-1017)

Qy         56 GlnLysAlaArgGlnThrLeuGlu 63
              |||||||||||||||||||||||
Db         61 CAAAAAGCCAGGCAGACCCTGGAG 84

RESULT 5
US-10-322-836-27
; Sequence 27, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
```

```
 TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
 TITLE OF INVENTION:  ENCODED THEREBY
 FILE REFERENCE: 8535-0037-999
 CURRENT APPLICATION NUMBER: US/10/322,836
 CURRENT FILING DATE:  2002-12-18
 PRIOR APPLICATION NUMBER: US/09/579,114
 PRIOR FILING DATE: 2000-05-25
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 3.0
EQ ID NO 27
  LENGTH: 1248
  TYPE: DNA
  ORGANISM: Homo sapien
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)...(1245)
-10-322-836-27

ignment Scores:
ed. No.:                33.7          Length:        1248
re:                     8.00          Matches:       8
cent Similarity:        100.0%        Conservative:  0
t Local Similarity:     100.0%        Mismatches:    0
ry Match:               3.6%          Indels:        0
                        6             Gaps:          0

 10-821-670A-33 (1-222) x US-10-322-836-27 (1-1248)

         56 GlnLysAlaArgGlnThrLeuGlu 63
            ||||||||||||||||||||||||
        781 CAAAAAGCCAGGCAGACCCTGGAG 804

SULT 6
 10-471-571A-1475/c
equence 1475, Application US/10471571A
ublication No. US20060115490A1
ENERAL INFORMATION:
 APPLICANT: CHIRON SpA
 TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
 FILE REFERENCE: P026927WO
 CURRENT APPLICATION NUMBER: US/10/471,571A
 CURRENT FILING DATE:  2003-09-12
 PRIOR APPLICATION NUMBER: GB-0107661.1
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 5642
 SOFTWARE: SeqWin99, version 1.03
EQ ID NO 1475
  LENGTH: 1254
  TYPE: DNA
  ORGANISM: Staphylococcus aureus
-10-471-571A-1475

ignment Scores:
ed. No.:                33.8          Length:        1254
re:                     8.00          Matches:       8
cent Similarity:        100.0%        Conservative:  0
t Local Similarity:     100.0%        Mismatches:    0
ry Match:               3.6%          Indels:        0
                        6             Gaps:          0

 10-821-670A-33 (1-222) x US-10-471-571A-1475 (1-1254)

         12 IleLeuValLeuLeuAsnHisLeu 19
            |||||||||||||||||||||||
       1225 ATACTAGTTCTTTTGAACCATCTT 1202

ULT 7
 10-322-836-5
equence 5, Application US/10322836
ublication No. US20060090212A1
ENERAL INFORMATION:
 APPLICANT: Turner, Alexander C., Jr.
 APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;    LENGTH: 1293
;    TYPE: DNA
;    ORGANISM: Homo sapien
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)...(1290)
US-10-322-836-5

Alignment Scores:
Pred. No.:                34.8          Length:        1293
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              3.6%          Indels:        0
DB:                       6             Gaps:          0

US-10-821-670A-33 (1-222) x US-10-322-836-5 (1-1293)

Qy          56 GlnLysAlaArgGlnThrLeuGlu 63
               ||||||||||||||||||||||||
Db         826 CAAAAAGCCAGGCAGACCCTGGAG 849

RESULT 8
US-10-322-836-41
; Sequence 41, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, Alexander C., Jr.
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Freidrich, Glenn A.
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
;  TITLE OF INVENTION:  ENCODED THEREBY
;  FILE REFERENCE: 8535-0037-999
;  CURRENT APPLICATION NUMBER: US/10/322,836
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: US/09/579,114
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41
;    LENGTH: 1317
;    TYPE: DNA
;    ORGANISM: Homo sapien
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)...(1314)
US-10-322-836-41

Alignment Scores:
Pred. No.:                35.4          Length:        1317
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              3.6%          Indels:        0
DB:                       6             Gaps:          0

US-10-821-670A-33 (1-222) x US-10-322-836-41 (1-1317)
```

```
        56 GlnLysAlaArgGlnThrLeuGlu 63
           ||||||||||||||||||||||||
        61 CAAAAAGCCAGGCAGACCCTGGAG 84
```

SULT 9
-10-322-836-39
Sequence 39, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 1455
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1452)
-10-322-836-39

ignment Scores:			
ed. No.:	38.9	Length:	1455
ore:	8.00	Matches:	8
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
:	6	Gaps:	0

-10-821-670A-33 (1-222) x US-10-322-836-39 (1-1455)

```
        56 GlnLysAlaArgGlnThrLeuGlu 63
           ||||||||||||||||||||||||
        61 CAAAAAGCCAGGCAGACCCTGGAG 84
```

SULT 10
-10-322-836-25
Sequence 25, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 1599
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1596)
-10-322-836-25

Alignment Scores:			
Pred. No.:	42.6	Length:	1599
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-322-836-25 (1-1599)

```
Qy         56 GlnLysAlaArgGlnThrLeuGlu 63
              ||||||||||||||||||||||||
Db        781 CAAAAAGCCAGGCAGACCCTGGAG 804
```

RESULT 11
US-10-322-836-3
; Sequence 3, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1644
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1641)
US-10-322-836-3

Alignment Scores:			
Pred. No.:	43.7	Length:	1644
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-322-836-3 (1-1644)

```
Qy         56 GlnLysAlaArgGlnThrLeuGlu 63
              ||||||||||||||||||||||||
Db        826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

RESULT 12
US-10-322-836-23
; Sequence 23, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114

PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 1737
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1734)
-10-322-836-23

ignment Scores:

ed. No.:	46.1	Length:	1737
ore:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
	6	Gaps:	0

-10-821-670A-33 (1-222) x US-10-322-836-23 (1-1737)

```
        56 GlnLysAlaArgGlnThrLeuGlu 63
           ||||||||||||||||||||||||
       781 CAAAAAGCCAGGCAGACCCTGGAG 804
```

SULT 13
-10-322-836-1
equence 1, Application US/10322836
ublication No. US20060090212A1
ENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1782
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1779)
-10-322-836-1

ignment Scores:

ed. No.:	47.2	Length:	1782
ore:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
	6	Gaps:	0

10-821-670A-33 (1-222) x US-10-322-836-1 (1-1782)

```
        56 GlnLysAlaArgGlnThrLeuGlu 63
           ||||||||||||||||||||||||
       826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

SULT 14
10-953-349-4560
equence 4560, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4560
; LENGTH: 2021
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4560

Alignment Scores:

Pred. No.:	53.2	Length:	2021
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-4560 (1-2021)

```
Qy        124 ThrLeuCysLeuSerSerIleTyr 131
              |||||||||||||||||||||||
Db       1004 ACCTTGTGTTTGTCTTCTATCTAT 1027
```

RESULT 15
US-10-322-836-45
; Sequence 45, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2034)
US-10-322-836-45

Alignment Scores:

Pred. No.:	53.6	Length:	2037
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-322-836-45 (1-2037)

```
Qy         56 GlnLysAlaArgGlnThrLeuGlu 63
              ||||||||||||||||||||||||
Db        781 CAAAAAGCCAGGCAGACCCTGGAG 804
```

RESULT 16
US-10-322-836-33
; Sequence 33, Application US/10322836

Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 2082
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2079)
-10-322-836-33

gnment Scores:

ed. No.:	54.7	Length:	2082
ore:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
	6	Gaps:	0

-10-821-670A-33 (1-222) x US-10-322-836-33 (1-2082)

```
         56 GlnLysAlaArgGlnThrLeuGlu 63
            |||||||||||||||||||||||
        826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

SULT 17
-10-322-836-43
Sequence 43, Application US/10322836
Publication No. US20060090212A1
GENERAL INFORMATION:
APPLICANT: Turner, Alexander C., Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Nehls, Michael
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 2175
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2172)
-10-322-836-43

gnment Scores:

ed. No.:	57	Length:	2175
ore:	8.00	Matches:	8
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-322-836-43 (1-2175)

```
Qy         56 GlnLysAlaArgGlnThrLeuGlu 63
              |||||||||||||||||||||||
Db        781 CAAAAAGCCAGGCAGACCCTGGAG 804
```

RESULT 18
US-10-322-836-31
; Sequence 31, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2217)
US-10-322-836-31

Alignment Scores:

Pred. No.:	58.1	Length:	2220
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-322-836-31 (1-2220)

```
Qy         56 GlnLysAlaArgGlnThrLeuGlu 63
              |||||||||||||||||||||||
Db        826 CAAAAAGCCAGGCAGACCCTGGAG 849
```

RESULT 19
US-10-530-792A-1
; Sequence 1, Application US/10530792A
; Publication No. US20060105340A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-008
; CURRENT APPLICATION NUMBER: US/10/530,792A
; CURRENT FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-530-792A-1

```
Alignment Scores:
Pred. No.:                96.6          Length:         3791
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              3.6%          Indels:         0
DB:                       6             Gaps:           0

US-10-821-670A-33 (1-222) x US-10-530-792A-1 (1-3791)

Qy        111 GlySerCysLeuAlaSerArgLys 118
              ||||||||||||||||||||||||
Db        231 GGGTCATGCCTGGCCAGCAGAAAG 254

RESULT 20
US-11-217-529-3234
; Sequence 3234, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT:  NAKAO, YOSHIHIRO
; APPLICANT:  NAKAMURA, NORIHISA
; APPLICANT:  KODAMA, YUKIKO
; APPLICANT:  FUJIMURA, TOMOKO
; APPLICANT:  ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE:  2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3234
;   LENGTH: 6663
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-3234

Alignment Scores:
Pred. No.:                165           Length:         6663
Score:                    8.00          Matches:        8
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              3.6%          Indels:         0
DB:                       7             Gaps:           0

US-10-821-670A-33 (1-222) x US-11-217-529-3234 (1-6663)

Qy        164 ThrAlaIleAspGluLeuLeuGln 171
              ||||||||||||||||||||||||
Db       1729 ACTGCCATTGATGAACTATTACAA 1752

RESULT 21
US-10-488-619-837
; Sequence 837, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE:  2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 837
;   LENGTH: 331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(331)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-837

Alignment Scores:
Pred. No.:                97.6          Length:         331
Score:                    7.00          Matches:        7
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              3.2%          Indels:         0
DB:                       6             Gaps:           0

US-10-821-670A-33 (1-222) x US-10-488-619-837 (1-331)

Qy        111 GlySerCysLeuAlaSerArg 117
              |||||||||||||||||||||
Db        108 GGCTCCTGCCTGGCCTCTAGG 128

RESULT 22
US-10-148-883-27/c
; Sequence 27, Application US/10148883
; Publication No. US20060115811A1
; GENERAL INFORMATION:
;  APPLICANT: Jay White et al.
;  TITLE OF INVENTION: Cytochrome P450RA1-2 and Related Proteins
;  FILE REFERENCE: 11812-49
;  CURRENT APPLICATION NUMBER: US/10/148,883
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US 60/171,110
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: US 60/178,314
;  PRIOR FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 399
;   TYPE: DNA
;   ORGANISM: Rattus rattus
US-10-148-883-27

Alignment Scores:
Pred. No.:                117           Length:         399
Score:                    7.00          Matches:        7
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              3.2%          Indels:         0
DB:                       6             Gaps:           0

US-10-821-670A-33 (1-222) x US-10-148-883-27 (1-399)

Qy         29 ProThrProThrProSerPro 35
              |||||||||||||||||||||
Db         42 CCGACACCAACTCCAAGCCCT 22

RESULT 23
US-10-953-349-25251/c
; Sequence 25251, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25251
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-25251
```

```
:gnment Scores:
ed. No.:                167             Length:         582
:re:                    7.00            Matches:        7
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              3.2%            Indels:         0
:                       6               Gaps:           0

-10-821-670A-33 (1-222) x US-10-953-349-25251 (1-582)

        164 ThrAlaIleAspGluLeuLeu 170
            ||||||||||||||||||||
         88 ACGGCCATAGATGAGTTGCTG 68

SULT 24
-11-217-529-81369
Sequence 81369, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 81369
  LENGTH: 660
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
-11-217-529-81369

:gnment Scores:
ed. No.:                188             Length:         660
:re:                    7.00            Matches:        7
:cent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              3.2%            Indels:         0
:                       7               Gaps:           0

-10-821-670A-33 (1-222) x US-11-217-529-81369 (1-660)

        131 TyrGluAspLeuLysMetTyr 137
            |||||||||||||||||||||
        124 TATGAAGACCTGAAGATGTAT 144

SULT 25
-10-488-619-2648/c
Sequence 2648, Application US/10488619
Publication No. US20060099578A1
GENERAL INFORMATION:
 APPLICANT: Greenlee, Winner and Sullivan, P.C.
 TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
 TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
 FILE REFERENCE: 98-01 WO
 CURRENT APPLICATION NUMBER: US/10/488,619
 CURRENT FILING DATE:  2004-03-01
 NUMBER OF SEQ ID NOS: 3040
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 2648
  LENGTH: 704
  TYPE: DNA
  ORGANISM: Mus musculus
-10-488-619-2648

:gnment Scores:
Pred. No.:              200             Length:         704
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.2%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-488-619-2648 (1-704)

Qy        169 LeuLeuGlnAlaLeuAsnVal 175
              |||||||||||||||||||
Db        154 CTTCTCCAAGCTCTGAATGTC 134

RESULT 26
US-10-471-571A-717
; Sequence 717, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 717
;   LENGTH: 759
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-717

Alignment Scores:
Pred. No.:              214             Length:         759
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.2%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-471-571A-717 (1-759)

Qy          7 LeuLeuLeuValThrIleLeu 13
              |||||||||||||||||||||
Db        409 TTGTTATTGGTGACAATATTG 429

RESULT 27
US-11-217-529-1263
; Sequence 1263, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1263
;   LENGTH: 894
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1263

Alignment Scores:
```

```
ed. No.:              250          Length:        894
re:                   7.00         Matches:       7
cent Similarity:      100.0%       Conservative:  0
t Local Similarity:   100.0%       Mismatches:    0
ry Match:             3.2%         Indels:        0
                      7            Gaps:          0

10-821-670A-33 (1-222) x US-11-217-529-1263 (1-894)

        29 ProThrProThrProSerPro 35
           ||||||||||||||||||||
       766 CCAACTCCAACTCCGTCGCCA 786

SULT 28
11-264-737-102
Sequence 102, Application US/11264737
Publication No. US20060110806A1
GENERAL INFORMATION:
 APPLICANT: E.I. duPont de Nemours & Co., Inc.
 APPLICANT:  Damude, Howard Glenn
 APPLICANT:  Gillies, Peter J.
 APPLICANT:  Macool, Daniel Joseph
 APPLICANT:  Pictaggio, Stephen K.
 APPLICANT:  Ragghianti, James John
 APPLICANT:  Seip, John E.
 APPLICANT:  Xue, Zhixiong
 APPLICANT:  Yadav, Narendra S.
 APPLICANT:  Zhang, Hongxiang
 APPLICANT:  Zhu, Quinn Qun
 TITLE OF INVENTION: DOCOSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
 FILE REFERENCE: CL3160 US NA
 CURRENT APPLICATION NUMBER: US/11/264,737
 CURRENT FILING DATE:  2005-11-01
 NUMBER OF SEQ ID NOS: 467
 SOFTWARE: PatentIn version 3.3
EQ ID NO 102
  LENGTH: 903
  TYPE: DNA
  ORGANISM: Ostreococcus tauri
  FEATURE:
  NAME/KEY: misc_feature
  OTHER INFORMATION: synthetic C20/22 fatty acid elongase (codon-optimized)
 11-264-737-102

lgnment Scores:
ed. No.:              253          Length:        903
re:                   7.00         Matches:       7
cent Similarity:      100.0%       Conservative:  0
t Local Similarity:   100.0%       Mismatches:    0
ry Match:             3.2%         Indels:        0
                      7            Gaps:          0

10-821-670A-33 (1-222) x US-11-264-737-102 (1-903)

        28 LeuProThrProThrProSer 34
           ||||||||||||||||||||
        56 CTACCTACGCCTACGCCTTCG 76

SULT 29
10-953-349-4834
Sequence 4834, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
EQ ID NO 4834
  LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-4834

Alignment Scores:
Pred. No.:            254          Length:        906
Score:                7.00         Matches:       7
Percent Similarity:   100.0%       Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:          3.2%         Indels:        0
DB:                   6            Gaps:          0

US-10-821-670A-33 (1-222) x US-10-953-349-4834 (1-906)

Qy        100 LeuAlaSerArgGluIleSer 106
              |||||||||||||||||||
Db        681 TTGGCTAGCAGAGAAATCAGT 701

RESULT 30
US-11-217-529-4191
; Sequence 4191, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4191
;   LENGTH: 912
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4191

Alignment Scores:
Pred. No.:            255          Length:        912
Score:                7.00         Matches:       7
Percent Similarity:   100.0%       Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:          3.2%         Indels:        0
DB:                   7            Gaps:          0

US-10-821-670A-33 (1-222) x US-11-217-529-4191 (1-912)

Qy         11 ThrIleLeuValLeuLeuAsn 17
              ||||||||||||||||||||
Db         22 ACTATATTAGTCTTGTTGAAC 42

RESULT 31
US-10-953-349-36136
; Sequence 36136, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36136
;   LENGTH: 915
;   TYPE: DNA
```

ORGANISM: Zea mays subsp. mays
-10-953-349-36136

ignment Scores:
ed. No.: 256 Length: 915
ore: 7.00 Matches: 7
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 3.2% Indels: 0
: 6 Gaps: 0

-10-821-670A-33 (1-222) x US-10-953-349-36136 (1-915)

4 ProArgGlyLeuLeuLeuVal 10
||||||||||||||||||||
181 CCGCGCGGACTCCTCCTCGTC 201

SULT 32
-11-217-529-5460
Sequence 5460, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5460
LENGTH: 921
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-5460

ignment Scores:
ed. No.: 258 Length: 921
ore: 7.00 Matches: 7
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 3.2% Indels: 0
: 7 Gaps: 0

-10-821-670A-33 (1-222) x US-11-217-529-5460 (1-921)

205 PheArgIleArgAlaValThr 211
||||||||||||||||||||
867 TTTCGAATTCGAGCGGTTACC 887

SULT 33
-10-953-349-38906
Sequence 38906, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38906
LENGTH: 932
TYPE: DNA
ORGANISM: Zea mays subsp. mays
US-10-953-349-38906

Alignment Scores:
Pred. No.: 261 Length: 932
Score: 7.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 3.2% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-33 (1-222) x US-10-953-349-38906 (1-932)

Qy 4 ProArgGlyLeuLeuLeuVal 10
||||||||||||||||||||
Db 192 CCGCGCGGACTCCTCCTCGTC 212

RESULT 34
US-11-311-754-5
; Sequence 5, Application US/11311754
; Publication No. US20060099635A1
; GENERAL INFORMATION:
; APPLICANT: Vincent Ling
; APPLICANT: Kyriaki Dunussi-Joannopoulos
; TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
; FILE REFERENCE: GNN-007
; CURRENT APPLICATION NUMBER: US/11/311,754
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: US/09/667,135
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (24)..(950)
US-11-311-754-5

Alignment Scores:
Pred. No.: 266 Length: 953
Score: 7.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 3.2% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-33 (1-222) x US-11-311-754-5 (1-953)

Qy 181 ProGlnAsnSerSerLeuGlu 187
||||||||||||||||||||
Db 225 CCACAGAACAGCTCCTTGGAA 245

RESULT 35
US-10-488-619-3026/c
; Sequence 3026, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3026
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-3026

```
gnment Scores:
d. No.:                 267             Length:         955
re:                     7.00            Matches:        7
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.2%            Indels:         0
                        6               Gaps:           0

10-821-670A-33 (1-222) x US-10-488-619-3026 (1-955)

        24 LeuAlaArgAsnLeuProThr 30
           ||||||||||||||||||||
       243 CTGGCACGAAATTTACCAACC 223

ULT 36
10-953-349-12779
equence 12779, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION:  ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE:  2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 12779
 LENGTH: 979
 TYPE: DNA
 ORGANISM: Glycine max
10-953-349-12779

gnment Scores:
d. No.:                 273             Length:         979
re:                     7.00            Matches:        7
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.2%            Indels:         0
                        6               Gaps:           0

10-821-670A-33 (1-222) x US-10-953-349-12779 (1-979)

        30 ThrProThrProSerProGly 36
           ||||||||||||||||||||
       412 ACACCAACACCGTCGCCGGGG 432

ULT 37
10-953-349-28356/c
equence 28356, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION:  ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE:  2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 28356
 LENGTH: 994
 TYPE: DNA
 ORGANISM: Triticum aestivum
10-953-349-28356

gnment Scores:
d. No.:                 277             Length:         994
re:                     7.00            Matches:        7
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.2%            Indels:         0
                        6               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-953-349-28356 (1-994)

Qy          117 ArgLysThrSerPheMetThr 123
                ||||||||||||||||||||
Db          340 AGGAAGACCAGCTTCATGACG 320

RESULT 38
US-10-560-723-79/c
; Sequence 79, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
;  APPLICANT: EXONHIT THERAPEUTICALS
;  TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
;  TITLE OF INVENTION:  CANCER THERAPY AND DIAGNOSIS
;  FILE REFERENCE: B0213WO
;  CURRENT APPLICATION NUMBER: US/10/560,723
;  CURRENT FILING DATE:  2005-12-15
;  NUMBER OF SEQ ID NOS: 185
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
;   LENGTH: 997
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-560-723-79

Alignment Scores:
Pred. No.:              278             Length:         997
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.2%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-560-723-79 (1-997)

Qy          111 GlySerCysLeuAlaSerArg 117
                ||||||||||||||||||||
Db          839 GGCTCCTGCCTGGCCTCTAGG 819

RESULT 39
US-10-953-349-26293
; Sequence 26293, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26293
;   LENGTH: 1056
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-26293

Alignment Scores:
Pred. No.:              293             Length:         1056
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.2%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-953-349-26293 (1-1056)

Qy           29 ProThrProThrProSerPro 35
                ||||||||||||||||||||
Db          432 CCGACTCCGACTCCGTCACCT 452
```

SULT 40
-10-953-349-39566
Sequence 39566, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 39566
LENGTH: 1062
TYPE: DNA
ORGANISM: Zea mays subsp. mays
-10-953-349-39566

ignment Scores:

ed. No.:	295	Length:	1062
ore:	7.00	Matches:	7
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.2%	Indels:	0
:	6	Gaps:	0

-10-821-670A-33 (1-222) x US-10-953-349-39566 (1-1062)

```
       123 ThrThrLeuCysLeuSerSer 129
           ||||||||||||||||||||
       188 ACTACGTTGTGTCTGAGTTCA 208
```

SULT 41
-11-217-529-76797
Sequence 76797, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 76797
LENGTH: 1131
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-76797

ignment Scores:

ed. No.:	313	Length:	1131
ore:	7.00	Matches:	7
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.2%	Indels:	0
:	7	Gaps:	0

-10-821-670A-33 (1-222) x US-11-217-529-76797 (1-1131)

```
        11 ThrIleLeuValLeuLeuAsn 17
           ||||||||||||||||||||
       238 ACTATATTAGTCTTGCTGAAC 258
```

SULT 42

US-10-953-349-26634
; Sequence 26634, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26634
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-26634

Alignment Scores:

Pred. No.:	314	Length:	1133
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-26634 (1-1133)

```
Qy          3 ProProArgGlyLeuLeuLeu 9
              |||||||||||||||||||||
Db         73 CCGCCGCGCGGCCTCCTCCTC 93
```

RESULT 43
US-10-953-349-16752
; Sequence 16752, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16752
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-16752

Alignment Scores:

Pred. No.:	329	Length:	1193
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-16752 (1-1193)

```
Qy          7 LeuLeuLeuValThrIleLeu 13
              |||||||||||||||||||||
Db        296 TTGCTGCTGGTAACTATCCTG 316
```

RESULT 44
US-10-953-349-17414/c
; Sequence 17414, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17414
LENGTH: 1202
TYPE: DNA
ORGANISM: Glycine max
10-953-349-17414

gnment Scores:

d. No.:	332	Length:	1202
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	6	Gaps:	0

10-821-670A-33 (1-222) x US-10-953-349-17414 (1-1202)

```
       196 IleLysLeuCysIleLeuLeu 202
           ||||||||||||||||||||||
       882 ATTAAACTCTGTATTTTACTT 862
```

ULT 45
11-217-529-1292/c
equence 1292, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1292
LENGTH: 1236
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-1292

gnment Scores:

d. No.:	341	Length:	1236
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	7	Gaps:	0

10-821-670A-33 (1-222) x US-11-217-529-1292 (1-1236)

```
        30 ThrProThrProSerProGly 36
           ||||||||||||||||||||||
       328 ACACCAACTCCTTCTCCAGGG 308
```

ULT 46
11-217-529-80501/c
equence 80501, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80501
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80501

Alignment Scores:

Pred. No.:	346	Length:	1257
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-217-529-80501 (1-1257)

```
Qy           9 LeuValThrIleLeuValLeu 15
               |||||||||||||||||||||
Db         701 CTTGTTACGATTTTAGTTCTT 681
```

RESULT 47
US-10-953-349-24555/c
; Sequence 24555, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24555
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-24555

Alignment Scores:

Pred. No.:	361	Length:	1313
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-24555 (1-1313)

```
Qy         177 SerValThrValProGlnAsn 183
               ||||||||||||||||||||||
Db         199 AGTGTTACTGTTCCCCAAAAC 179
```

RESULT 48
US-10-953-349-35965/c
; Sequence 35965, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35965
LENGTH: 1454
TYPE: DNA
ORGANISM: Zea mays subsp. mays
US-10-953-349-35965

Alignment Scores:

Pred. No.:	397	Length:	1454
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-35965 (1-1454)

```
Qy        197 LysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||||
Db        575 AAGCTCTGTATTCTGCTACAT 555
```

RESULT 49
US-10-953-349-32584
Sequence 32584, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 32584
LENGTH: 1481
TYPE: DNA
ORGANISM: Triticum aestivum
US-10-953-349-32584

Alignment Scores:

Pred. No.:	404	Length:	1481
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-32584 (1-1481)

```
Qy          3 ProProArgGlyLeuLeuLeu 9
              |||||||||||||||||||||
Db        261 CCTCCTCGCGGCCTTCTGCTT 281
```

RESULT 50
US-10-953-349-36433
Sequence 36433, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 36433
LENGTH: 1483
TYPE: DNA
ORGANISM: Zea mays subsp. mays
US-10-953-349-36433

Alignment Scores:

Pred. No.:	405	Length:	1483
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-36433 (1-1483)

```
Qy         46 ThrLeuLeuArgAlaIleSer 52
              |||||||||||||||||||||
Db       1092 ACACTCTTGCGAGCCATCTCT 1112
```

RESULT 51
US-11-264-784-73
; Sequence 73, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
; LENGTH: 1495
; TYPE: DNA
; ORGANISM: Yarrowia lipolytica
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: LPAAT2
US-11-264-784-73

Alignment Scores:

Pred. No.:	408	Length:	1495
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-264-784-73 (1-1495)

```
Qy          8 LeuLeuValThrIleLeuVal 14
              ||||||||||||||||||||
Db        379 CTGCTGGTGACCATCCTGGTG 399
```

RESULT 52
US-11-264-737-114
; Sequence 114, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Pictaggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.

APPLICANT: Xue, Zhixiong
APPLICANT: Yadav, Narendra S.
APPLICANT: Zhang, Hongxiang
APPLICANT: Zhu, Quinn Qun
TITLE OF INVENTION: DOCOSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
FILE REFERENCE: CL3160 US NA
CURRENT APPLICATION NUMBER: US/11/264,737
CURRENT FILING DATE: 2005-11-01
NUMBER OF SEQ ID NOS: 467
SOFTWARE: PatentIn version 3.3
SEQ ID NO 114
LENGTH: 1495
TYPE: DNA
ORGANISM: Yarrowia lipolytica
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: LPAAT2
11-264-737-114

gnment Scores:

d. No.:	408	Length:	1495
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	7	Gaps:	0

10-821-670A-33 (1-222) x US-11-264-737-114 (1-1495)

```
          8 LeuLeuValThrIleLeuVal 14
            ||||||||||||||||||||
        379 CTGCTGGTGACCATCCTGGTG 399
```

ULT 53
11-265-761-86
equence 86, Application US/11265761
ublication No. US20060115881A1
ENERAL INFORMATION:
APPLICANT: E.I. duPont de Nemours and Co., Inc.
APPLICANT: Damude, Howard Glenn
APPLICANT: Gillies, Peter John
APPLICANT: Macool, Daniel Joseph
APPLICANT: Picataggio, Stephen K.
APPLICANT: Pollak, Dana M. Walters
APPLICANT: Ragghianti, James John
APPLICANT: Xue, Zhixiong
APPLICANT: Yadav, Narendra S.
APPLICANT: Zhang, Hongxiang
APPLICANT: Zhu, Quinn
TITLE OF INVENTION: HIGH EICOSAPENTAENOIC ACID PRODUCING STRAINS OF YARROWIA
TITLE OF INVENTION: LIPOLYTICA
FILE REFERENCE: CL2698 USNA
CURRENT APPLICATION NUMBER: US/11/265,761
CURRENT FILING DATE: 2005-11-02
PRIOR APPLICATION NUMBER: US 60/624812
PRIOR FILING DATE: 2004-11-04
NUMBER OF SEQ ID NOS: 414
SOFTWARE: PatentIn version 3.3
EQ ID NO 86
LENGTH: 1495
TYPE: DNA
ORGANISM: Yarrowia lipolytica
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: LPAAT2
11-265-761-86

gnment Scores:

d. No.:	408	Length:	1495
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-265-761-86 (1-1495)

```
Qy          8 LeuLeuValThrIleLeuVal 14
              ||||||||||||||||||||
Db        379 CTGCTGGTGACCATCCTGGTG 399
```

RESULT 54
US-10-953-349-33213
; Sequence 33213, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33213
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33213

Alignment Scores:

Pred. No.:	410	Length:	1504
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-33213 (1-1504)

```
Qy         28 LeuProThrProThrProSer 34
              ||||||||||||||||||||
Db         40 CTCCCAACCCCAACCCCGTCC 60
```

RESULT 55
US-10-953-349-17700/c
; Sequence 17700, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17700
; LENGTH: 1538
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17700

Alignment Scores:

Pred. No.:	419	Length:	1538
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-17700 (1-1538)

```
Qy        184 SerSerLeuGluGluProAsp 190
              ||||||||||||||||||||
Db        368 TCTTCACTTGAAGAACCCGAT 348
```

```
SULT 56
-10-953-349-21291/c
Sequence 21291, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 21291
  LENGTH: 1575
  TYPE: DNA
  ORGANISM: Glycine max
-10-953-349-21291

ignment Scores:
ed. No.:                429             Length:         1575
ore:                    7.00            Matches:        7
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              3.2%            Indels:         0
:                       6               Gaps:           0

-10-821-670A-33 (1-222) x US-10-953-349-21291 (1-1575)

         12 IleLeuValLeuLeuAsnHis 18
            ||||||||||||||||||||
        565 ATTTTAGTGTTGCTGAACCAC 545

SULT 57
-10-953-349-24275/c
Sequence 24275, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 24275
  LENGTH: 1660
  TYPE: DNA
  ORGANISM: Glycine max
-10-953-349-24275

ignment Scores:
ed. No.:                451             Length:         1660
ore:                    7.00            Matches:        7
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              3.2%            Indels:         0
:                       6               Gaps:           0

-10-821-670A-33 (1-222) x US-10-953-349-24275 (1-1660)

        197 LysLeuCysIleLeuLeuHis 203
            ||||||||||||||||||||
        965 AAGTTGTGTATTCTGTTGCAC 945

SULT 58
-11-217-529-78924
Sequence 78924, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78924
;    LENGTH: 1674
;    TYPE: DNA
;    ORGANISM: Saccharomyces pastorianus
US-11-217-529-78924

Alignment Scores:
Pred. No.:              454             Length:         1674
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.2%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-33 (1-222) x US-11-217-529-78924 (1-1674)

Qy           3 ProProArgGlyLeuLeuLeu 9
               |||||||||||||||||||||
Db        1427 CCTCCCAGAGGACTTCTATTG 1447

RESULT 59
US-10-953-349-16452
; Sequence 16452, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16452
;    LENGTH: 1699
;    TYPE: DNA
;    ORGANISM: Glycine max
US-10-953-349-16452

Alignment Scores:
Pred. No.:              461             Length:         1699
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.2%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-953-349-16452 (1-1699)

Qy           7 LeuLeuLeuValThrIleLeu 13
               |||||||||||||||||||||
Db         813 TTGCTGCTGGTAACTATCCTG 833

RESULT 60
US-10-953-349-6606
; Sequence 6606, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
```

```
TITLE OF INVENTION:  ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE:  2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 6606
 LENGTH: 1703
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (177)..(177)
 OTHER INFORMATION: n is a, c, g, or t
10-953-349-6606

gnment Scores:
d. No.:              462          Length:         1703
re:                  7.00         Matches:        7
cent Similarity:     100.0%       Conservative:   0
t Local Similarity:  100.0%       Mismatches:     0
ry Match:            3.2%         Indels:         0
                     6            Gaps:           0

10-821-670A-33 (1-222) x US-10-953-349-6606 (1-1703)

          9 LeuValThrIleLeuValLeu 15
            ||||||||||||||||||||
        181 CTCGTGACAATCCTGGTCTTG 201

ULT 61
11-313-556-3/c
equence 3, Application US/11313556
ublication No. US20060099195A1
 GENERAL INFORMATION:
      APPLICANT: Ostrand-Rosenberg, Suzanne
                 Baskar, Sivasubramanian
                 Glimcher, Laurie H.
                 Freeman, Gordon J.
                 Nadler, Lee M.
      TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
      NUMBER OF SEQUENCES: 4
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: LAHIVE & COCKFIELD
           STREET: 60 State Street, Suite 510
           CITY: Boston
           STATE: Massachusetts
           COUNTRY: USA
           ZIP: 02109
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/11/313,556
           FILING DATE: 20-Dec-2005
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: US/09/966,148
           FILING DATE: 27-Sep-2001
           APPLICATION NUMBER: 08/147,772
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Mandragouras, Amy E.
           REGISTRATION NUMBER: 36,207
           REFERENCE/DOCKET NUMBER: RPI-003
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (617) 227-7400
           TELEFAX: (617) 227-5941
  INFORMATION FOR SEQ ID NO: 3:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 1716 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA to mRNA
      HYPOTHETICAL: no
      ORIGINAL SOURCE:
           ORGANISM: Mus musculus
           DEVELOPMENTAL STAGE: germ line
           TISSUE TYPE: lymphoid
           CELL TYPE: B lymphocyte
           CELL LINE: 70Z and A20
      IMMEDIATE SOURCE:
           LIBRARY: cDNA in pCDM8 vector
           CLONE: B7 #'s 1 and 29
      FEATURE:
           NAME/KEY:  translated region
           LOCATION:  249 to 1166 bp
           IDENTIFICATION METHOD:  similarity to other pattern
      FEATURE:
           NAME/KEY:  Alternate ATG initiation codons
           LOCATION:  225 to 227 and 270 to 272
           IDENTIFICATION METHOD:  similarity to other pattern
      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-11-313-556-3

Alignment Scores:
Pred. No.:              465          Length:         1716
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            3.2%         Indels:         0
DB:                     7            Gaps:           0

US-10-821-670A-33 (1-222) x US-11-313-556-3 (1-1716)

Qy         29 ProThrProThrProSerPro 35
              ||||||||||||||||||||
Db       1631 CCCACCCCCACCCCGTCCCCC 1611

RESULT 62
US-10-953-349-34792
; Sequence 34792, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34792
;   LENGTH: 1750
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (63)..(63)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-34792

Alignment Scores:
Pred. No.:              474          Length:         1750
Score:                  7.00         Matches:        7
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            3.2%         Indels:         0
DB:                     6            Gaps:           0

US-10-821-670A-33 (1-222) x US-10-953-349-34792 (1-1750)

Qy         28 LeuProThrProThrProSer 34
```

```
              ||||||||||||||||||||
        90 CTCCCAACCCCAACCCCGTCC 110

SULT 63
-11-217-529-174380/c
Sequence 174380, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 174380
  LENGTH: 1761
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
-11-217-529-174380

gnment Scores:
ed. No.:              477          Length:        1761
ore:                  7.00         Matches:       7
cent Similarity:      100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            3.2%         Indels:        0
:                     7            Gaps:          0

-10-821-670A-33 (1-222) x US-11-217-529-174380 (1-1761)

        47 LeuLeuArgAlaIleSerAsn 53
              ||||||||||||||||||||
       307 TTATTACGGGCGATATCAAAT 287

SULT 64
-11-251-465-7/c
Sequence 7, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
 APPLICANT: Brys, Reginald
 APPLICANT:  Vandeghinste, Nick
 APPLICANT:  Tomme, Peter
 APPLICANT:  Klaassen, Hubertus
 TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
 TITLE OF INVENTION:  Same, Useful In The Treatment Of Joint Degenerative And
 TITLE OF INVENTION:  Inflammatory Diseases
 FILE REFERENCE: P30,172-A USA
 CURRENT APPLICATION NUMBER: US/11/251,465
 CURRENT FILING DATE:  2005-10-14
 PRIOR APPLICATION NUMBER: 60/619,384
 PRIOR FILING DATE: 2004-10-15
 NUMBER OF SEQ ID NOS: 880
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
  LENGTH: 1804
  TYPE: DNA
  ORGANISM: Homo sapiens
-11-251-465-7

gnment Scores:
ed. No.:              488          Length:        1804
ore:                  7.00         Matches:       7
cent Similarity:      100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            3.2%         Indels:        0
DB:                   7            Gaps:          0

US-10-821-670A-33 (1-222) x US-11-251-465-7 (1-1804)

Qy        169 LeuLeuGlnAlaLeuAsnVal 175
              |||||||||||||||||||||
Db       1109 CTCCTGCAGGCTCTCAACGTG 1089

RESULT 65
US-11-311-754-27
; Sequence 27, Application US/11311754
; Publication No. US20060099635A1
; GENERAL INFORMATION:
;  APPLICANT: Vincent Ling
;  APPLICANT:  Kyriaki Dunussi-Joannopoulos
;  TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: GNN-007
;  CURRENT APPLICATION NUMBER: US/11/311,754
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: US/09/667,135
;  PRIOR FILING DATE: 2000-09-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 1831
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: hGL50-mIgG2am nucleotide sequence
US-11-311-754-27

Alignment Scores:
Pred. No.:            494          Length:        1831
Score:                7.00         Matches:       7
Percent Similarity:   100.0%       Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:          3.2%         Indels:        0
DB:                   7            Gaps:          0

US-10-821-670A-33 (1-222) x US-11-311-754-27 (1-1831)

Qy        181 ProGlnAsnSerSerLeuGlu 187
              |||||||||||||||||||||
Db        237 CCACAGAACAGCTCCTTGGAA 257

RESULT 66
US-10-505-928-693
; Sequence 693, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 693
;   LENGTH: 1868
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-693

Alignment Scores:
Pred. No.:            504          Length:        1868
Score:                7.00         Matches:       7
Percent Similarity:   100.0%       Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:          3.2%         Indels:        0
DB:                   6            Gaps:          0
```

10-821-670A-33 (1-222) x US-10-505-928-693 (1-1868)

```
        79 LysAspLysThrSerThrVal 85
           ||||||||||||||||||||
       708 AAAGACAAAACTTCAACAGTG 728
```

ULT 67
10-953-349-11252/c
equence 11252, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 11252
LENGTH: 1914
TYPE: DNA
ORGANISM: Arabidopsis thaliana
10-953-349-11252

gnment Scores:

d. No.:	516	Length:	1914
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	6	Gaps:	0

10-821-670A-33 (1-222) x US-10-953-349-11252 (1-1914)

```
        86 GluAlaCysLeuProLeuGlu 92
           ||||||||||||||||||||
       932 GAAGCCTGTCTTCCTCTGGAA 912
```

ULT 68
11-293-697-275
equence 275, Application US/11293697
ublication No. US20060105376A1
ENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 275
LENGTH: 1933
TYPE: DNA
ORGANISM: Homo sapiens
11-293-697-275

gnment Scores:

d. No.:	521	Length:	1933
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	7	Gaps:	0

10-821-670A-33 (1-222) x US-11-293-697-275 (1-1933)

```
        28 LeuProThrProThrProSer 34
           ||||||||||||||||||||
      1778 CTCCCCACCCCCACACCATCT 1798
```

RESULT 69
US-10-953-349-1534
; Sequence 1534, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1534
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1534

Alignment Scores:

Pred. No.:	532	Length:	1977
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-953-349-1534 (1-1977)

```
Qy         10 ValThrIleLeuValLeuLeu 16
              ||||||||||||||||||||
Db       1795 GTCACCATTCTTGTTTTGTTG 1815
```

RESULT 70
US-11-293-697-1094/c
; Sequence 1094, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1094
; LENGTH: 2036
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1094

Alignment Scores:

Pred. No.:	547	Length:	2036
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-293-697-1094 (1-2036)

```
Qy         85 ValGluAlaCysLeuProLeu 91
              ||||||||||||||||||||
Db       582 GTTGAAGCTTGTCTCCCACTT 562
```

RESULT 71
US-11-217-529-77609/c
; Sequence 77609, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 77609
LENGTH: 2037
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-77609

gnment Scores:

ed. No.:	547	Length:	2037
ore:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.2%	Indels:	0
:	7	Gaps:	0

-10-821-670A-33 (1-222) x US-11-217-529-77609 (1-2037)

```
        116 SerArgLysThrSerPheMet 122
            |||||||||||||||||||||
        314 TCTCGCAAAACTAGCTTTATG 294
```

SULT 72
-11-293-697-1972
Sequence 1972, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1972
LENGTH: 2126
TYPE: DNA
ORGANISM: Homo sapiens
-11-293-697-1972

gnment Scores:

ed. No.:	570	Length:	2126
ore:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.2%	Indels:	0
:	7	Gaps:	0

-10-821-670A-33 (1-222) x US-11-293-697-1972 (1-2126)

```
         30 ThrProThrProSerProGly 36
            ||||||||||||||||||||||
       1992 ACCCCTACCCCATCTCCAGGC 2012
```

SULT 73
-11-293-697-374
Sequence 374, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 374
; LENGTH: 2152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-374

Alignment Scores:

Pred. No.:	576	Length:	2152
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-293-697-374 (1-2152)

```
Qy          9 LeuValThrIleLeuValLeu 15
              |||||||||||||||||||||
Db        950 CTTGTCACCATTTTGGTTTTG 970
```

RESULT 74
US-11-217-529-2489
; Sequence 2489, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2489
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2489

Alignment Scores:

Pred. No.:	599	Length:	2241
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-217-529-2489 (1-2241)

```
Qy        131 TyrGluAspLeuLysMetTyr 137
              ||||||||||||||||||||
Db       1705 TATGAAGACTTGAAGATGTAC 1725
```

RESULT 75
US-11-293-697-507
; Sequence 507, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 507
LENGTH: 2275
TYPE: DNA
ORGANISM: Homo sapiens
11-293-697-507

gnment Scores:

d. No.:	608	Length:	2275
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t. Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	7	Gaps:	0

10-821-670A-33 (1-222) x US-11-293-697-507 (1-2275)

```
        97 GluSerCysLeuAlaSerArg 103
           ||||||||||||||||||||
      1307 GAGAGCTGCTTGGCTTCAAGG 1327
```

ULT 76
10-511-937-649/c
equence 649, Application US/10511937
ublication No. US20060088836A1
ENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 649
LENGTH: 2315
TYPE: DNA
ORGANISM: Homo sapiens
10-511-937-649

gnment Scores:

d. No.:	618	Length:	2315
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t. Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	6	Gaps:	0

10-821-670A-33 (1-222) x US-10-511-937-649 (1-2315)

```
       182 GlnAsnSerSerLeuGluGlu 188
           ||||||||||||||||||||
      1460 CAGAATTCTTCATTAGAGGAA 1440
```

RESULT 77
US-11-293-697-1101
; Sequence 1101, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1101
; LENGTH: 2558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1101

Alignment Scores:

Pred. No.:	679	Length:	2558
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-293-697-1101 (1-2558)

```
Qy          9 LeuValThrIleLeuValLeu 15
              |||||||||||||||||||||
Db         47 TTGGTCACCATCTTGGTTTTG 67
```

RESULT 78
US-10-196-749-135
; Sequence 135, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 135
LENGTH: 2651
TYPE: DNA
ORGANISM: Homo Sapien
-10-196-749-135

:gnment Scores:

ed. No.:	702	Length:	2651
ore:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.2%	Indels:	0
	6	Gaps:	0

-10-821-670A-33 (1-222) x US-10-196-749-135 (1-2651)

```
        29 ProThrProThrProSerPro 35
           ||||||||||||||||||||
       370 CCAACTCCAACTCCTTCTCCC 390
```

SULT 79
-11-101-316-23
Sequence 23, Application US/11101316
Publication No. US20060099657A1
GENERAL INFORMATION:
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Grimaldi,Christopher J.
APPLICANT: Gurney,Austin L.
APPLICANT: Wood,William I.
TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
FILE REFERENCE: P3230R1C17C1
CURRENT APPLICATION NUMBER: US/11/101,316
CURRENT FILING DATE: 2005-04-06
PRIOR APPLICATION NUMBER: 10/063526
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 23
LENGTH: 2651
TYPE: DNA
ORGANISM: Homo Sapien
-11-101-316-23

:gnment Scores:

ed. No.:	702	Length:	2651
ore:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.2%	Indels:	0
	7	Gaps:	0

-10-821-670A-33 (1-222) x US-11-101-316-23 (1-2651)

```
        29 ProThrProThrProSerPro 35
           ||||||||||||||||||||
       370 CCAACTCCAACTCCTTCTCCC 390
```

RESULT 80
US-11-293-697-753
; Sequence 753, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 753
; LENGTH: 2662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-753

Alignment Scores:

Pred. No.:	705	Length:	2662
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-293-697-753 (1-2662)

```
Qy        174 AsnValAsnSerValThrVal 180
              ||||||||||||||||||||
Db       1505 AATGTGAATTCAGTAACTGTG 1525
```

RESULT 81
US-11-293-697-2253
; Sequence 2253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2253
; LENGTH: 2688
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2253

Alignment Scores:

Pred. No.:	712	Length:	2688
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-293-697-2253 (1-2688)

```
Qy          3 ProProArgGlyLeuLeuLeu 9
              ||||||||||||||||||||
Db       2570 CCGCCAAGGGGACTGCTGCTT 2590
```

RESULT 82
US-10-511-937-551/c
; Sequence 551, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 551
LENGTH: 2692
TYPE: DNA
ORGANISM: Homo sapiens
10-511-937-551

gnment Scores:

d. No.:	713	Length:	2692
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	6	Gaps:	0

10-821-670A-33 (1-222) x US-10-511-937-551 (1-2692)

```
        10 ValThrIleLeuValLeuLeu 16
           ||||||||||||||||||||||
        65 GTAACAATCCTCGTCCTCCTC 45
```

ULT 83
11-293-697-1902/c
equence 1902, Application US/11293697
ublication No. US20060105376A1
ENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 1902
LENGTH: 2792
TYPE: DNA
ORGANISM: Homo sapiens
11-293-697-1902

gnment Scores:

d. No.:	738	Length:	2792
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	7	Gaps:	0

10-821-670A-33 (1-222) x US-11-293-697-1902 (1-2792)

```
        10 ValThrIleLeuValLeuLeu 16
           ||||||||||||||||||||||
```

```
Db        178 GTAACAATCCTCGTCCTCCTC 158
```

RESULT 84
US-11-217-529-82539
; Sequence 82539, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82539
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82539

Alignment Scores:

Pred. No.:	741	Length:	2805
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-217-529-82539 (1-2805)

```
Qy        165 AlaIleAspGluLeuLeuGln 171
              |||||||||||||||||||||
Db       1738 GCCATTGATGAATTATTACAA 1758
```

RESULT 85
US-11-293-697-74/c
; Sequence 74, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-74

Alignment Scores:

Pred. No.:	766	Length:	2905
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-293-697-74 (1-2905)

```
Qy        181 ProGlnAsnSerSerLeuGlu 187
              |||||||||||||||||||||
```

```
       246 CCGCAAAACTCTTCGCTGGAG 226

SULT 86
-11-312-958-55
Sequence 55, Application US/11312958
Publication No. US20060100152A1
GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT:  Rosenfeld, Julie Beth
 APPLICANT:  Silos-Santiago, Inmaculada
 TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
 TITLE OF INVENTION:  PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
 TITLE OF INVENTION:  12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
 TITLE OF INVENTION:  27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
 TITLE OF INVENTION:  95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
 TITLE OF INVENTION:  13424 MOLECULES
 FILE REFERENCE: MPI02-027P1RNOMNIM
 CURRENT APPLICATION NUMBER: US/11/312,958
 CURRENT FILING DATE:  2005-12-20
 PRIOR APPLICATION NUMBER: US/10/369,022
 PRIOR FILING DATE: 2003-02-19
 PRIOR APPLICATION NUMBER: US 60/360,495
 PRIOR FILING DATE: 2002-02-28
 PRIOR APPLICATION NUMBER: US 60/370,121
 PRIOR FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: US 60/373,010
 PRIOR FILING DATE: 2002-04-16
 PRIOR APPLICATION NUMBER: US 60/373,908
 PRIOR FILING DATE: 2002-04-19
 PRIOR APPLICATION NUMBER: US 60/377,717
 PRIOR FILING DATE: 2002-05-03
 PRIOR APPLICATION NUMBER: US 60/379,949
 PRIOR FILING DATE: 2002-05-13
 PRIOR APPLICATION NUMBER: US 60/382,409
 PRIOR FILING DATE: 2002-05-21
 PRIOR APPLICATION NUMBER: US 60/385,280
 PRIOR FILING DATE: 2002-06-03
 PRIOR APPLICATION NUMBER: US 60/386,879
 PRIOR FILING DATE: 2002-06-06
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
  LENGTH: 3138
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (161)...(3022)
-11-312-958-55

gnment Scores:
d. No.:                824          Length:        3138
re:                    7.00         Matches:       7
cent Similarity:       100.0%       Conservative:  0
st Local Similarity:   100.0%       Mismatches:    0
ery Match:             3.2%         Indels:        0
:                      7            Gaps:          0

-10-821-670A-33 (1-222) x US-11-312-958-55 (1-3138)

         29 ProThrProThrProSerPro 35
            ||||||||||||||||||||
       2504 CCCACACCCACGCCCTCGCCC 2524

SULT 87
-11-293-697-1397
Sequence 1397, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
 APPLICANT: HELIX RESEARCH INSTITUTE
 TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: H1-A0106
 CURRENT APPLICATION NUMBER: US/11/293,697
 CURRENT FILING DATE:  2005-12-05
 PRIOR APPLICATION NUMBER: US/10/108,260
 PRIOR FILING DATE: 2002-03-28
 NUMBER OF SEQ ID NOS: 5458
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1397
  LENGTH: 3294
  TYPE: DNA
  ORGANISM: Homo sapiens
US-11-293-697-1397

Alignment Scores:
Pred. No.:             863          Length:        3294
Score:                 7.00         Matches:       7
Percent Similarity:    100.0%       Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:           3.2%         Indels:        0
DB:                    7            Gaps:          0

US-10-821-670A-33 (1-222) x US-11-293-697-1397 (1-3294)

Qy          98 SerCysLeuAlaSerArgGlu 104
               ||||||||||||||||||||
Db        1271 AGTTGCTTAGCAAGCAGGGAA 1291

RESULT 88
US-10-505-928-814/c
SEQ ID NO 814, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
 APPLICANT: Ludwig Institute for Cancer Research et al.
 TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 FILE REFERENCE: 28967/39178
 CURRENT APPLICATION NUMBER: US/10/505,928
 CURRENT FILING DATE:  2004-08-27
 PRIOR APPLICATION NUMBER: US 60/363,019
 PRIOR FILING DATE: 2002-03-07
 NUMBER OF SEQ ID NOS: 866
 SOFTWARE: PatentIn 3.2
SEQ ID NO 814
  LENGTH: 3558
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-505-928-814

Alignment Scores:
Pred. No.:             929          Length:        3558
Score:                 7.00         Matches:       7
Percent Similarity:    100.0%       Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:           3.2%         Indels:        0
DB:                    6            Gaps:          0

US-10-821-670A-33 (1-222) x US-10-505-928-814 (1-3558)

Qy         114 LeuAlaSerArgLysThrSer 120
               ||||||||||||||||||||
Db         460 CTTGCAAGCCGTAAAACTTCT 440

RESULT 89
US-11-293-697-799/c
Sequence 799, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
 APPLICANT: HELIX RESEARCH INSTITUTE
 TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: H1-A0106
 CURRENT APPLICATION NUMBER: US/11/293,697
 CURRENT FILING DATE:  2005-12-05
 PRIOR APPLICATION NUMBER: US/10/108,260
 PRIOR FILING DATE: 2002-03-28
 NUMBER OF SEQ ID NOS: 5458
```

SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 799
LENGTH: 4295
TYPE: DNA
ORGANISM: Homo sapiens
11-293-697-799

gnment Scores:

d. No.:	1.11e+03	Length:	4295
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	7	Gaps:	0

10-821-670A-33 (1-222) x US-11-293-697-799 (1-4295)

```
        13 LeuValLeuLeuAsnHisLeu 19
           ||||||||||||||||||||
       553 CTCGTCCTGCTGAACCATCTC 533
```

ULT 90
11-217-529-1506/c
equence 1506, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
ILE REFERENCE: S-38-285
URRENT APPLICATION NUMBER: US/11/217,529
URRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
RIOR FILING DATE: 2004-09-02
UMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 1506
LENGTH: 7422
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-1506

gnment Scores:

d. No.:	1.87e+03	Length:	7422
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	3.2%	Indels:	0
	7	Gaps:	0

10-821-670A-33 (1-222) x US-11-217-529-1506 (1-7422)

```
        88 CysLeuProLeuGluLeuThr 94
           ||||||||||||||||||||
       685 TGTCTGCCGTTAGAGTTAACC 665
```

ULT 91
10-505-928-236/c
equence 236, Application US/10505928
ublication No. US20060088532A1
ENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
ITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
ILE REFERENCE: 28967/39178
URRENT APPLICATION NUMBER: US/10/505,928
URRENT FILING DATE: 2004-08-27
RIOR APPLICATION NUMBER: US 60/363,019
RIOR FILING DATE: 2002-03-07
UMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2
; SEQ ID NO 236
; LENGTH: 7758
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-236

Alignment Scores:

Pred. No.:	1.95e+03	Length:	7758
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x US-10-505-928-236 (1-7758)

```
Qy         29 ProThrProThrProSerPro 35
              ||||||||||||||||||||
Db       6809 CCCACCCCCACCCCCAGCCCC 6789
```

RESULT 92
US-11-264-737-165/c
; Sequence 165, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Pictaggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn Qun
; TITLE OF INVENTION: DOCOSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 165
; LENGTH: 10660
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pZP2FOEN4
US-11-264-737-165

Alignment Scores:

Pred. No.:	2.63e+03	Length:	10660
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-33 (1-222) x US-11-264-737-165 (1-10660)

```
Qy         28 LeuProThrProThrProSer 34
              ||||||||||||||||||||
Db       9542 CTACCTACGCCTACGCCTTCG 9522
```

RESULT 93
US-11-293-697-5328/c
; Sequence 5328, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5328
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
-11-293-697-5328

Alignment Scores:
ed. No.: 62.9 Length: 18
ore: 6.00 Matches: 6
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 2.7% Indels: 0
7 Gaps: 0

-10-821-670A-33 (1-222) x US-11-293-697-5328 (1-18)

7 LeuLeuLeuValThrIle 12
||||||||||||||||||
18 CTGCTGCTTGTCACAATT 1

SULT 94
-11-266-409-9
Sequence 9, Application US/11266409
Publication No. US20060093578A1
GENERAL INFORMATION:
APPLICANT: SUZUMURA, AKIO
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
FILE REFERENCE: 279847US40
CURRENT APPLICATION NUMBER: US/11/266,409
CURRENT FILING DATE: 2005-11-04
PRIOR APPLICATION NUMBER: US 60/624,851
PRIOR FILING DATE: 2004-11-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
-11-266-409-9

Alignment Scores:
ed. No.: 76.1 Length: 22
ore: 6.00 Matches: 6
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 2.7% Indels: 0
7 Gaps: 0

-10-821-670A-33 (1-222) x US-11-266-409-9 (1-22)

133 AspLeuLysMetTyrGln 138
|||||||||||||||||||
1 GACTTGAAGATGTACCAG 18

SULT 95
-11-217-529-36402
Sequence 36402, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36402
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-36402

Alignment Scores:
Pred. No.: 85.9 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-33 (1-222) x US-11-217-529-36402 (1-25)

Qy 81 LysThrSerThrValGlu 86
|||||||||||||||||||
Db 3 AAAACCTCCACCGTAGAG 20

RESULT 96
US-11-217-529-43879
; Sequence 43879, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43879
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-43879

Alignment Scores:
Pred. No.: 85.9 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-33 (1-222) x US-11-217-529-43879 (1-25)

Qy 23 SerLeuAlaArgAsnLeu 28
|||||||||||||||||||
Db 6 AGCCTCGCAAGGAACTTA 23

RESULT 97
US-11-217-529-47657/c
; Sequence 47657, Application US/11217529
; Publication No. US20060099612A1

```
ENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
EQ ID NO 47657
  LENGTH: 25
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
11-217-529-47657

gnment Scores:
d. No.:                 85.9            Length:         25
re:                     6.00            Matches:        6
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               2.7%            Indels:         0
                        7               Gaps:           0

10-821-670A-33 (1-222) x US-11-217-529-47657 (1-25)

        26 ArgAsnLeuProThrPro 31
           |||||||||||||||||||
        21 CGTAATTTACCCACGCCA 4

ULT 98
11-217-529-53284/c
equence 53284, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
EQ ID NO 53284
  LENGTH: 25
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
11-217-529-53284

gnment Scores:
d. No.:                 85.9            Length:         25
re:                     6.00            Matches:        6
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               2.7%            Indels:         0
                        7               Gaps:           0

10-821-670A-33 (1-222) x US-11-217-529-53284 (1-25)

        23 SerLeuAlaArgAsnLeu 28
           |||||||||||||||||||
        18 TCGTTAGCCAGGAACTTG 1

RESULT 99
US-11-217-529-84821/c
; Sequence 84821, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84821
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-84821

Alignment Scores:
Pred. No.:                 85.9            Length:         25
Score:                     6.00            Matches:        6
Percent Similarity:        100.0%          Conservative:   0
Best Local Similarity:     100.0%          Mismatches:     0
Query Match:               2.7%            Indels:         0
DB:                        7               Gaps:           0

US-10-821-670A-33 (1-222) x US-11-217-529-84821 (1-25)

Qy          23 SerLeuAlaArgAsnLeu 28
               |||||||||||||||||||
Db          25 TCTCTGGCCCGAAACCTC 8

RESULT 100
US-11-217-529-87245
; Sequence 87245, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87245
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-87245

Alignment Scores:
Pred. No.:                 85.9            Length:         25
Score:                     6.00            Matches:        6
Percent Similarity:        100.0%          Conservative:   0
Best Local Similarity:     100.0%          Mismatches:     0
Query Match:               2.7%            Indels:         0
DB:                        7               Gaps:           0
```

-10-821-670A-33 (1-222) x US-11-217-529-87245 (1-25)

```
        82 ThrSerThrValGluAla 87
           |||||||||||||||||
         3 ACCTCTACTGTGGAGGCA 20
```

arch completed: June 10, 2006, 02:12:30
) time : 53.1299 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

M protein - nucleic search, using frame_plus_p2n model

un on: June 10, 2006, 01:33:29 ; Search time 7495.33 Seconds
(without alignments)
4210.361 Million cell updates/sec

itle: US-10-821-670A-30
erfect score: 329
equence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

coring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

earched: 6366136 seqs, 31973710525 residues

ord size: 1

otal number of hits satisfying chosen parameters: 12722146

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Listing first 200 summaries

ommand line parameters:
MODEL=frame+_p2n.model -DEV=xlh
Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110449_27523/app_query.fasta_1
DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rge -MINMATCH=0.1
LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
MAXLEN=2000000000 -HOST=abss08
USER=US10821670_@CGN_1_1_6646_@runat_07062006_110449_27523 -NCPU=6 -ICPU=3
NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

atabase : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.		Score	% Query Match	Length	DB	ID	Description
1		329	100.0	987	2	AR595950	AR595950 Sequence
2	c	329	100.0	987	2	AR595951	AR595951 Sequence
3		329	100.0	990	2	AX076200	AX076200 Sequence
4		329	100.0	990	2	AX076482	AX076482 Sequence
5		329	100.0	4522	2	AX076209	AX076209 Sequence
6		329	100.0	4522	2	AX076476	AX076476 Sequence
7		328	99.7	985	2	AR595967	AR595967 Sequence
8	c	328	99.7	985	2	AR595968	AR595968 Sequence
9		317	96.4	2193	2	AR242435	AR242435 Sequence
10		317	96.4	2193	2	AR280203	AR280203 Sequence
11		317	96.4	2193	2	AR322418	AR322418 Sequence
12		307	93.3	921	2	AR242436	AR242436 Sequence
13		307	93.3	921	2	AR242437	AR242437 Sequence
14		307	93.3	921	2	AR280204	AR280204 Sequence
15		307	93.3	921	2	AR280205	AR280205 Sequence
16		307	93.3	921	2	AR322419	AR322419 Sequence
17		307	93.3	921	2	AR322420	AR322420 Sequence
18		278	84.5	990	14	FCU83184	U83184 Felis catus
19		217	66.0	1006	14	FCIL12P40	Y07762 Felis catus
20		217	66.0	1599	2	AR595956	AR595956 Sequence
21	c	217	66.0	1599	2	AR595957	AR595957 Sequence
22		206	62.6	921	2	AR595948	AR595948 Sequence
23	c	206	62.6	921	2	AR595949	AR595949 Sequence
24		206	62.6	1533	2	AR595959	AR595959 Sequence
25	c	206	62.6	1533	2	AR595960	AR595960 Sequence
26		126	38.3	431	14	AF054607	AF054607 Felis cat
27		52	15.8	990	2	AX154603	AX154603 Sequence
28		49	14.9	984	2	AX154600	AX154600 Sequence
29		42	12.8	984	2	AX154599	AX154599 Sequence
30		41	12.5	972	8	AY191829	AY191829 Synthetic
31		41	12.5	975	2	AX154597	AX154597 Sequence
32		39	11.9	993	14	AB107654	AB107654 Lama glam
33		39	11.9	1005	5	AY234218	AY234218 Papio anu
34		39	11.9	1005	5	CTU19834	U19834 Cercocebus
35		39	11.9	1080	5	MMU19841	U19841 Macaca mula
36		37	11.2	921	2	AR595965	AR595965 Sequence
37	c	37	11.2	921	2	AR595966	AR595966 Sequence
38		37	11.2	924	2	BD171282	BD171282 Novel can
39		37	11.2	987	2	AR595969	AR595969 Sequence
40	c	37	11.2	987	2	AR595970	AR595970 Sequence
41		37	11.2	990	2	AR151061	AR151061 Sequence
42		37	11.2	990	2	AR151071	AR151071 Sequence
43		37	11.2	990	2	BD014653	BD014653 Process f
44		37	11.2	990	2	BD014663	BD014663 Process f
45		37	11.2	990	2	E15017	E15017 Canine mRNA
46		37	11.2	990	2	AR316460	AR316460 Sequence
47		37	11.2	990	2	AR316470	AR316470 Sequence
48		37	11.2	1015	14	CFU49100	U49100 Canis famil
49		37	11.2	1533	2	AR595973	AR595973 Sequence
50	c	37	11.2	1533	2	AR595974	AR595974 Sequence
51		37	11.2	1599	2	AR595971	AR595971 Sequence
52	c	37	11.2	1599	2	AR595972	AR595972 Sequence
53		37	11.2	2154	2	BD171281	BD171281 Novel can
54		37	11.2	2267	2	AR596011	AR596011 Sequence
55	c	37	11.2	2267	2	AR596012	AR596012 Sequence
56		36	10.9	446	14	AF091134	AF091134 Canis fam
57		36	10.9	452	14	AF333121	AF333121 Canis fam
58		36	10.9	588	14	AF349536	AF349536 Canis fam
59		35	10.6	906	2	BD021808	BD021808 Natural k
60		35	10.6	906	2	BD021809	BD021809 Natural k
61		35	10.6	975	2	AX154602	AX154602 Sequence
62		35	10.6	987	2	AR008950	AR008950 Sequence
63		35	10.6	987	2	BD007070	BD007070 IL-12 gen
64		35	10.6	987	2	BD007076	BD007076 Gene expr
65		35	10.6	987	2	BD007077	BD007077 Gene expr
66		35	10.6	987	2	BD007078	BD007078 Gene expr
67		35	10.6	987	2	BD136034	BD136034 Interfero
68		35	10.6	987	2	BD136035	BD136035 Interfero
69		35	10.6	987	2	BD136036	BD136036 Interfero
70		35	10.6	987	2	CQ803342	CQ803342 Sequence
71		35	10.6	987	2	CS131491	CS131491 Sequence
72		35	10.6	987	2	I28591	I28591 Sequence 1
73		35	10.6	987	2	AX154633	AX154633 Sequence
74		35	10.6	1007	5	AF180563	AF180563 Homo sapi
75		35	10.6	1008	14	AB246353	AB246353 Bubalus b

76	35	10.6	1012	14	AY198121	AY198121 Bubalus b
77	35	10.6	1018	2	AR052857	AR052857 Sequence
78	35	10.6	1018	2	AR288169	AR288169 Sequence
79	35	10.6	1018	2	AR567156	AR567156 Sequence
80	35	10.6	1029	2	CQ829448	CQ829448 Sequence
81	35	10.6	1046	5	BC074723	BC074723 Homo sapi
82	35	10.6	1073	5	BC067498	BC067498 Homo sapi
83	35	10.6	1073	5	BC067499	BC067499 Homo sapi
84	35	10.6	1073	5	BC067500	BC067500 Homo sapi
85	35	10.6	1073	5	BC067501	BC067501 Homo sapi
86	35	10.6	1073	5	BC067502	BC067502 Homo sapi
87	35	10.6	1389	2	AR393788	AR393788 Sequence
88	35	10.6	1389	2	AX084106	AX084106 Sequence
89	35	10.6	1397	2	BD165800	BD165800 Antibody
90	35	10.6	1399	2	AR091391	AR091391 Sequence
91	35	10.6	1399	5	HUMCLMF40	M65272 Human cytot
92	35	10.6	1560	2	AR091395	AR091395 Sequence
93	35	10.6	1623	2	AR091394	AR091394 Sequence
94	35	10.6	2307	2	CQ715179	CQ715179 Sequence
95	35	10.6	2362	2	AR082684	AR082684 Sequence
96	35	10.6	2362	2	AR122960	AR122960 Sequence
97	35	10.6	2362	2	I28325	I28325 Sequence 1
98	35	10.6	2362	2	AR309636	AR309636 Sequence
99	35	10.6	2362	2	I89770	I89770 Sequence 1
100	35	10.6	5686	2	BD136048	BD136048 Interfero
101	35	10.6	6139	2	AR091393	AR091393 Sequence
102	33	10.0	681	7	BV440664	BV440664 S237P6324
103	30	9.1	621	7	BV242752	BV242752 S234P6134
104	28	8.5	224	14	DQ152965	DQ152965 Ovis arie
105	28	8.5	525	14	CEU10160	U10160 Cervus elap
106	28	8.5	969	2	AX154601	AX154601 Sequence
107	28	8.5	984	2	AX154598	AX154598 Sequence
108	28	8.5	984	14	AF004024	AF004024 Ovis arie
109	28	8.5	984	14	AF209435	AF209435 Ovis arie
110	28	8.5	993	14	AY603406	AY603406 Capra hir
111	28	8.5	993	14	CEU57752	U57752 Cervus elap
112	28	8.5	1008	14	AB246273	AB246273 Bubalus c
113	28	8.5	1008	14	AB246358	AB246358 Bubalus b
114	28	8.5	1012	14	AF007576	AF007576 Capra hir
115	28	8.5	1012	14	BTU11815	U11815 Bos taurus
116	28	8.5	1019	2	E35794	E35794 Process for
117	28	8.5	2090	14	SSU08317	U08317 Sus scrofa
118	27	8.2	932	14	AY686641S1	AY686641 Equus cab
119	27	8.2	1058	14	ECIL12P40	Y11129 Equus cabal
120	27	8.2	1626	8	AF401989	AF401989 Synthetic
121	23	7.0	987	2	BD105974	BD105974 Animal mo
122	23	7.0	987	2	AR533404	AR533404 Sequence
123	23	7.0	1870	2	A92079	A92079 Sequence 3
124	23	7.0	1870	2	AR230691	AR230691 Sequence
125	23	7.0	2318	2	AR228993	AR228993 Sequence
126	23	7.0	2318	5	HUMNKSFP40	M65290 Human natur
127	22	6.7	200	5	AY591921	AY591921 Macaca fa
128	22	6.7	999	6	AB025724	AB025724 Cavia por
129	22	6.7	15648	5	AF512686	AF512686 Homo sapi
130	22	6.7	18340	5	AY008847	AY008847 Homo sapi
131	22	6.7	108511	5	AC011418	AC011418 Homo sapi
132	21	6.4	528	6	AF082494	AF082494 Marmota m
133	21	6.4	984	6	AF288519	AF288519 Marmota m
134	21	6.4	984	6	MMIL12P40	X97019 M.monax mRN
135	21	6.4	1425	6	AF421395	AF421395 Sigmodon
136	20	6.1	399	2	CS211342	CS211342 Sequence
137	20	6.1	399	2	CS214984	CS214984 Sequence
138	20	6.1	399	6	AF046211	AF046211 Mesocrice
139	20	6.1	2276	6	AB085792	AB085792 Mesocrice
140	19	5.8	928	11	MGA564203	AJ564203 Meleagris
141	19	5.8	948	2	CQ760887	CQ760887 Sequence
142	19	5.8	948	2	CQ760890	CQ760890 Sequence
143	19	5.8	948	2	CQ760892	CQ760892 Sequence
144	19	5.8	948	11	DQ202328	DQ202328 Gallus ga
145	19	5.8	948	11	AY262752	AY262752 Gallus ga
146	17	5.2	73	2	AR439759	AR439759 Sequence
147	17	5.2	73	2	AX268996	AX268996 Sequence
148	17	5.2	508	6	AF097507	AF097507 Cavia por
149	17	5.2	600	2	E26663	E26663 Improved me
150	17	5.2	821	6	RNU16674	U16674 Rattus norv
151	17	5.2	1008	6	AF133197	AF133197 Rattus no
152	17	5.2	1061	2	AR069654	AR069654 Sequence
153	17	5.2	1143	6	AF128214	AF128214 Mus muscu
154	17	5.2	1143	6	AF128215	AF128215 Mus muscu
155	17	5.2	1381	6	BC103608	BC103608 Mus muscu
156	17	5.2	1381	6	BC103609	BC103609 Mus muscu
157	17	5.2	1381	6	BC103610	BC103610 Mus muscu
158	17	5.2	1381	6	BC103614	BC103614 Mus muscu
159	17	5.2	1409	2	AR393787	AR393787 Sequence
160	17	5.2	1409	2	AX084105	AX084105 Sequence
161	17	5.2	1472	2	AR393786	AR393786 Sequence
162	17	5.2	1472	2	AX084104	AX084104 Sequence
163	17	5.2	1569	2	AR393796	AR393796 Sequence
164	17	5.2	1569	2	AX084114	AX084114 Sequence
165	17	5.2	1582	14	AY686641S2	AY686644 Equus cab
166	17	5.2	1669	8	AF411293	AF411293 Synthetic
167	17	5.2	1840	6	MUSIL40A	M86671 Mus musculu
168	17	5.2	2013	2	AR393795	AR393795 Sequence
169	17	5.2	2013	2	AX084113	AX084113 Sequence
170	17	5.2	2438	2	CQ812173	CQ812173 Sequence
171	17	5.2	2709	2	AR393797	AR393797 Sequence
172	17	5.2	2709	2	AX084115	AX084115 Sequence
173	17	5.2	5252	2	CQ803341	CQ803341 Sequence
174	17	5.2	5966	2	BD136050	BD136050 Interfero
175	17	5.2	9049	2	CQ803350	CQ803350 Sequence
176	17	5.2	10633	2	CQ803349	CQ803349 Sequence
177	17	5.2	11746	2	CQ803348	CQ803348 Sequence
178	17	5.2	38246	2	CQ803351	CQ803351 Sequence
179	16	4.9	1062	6	AF288612	AF288612 Meriones
180	13	4.0	987	2	BD136055	BD136055 Interfero
181	13	4.0	1000	6	S82420S3	S82422 interleukin
182	13	4.0	76047	6	AL669944	AL669944 Mouse DNA
183	13	4.0	110000	12	AC073744_2	Continuation (3 of
184	13	4.0	110000	12	AC073744_3	Continuation (4 of
185	13	4.0	189236	6	AL607030	AL607030 Mouse DNA
c 186	13	4.0	268294	12	AC020885	AC020885 Mus muscu
187	13	4.0	287927	12	AC079530	AC079530 Mus muscu
188	12	3.6	38	2	AR242440	AR242440 Sequence
189	12	3.6	38	2	AR280208	AR280208 Sequence
190	12	3.6	38	2	AR322423	AR322423 Sequence
191	12	3.6	1897	11	GGA564201	AJ564201 Gallus ga
192	12	3.6	285389	12	AC096348	AC096348 Rattus no
193	11	3.3	9821	11	GGA564202	AJ564202 Gallus ga
c 194	10	3.0	30	2	AX027245	AX027245 Sequence
195	10	3.0	500	6	S82420S5	S82424 interleukin
c 196	10	3.0	2553	10	AF394057	AF394057 Porcine c
c 197	10	3.0	5668	10	AF268041	AF268041 Porcine c
c 198	10	3.0	6249	10	AF268039	AF268039 Porcine c
199	10	3.0	21925	2	AX647863	AX647863 Sequence
200	10	3.0	26184	2	AX647497	AX647497 Sequence

ALIGNMENTS

```
RESULT 1
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
```

```
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          987
Score:                    329.00         Matches:         329
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR595950 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 2
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          987
Score:                    329.00         Matches:         329
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR595951 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
```

```
                                                
```

```
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
EFERENCE   1
 AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
 TITLE     Vaccine against lentiviral infections, such as the feline immune
           deficiency virus of the cat
 JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
           Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
           Universitaet Zuerich (CH)
EATURES              Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
RIGIN

lignment Scores:
red. No.:              0              Length:        990
core:                  329.00         Matches:       329
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-30 (1-329) x AX076482 (1-990)

y          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

y         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

y         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

y         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

y         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

y        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

y        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

y        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

y        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

y        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

y        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

y        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy       321 SerAsnTrpAlaSerValSerCysSer 329
             |||||||||||||||||||||||||||
Db       961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 5
AX076209
LOCUS       AX076209                4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
ORIGIN

Alignment Scores:
Pred. No.:             0              Length:        4522
Score:                 329.00         Matches:       329
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           100.0%         Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-30 (1-329) x AX076209 (1-4522)

Qy         1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy        21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286
```

```
Qy          81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy         101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy         121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy         141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy         161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy         181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy         201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy         221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy         241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy         261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy         281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy         301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy         321 SerAsnTrpAlaSerValSerCysSer 329
               |||||||||||||||||||||||||||
Db        4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033

ESULT 6
X076476
CUS       AX076476                4522 bp    DNA     linear   PAT 06-FEB-2001
EFINITION  Sequence 2 from Patent WO0104280.
CCESSION   AX076476
ERSION     AX076476.1  GI:12711028
EYWORDS    .
URCE       synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
EFERENCE   1
 AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
 TITLE     Vaccine against lentiviral infections, such as the feline immune
           deficiency virus of the cat
 JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
           Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
           Universitaet Zuerich (CH)
EATURES             Location/Qualifiers
    source          1. .4522
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="IL-12p40"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          4522
Score:                    329.00         Matches:         329
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AX076476 (1-4522)

Qy           1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy          21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy          41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy          61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy          81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy         101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy         121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy         141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy         161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy         181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy         201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy         221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy         241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy         261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy         281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946
```

```
Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033

RESULT 7
AR595967
LOCUS       AR595967                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 55 from patent US 6818444.
ACCESSION   AR595967
VERSION     AR595967.1  GI:56646948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 55 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0             Length:         985
Score:                    328.00        Matches:        328
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              99.7%         Indels:         0
DB:                       2             Gaps:           0

US-10-821-670A-30 (1-329) x AR595967 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 8
AR595968/c
LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0             Length:         985
Score:                    328.00        Matches:        328
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              99.7%         Indels:         0
DB:                       2             Gaps:           0

US-10-821-670A-30 (1-329) x AR595968 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866
```

```
Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
               |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2
```

```
RESULT 9
AR242435
LOCUS       AR242435               2193 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6472509.
ACCESSION   AR242435
VERSION     AR242435.1  GI:27288852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          2193
Score:                    317.00         Matches:         317
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              96.4%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR242435 (1-2193)

Qy         13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

Qy         33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy         53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy         73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

Qy         93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

Qy        113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

Qy        133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

Qy        153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

Qy        173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

Qy        193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

Qy        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879
```

```
Qy        273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

Qy        293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

Qy        313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 10
AR280203
LOCUS       AR280203                2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          2193
Score:                    317.00         Matches:         317
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              96.4%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR280203 (1-2193)

Qy         13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

Qy         33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy         53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy         73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

Qy         93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

Qy        113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

Qy        133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

Qy        153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

Qy        173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

Qy        193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

Qy        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

Qy        273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

Qy        293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

Qy        313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 11
AR322418
LOCUS       AR322418                2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          2193
Score:                    317.00         Matches:         317
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              96.4%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR322418 (1-2193)

Qy         13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159
```

```
Qy         33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy         53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy         73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

Qy         93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

Qy        113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

Qy        133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

Qy        153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

Qy        173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

Qy        193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

Qy        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

Qy        273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

Qy        293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

Qy        313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050
```

```
ESULT 12
R242436
CUS       AR242436                921 bp    mRNA    linear   PAT 20-DEC-2002
EFINITION  Sequence 6 from patent US 6472509.
CCESSION   AR242436
ERSION     AR242436.1  GI:27288853
EYWORDS    .
URCE       Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 921)
 AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
 TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 6 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          921
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              93.3%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR242436 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
                 |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 13
AR242437
LOCUS       AR242437                 921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6472509.
ACCESSION   AR242437
VERSION     AR242437.1  GI:27288854
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 7 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:         921
Score:                    307.00         Matches:        307
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              93.3%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-30 (1-329) x AR242437 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
                 |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 14
AR280204
LOCUS       AR280204                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6518045.
ACCESSION   AR280204
VERSION     AR280204.1  GI:29715594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 6 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:         921
Score:                    307.00         Matches:        307
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              93.3%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-30 (1-329) x AR280204 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 15
R280205
OCUS       AR280205                921 bp    mRNA    linear   PAT 10-APR-2003
EFINITION  Sequence 7 from patent US 6518045.
CCESSION   AR280205
ERSION     AR280205.1  GI:29715595
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 921)
 AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
 TITLE     Feline cytokine protein
 JOURNAL   Patent: US 6518045-A 7 11-FEB-2003;
           Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
           Kumamoto-ken;
           EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          921
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              93.3%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR280205 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
)b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

)y        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

)y        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
)b        901 TGGGCATCCGTGTCCTGCAGT 921

:ESULT 16
:R322419
:OCUS       AR322419                 921 bp    mRNA    linear   PAT 17-AUG-2003
)EFINITION  Sequence 6 from patent US 6566097.
:CCESSION   AR322419
:ERSION     AR322419.1  GI:33708172
:EYWORDS    .
:OURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
:EFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 6 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
:EATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
)RIGIN

.lignment Scores:
:ed. No.:                0              Length:         921
:core:                   307.00         Matches:        307
:ercent Similarity:      100.0%         Conservative:   0
:est Local Similarity:   100.0%         Mismatches:     0
)uery Match:             93.3%          Indels:         0
)B:                      2              Gaps:           0

:S-10-821-670A-30 (1-329) x AR322419 (1-921)

)y         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

)y         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

)y         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

)y         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

)y        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

)y        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

)y        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

)y        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 17
AR322420
LOCUS       AR322420                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 7 from patent US 6566097.
ACCESSION   AR322420
VERSION     AR322420.1  GI:33708173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 7 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:               0              Length:         921
Score:                   307.00         Matches:        307
Percent Similarity:      100.0%         Conservative:   0
Best Local Similarity:   100.0%         Mismatches:     0
Query Match:             93.3%          Indels:         0
DB:                      2              Gaps:           0

US-10-821-670A-30 (1-329) x AR322420 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy          63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy          83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy         183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         323 TrpAlaSerValSerCysSer 329
               |||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 18
CU83184
CUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
EFINITION Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
CCESSION  U83184
ERSION    U83184.1  GI:2735050
YWORDS    .
URCE      Felis catus (cat)
 ORGANISM  Felis catus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
           Felinae; Felis.
EFERENCE  1  (bases 1 to 990)
 AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
           Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCDTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:                0                Length:          990
Score:                    278.00           Matches:         278
Percent Similarity:       100.0%           Conservative:    0
Best Local Similarity:    100.0%           Mismatches:      0
Query Match:              84.5%            Indels:          0
DB:                       14               Gaps:            0

US-10-821-670A-30 (1-329) x FCU83184 (1-990)

Qy          52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 ACGCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy          72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy          92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy         112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy         132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy         152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGA 513

Qy         172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy         192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy         212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

Qy        312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 19
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
    PUBMED  9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1006
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .1006
                     /gene="IL-12.p40"
     CDS             1. .990
                     /gene="IL-12.p40"
                     /note="heterodimer with IL-12 p35 chain"
                     /codon_start=1
                     /product="interleukin-12 p40 chain"
                     /protein_id="CAA69068.1"
                     /db_xref="GI:2102665"
                     /db_xref="GOA:O02744"
                     /db_xref="InterPro:IPR002996"
                     /db_xref="InterPro:IPR003530"
                     /db_xref="InterPro:IPR003961"
                     /db_xref="InterPro:IPR007110"
                     /db_xref="InterPro:IPR008957"
                     /db_xref="UniProtKB/Swiss-Prot:O02744"
                     /translation="MHPQQLVIAWLSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:              3.29e-256       Length:         1006
Score:                  217.00          Matches:        317
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            66.0%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-30 (1-329) x FCIL12P40 (1-1006)

Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933
```

```
Qy        312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 20
AR595956
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                5.31e-256      Length:          1599
Score:                    217.00         Matches:         317
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              66.0%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR595956 (1-1599)

Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

Qy        312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 21
AR595957/c
LOCUS       AR595957                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                5.31e-256      Length:          1599
Score:                    217.00         Matches:         317
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              66.0%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR595957 (1-1599)

Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327
```

```
Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

Qy        312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613
```

ESULT 22
R595948
OCUS AR595948 921 bp DNA linear PAT 15-DEC-2004
EFINITION Sequence 26 from patent US 6818444.
CCESSION AR595948
ERSION AR595948.1 GI:56646929
EYWORDS .
OURCE Unknown.
ORGANISM Unknown.
Unclassified.
EFERENCE 1 (bases 1 to 921)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 26 16-NOV-2004;
Heska Corporation; Fort Collins, CO
EATURES Location/Qualifiers
source 1. .921
/organism="unknown"
/mol_type="genomic DNA"
RIGIN

lignment Scores:
ed. No.: 1.06e-242 Length: 921
core: 206.00 Matches: 306

```
Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            62.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x AR595948 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 23
AR595949/c

```
:CUS       AR595949                 921 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 28 from patent US 6818444.
:CESSION   AR595949
ERSION     AR595949.1  GI:56646930
EYWORDS    .
:URCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 921)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 28 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
     source         1. .921
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
ed. No.:              1.06e-242      Length:        921
core:                 206.00         Matches:       306
ercent Similarity:    99.7%          Conservative:  0
st Local Similarity:  99.7%          Mismatches:    1
uery Match:           62.6%          Indels:        0
B:                    2              Gaps:          0

-10-821-670A-30 (1-329) x AR595949 (1-921)

y         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

           43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

y         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

y         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

y        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

y        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

y        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

y        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
c        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

y        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy       323 TrpAlaSerValSerCysSer 329
             |||||||||||||||||||||
Db        21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 24
AR595959
LOCUS       AR595959                 1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.8e-242       Length:        1533
Score:                  206.00         Matches:       306
Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            62.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x AR595959 (1-1533)

Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 25
R595960/c
OCUS       AR595960                1533 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 45 from patent US 6818444.
CCESSION   AR595960
ERSION     AR595960.1  GI:56646941
EYWORDS    .
OURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
EFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
     source         1. .1533
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
ed. No.:              1.8e-242        Length:         1533
core:                 206.00          Matches:        306
ercent Similarity:    99.7%           Conservative:   0
est Local Similarity: 99.7%           Mismatches:     1
uery Match:           62.6%           Indels:         0
B:                    2               Gaps:           0

S-10-821-670A-30 (1-329) x AR595960 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 26
AF054607
LOCUS       AF054607                431 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p40 subunit mRNA, partial cds.
ACCESSION   AF054607
VERSION     AF054607.1  GI:3126822
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
```

```
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
          Felinae; Felis.
FERENCE   1  (bases 1 to 431)
 AUTHORS  Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
          Day,M.J.
 TITLE    Cytokine mRNA expression in lesions in cats with chronic
          gingivostomatitis
 JOURNAL  Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
  PUBMED  10391845
FERENCE   2  (bases 1 to 431)
 AUTHORS  Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
          Harbour,D.A.
 TITLE    Direct Submission
 JOURNAL  Submitted (19-MAR-1998) Clinical Veterinary Science, University of
          Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
ATURES             Location/Qualifiers
    source         1. .431
                   /organism="Felis catus"
                   /mol_type="mRNA"
                   /db_xref="taxon:9685"
                   /cell_line="FL4"
                   /cell_type="T cell"
                   /note="persistant FIV infection"
    CDS            <1. .>431
                   /codon_start=1
                   /product="interleukin 12 p40 subunit"
                   /protein_id="AAC15980.1"
                   /db_xref="GI:3126823"
                   /translation="CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEA
                   KNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYT
                   VECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRD"
RIGIN

lignment Scores:
ed. No.:              1.68e-144       Length:         431
core:                 126.00          Matches:        126
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
uery Match:           38.3%           Indels:         0
B:                    14              Gaps:           0

-10-821-670A-30 (1-329) x AF054607 (1-431)

       107 LysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLys 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        52 AAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAG 111

       127 IlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThr 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       112 ATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 171

       147 AlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGln 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       172 GCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAA 231

       167 GlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAsp 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       232 GGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGAT 291

       187 TyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSer 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       292 TATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGC 351

       207 LeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       352 CTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGC 411

       227 SerPhePheIleArgAsp 232
           ||||||||||||||||||
       412 AGCTTCTTCATCAGGGAC 429

ESULT 27
```

```
AX154603
LOCUS       AX154603                990 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 7 from Patent WO0140257.
ACCESSION   AX154603
VERSION     AX154603.1  GI:14536186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 7 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              5.62e-53        Length:         990
Score:                  52.00           Matches:        52
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            15.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x AX154603 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCTGACCCACCCAAGAACTTG 726

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGlu 254
              ||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTAAAGAATTCTCGACACGTGGAG 762

RESULT 28
AX154600
LOCUS       AX154600                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0140257.
ACCESSION   AX154600
VERSION     AX154600.1  GI:14536183
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 4 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              2.77e-49        Length:         984
Score:                  49.00           Matches:        49
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            14.9%           Indels:         0
```

```
)B:                    2             Gaps:          0

'S-10-821-670A-30 (1-329) x AX154600 (1-984)

'y        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        370 AAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGG 429

'y        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        430 TGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCT 489

'y        164 AspProGlnGlyValThrCysGlyAla 172
              ||||||||||||||||||||||||||||
)b        490 GACCCCCAAGGGGTGACTTGTGGAGCC 516

'ESULT 29
X154599
OCUS       AX154599                 984 bp    DNA     linear   PAT 22-JUN-2001
)EFINITION  Sequence 3 from Patent WO0140257.
CCESSION   AX154599
'ERSION     AX154599.1  GI:14536182
'EYWORDS    .
'OURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
'EFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 3 07-JUN-2001;
            Maxygen, Inc. (US)
'EATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
)RIGIN

.lignment Scores:
'red. No.:               1.16e-40       Length:         984
.core:                   42.00          Matches:        42
'ercent Similarity:      100.0%         Conservative:   0
.est Local Similarity:   100.0%         Mismatches:     0
)uery Match:             12.8%          Indels:         0
)B:                      2              Gaps:           0

'S-10-821-670A-30 (1-329) x AX154599 (1-984)

)y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

)y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACTTG 726

)y        243 GlnLeu 244
              ||||||
)b        727 CAGCTG 732

'ESULT 30
.Y191829
.OCUS       AY191829                 972 bp    mRNA    linear   SYN 04-FEB-2003
)EFINITION  Synthetic construct evolved IL-12 p40 precursor, mRNA, partial cds.
.CCESSION   AY191829
'ERSION     AY191829.1  GI:27729525
'EYWORDS    .
'OURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
'EFERENCE   1  (bases 1 to 972)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Optimized expression and specific activity of IL-12 by directed
            molecular evolution
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
  PUBMED    12529500
REFERENCE   2  (bases 1 to 972)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
            Drive, Redwood City, CA 94063, USA
FEATURES             Location/Qualifiers
     source          1. .972
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .>972
                     /codon_start=1
                     /transl_table=11
                     /product="evolved IL-12 p40 precursor"
                     /protein_id="AAO19112.1"
                     /db_xref="GI:27729526"
                     /translation="MCHQQLVISWFSLVLLASPLMAIWELKKDVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKNKSFLKCEAKNYSGRFTCWWLTTISTDLKFSVKSSR
                     GSTDPRGVTCGTATLSEDLGEYKKYRVECQEGSACPAAEESLPIEVVLEAVHKLKYEN
                     YTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWGYPDTWSTPHSYFSLTFCIQVQGK
                     SKREKKDRIFTDKTSATVICRKNAKIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide     1. .66
     mat_peptide     67. .972
                     /product="evolved IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:               1.95e-39       Length:         972
Score:                   41.00          Matches:        41
Percent Similarity:      100.0%         Conservative:   0
Best Local Similarity:   100.0%         Mismatches:     0
Query Match:             12.5%          Indels:         0
DB:                      8              Gaps:           0

US-10-821-670A-30 (1-329) x AY191829 (1-972)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

Qy        257 Trp 257
              |||
Db        754 TGG 756

RESULT 31
AX154597
LOCUS       AX154597                 975 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0140257.
ACCESSION   AX154597
VERSION     AX154597.1  GI:14536180
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 1 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .975
                     /organism="synthetic construct"
```

```
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:                1.96e-39       Length:         975
Score:                    41.00          Matches:        41
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              12.5%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-30 (1-329) x AX154597 (1-975)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 256
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

Qy         257 Trp 257
               |||
Db         754 TGG 756

RESULT 32
AX107654
LOCUS       AB107654                993 bp    mRNA    linear   MAM 29-APR-2004
DEFINITION  Lama glama IL-12 p40 mRNA for interleukin 12 p40 subunit, complete
            cds.
ACCESSION   AB107654
VERSION     AB107654.1  GI:29603618
KEYWORDS    .
SOURCE      Lama glama (llama)
  ORGANISM  Lama glama
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
            Camelidae; Lama.
REFERENCE   1
  AUTHORS   Odbileg,R., Lee,S.I., Yoshida,R., Chang,K.S., Ohashi,K.,
            Sugimoto,C. and Onuma,M.
  TITLE     Cloning and sequence analysis of llama cytokines related to
            cell-mediated immunity
  JOURNAL   Vet. Immunol. Immunopathol. 99 (1-2), 1-10 (2004)
    PUBMED  15113649
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Ohashi,K., Raadan,O. and Lee,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2003) Kazuhiko Ohashi, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control; Kita-ku Kita 18 Nishi 9, Sapporo, Hokkaido 060-0818, Japan
            (E-mail:okazu@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
            Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Lama glama"
                     /mol_type="mRNA"
                     /db_xref="taxon:9844"
                     /sex="Female"
                     /cell_type="PBMC"
                     /country="Japan"
     gene            1. .993
                     /gene="IL-12 p40"
     CDS             1. .993
                     /gene="IL-12 p40"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit"
                     /protein_id="BAC75391.1"
                     /db_xref="GI:29603619"
                     /translation="MHPQQLVVSWFSLVLLASPIMAIWELEKNVYVVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDHSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGVWSTDILKKDQKEPKSKTFLKCEAKNYSGHFTCWWLTAVSTDLKFSVKSS
                     RGSSDPRGVTCGAATLSAERVGVEHRDSWKYTVECQEGSSCPAAEESLPIELVVEAVH
                     KLKYENYSSSFFIRDIIRPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFC
                     VQVQGKHKREKKDKLFVDQTSAKVTCPKDASIRVQARDRYYSSSWSEWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:                5.81e-37       Length:         993
Score:                    39.00          Matches:        39
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              11.9%          Indels:         0
DB:                       14             Gaps:           0

US-10-821-670A-30 (1-329) x AB107654 (1-993)

Qy         236 ProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluVal 255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         709 CCAGACCCACCCAAGAATCTGCAGCTGAAGCCATTGAAGAATTCTCGGCACGTGGAGGTC 768

Qy         256 SerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPhe 274
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         769 AGCTGGGAGTACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACGTTT 825

RESULT 33
AY234218
LOCUS       AY234218                1005 bp    mRNA    linear   PRI 07-APR-2003
DEFINITION  Papio anubis interleukin-12 alpha p40 subunit precursor (IL12a)
            mRNA, complete cds.
ACCESSION   AY234218
VERSION     AY234218.1  GI:29569754
KEYWORDS    .
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Nonhuman primate cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2003) Pathology & Laboratory Medicine, Emory
            University School of Medicine, Woodruff Memorial Building Rm 2339,
            1639 Pierce Drive, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Papio anubis"
                     /mol_type="mRNA"
                     /db_xref="taxon:9555"
     gene            1. .1005
                     /gene="IL12a"
     CDS             9. .995
                     /gene="IL12a"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit precursor"
                     /protein_id="AAO85331.1"
                     /db_xref="GI:29569755"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQAEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
     sig_peptide     9. .74
                     /gene="IL12a"
     mat_peptide     75. .992
                     /gene="IL12a"
                     /product="interleukin-12 alpha p40 subunit"
ORIGIN
```

```
Alignment Scores:
Seq. No.:                5.88e-37        Length:          1005
Score:                   39.00           Matches:         39
Percent Similarity:      100.0%          Conservative:    0
Best Local Similarity:   100.0%          Mismatches:      0
Query Match:             11.9%           Indels:          0
DB:                      5               Gaps:            0

US-10-821-670A-30 (1-329) x AY234218 (1-1005)

Qy        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 701

Qy        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 758

RESULT 34
CTU19834
LOCUS       CTU19834                1005 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Cercocebus torquatus interleukin-12 alpha p40 subunit (IL-12a)
            mRNA, complete cds.
ACCESSION   U19834
VERSION     U19834.1  GI:644785
KEYWORDS    .
SOURCE      Cercocebus torquatus (red-crowned mangabey)
  ORGANISM  Cercocebus torquatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Cercocebus.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Cercocebus torquatus"
                     /mol_type="mRNA"
                     /sub_species="atys"
                     /db_xref="taxon:9530"
                     /clone="FPn IL-12a"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .1005
                     /gene="IL-12a"
     CDS             9. .995
                     /gene="IL-12a"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit"
                     /protein_id="AAA86701.1"
                     /db_xref="GI:644786"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LPHKKEDGIWSTDILKDQKEPKNETFLRCEAKNYSGRITCWWLSTISTDLTFSIISSR
                     GSSNPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWNEWTSVPCS"
ORIGIN

Alignment Scores:
Seq. No.:                5.88e-37        Length:          1005
Score:                   39.00           Matches:         39
Percent Similarity:      100.0%          Conservative:    0
Best Local Similarity:   100.0%          Mismatches:      0
Query Match:             11.9%           Indels:          0
DB:                      5               Gaps:            0

US-10-821-670A-30 (1-329) x CTU19834 (1-1005)

Qy        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 701

Qy        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 758

RESULT 35
MMU19841
LOCUS       MMU19841                1080 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Macaca mulatta interleukin-12 alpha (IL-12a) mRNA, complete cds.
ACCESSION   U19841
VERSION     U19841.1  GI:644799
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1080)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 1080)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1080
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /clone="RSo IL-12a clone 4"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .1080
                     /gene="IL-12a"
     CDS             13. .999
                     /gene="IL-12a"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 alpha"
                     /protein_id="AAB60397.1"
                     /db_xref="GI:644800"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
     variation       329
                     /gene="IL-12a"
                     /replace="t"
     variation       405
                     /gene="IL-12a"
                     /replace="c"
     variation       519
                     /gene="IL-12a"
                     /replace="a"
     variation       629
                     /gene="IL-12a"
                     /note="Leu to Pro"
                     /replace="c"
     variation       665
```

```
                     /gene="IL-12a"
                     /note="Leu to Pro"
                     /replace="c"
     variation       714
                     /gene="IL-12a"
                     /replace="g"
     variation       878
                     /gene="IL-12a"
                     /note="Ile to Thr"
                     /replace="c"
     variation       895
                     /gene="IL-12a"
                     /note="Ser to Pro"
                     /replace="c"
?IGIN

lignment Scores:
ted. No.:              6.34e-37       Length:        1080
core:                  39.00          Matches:       39
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.9%          Indels:        0
B:                     5              Gaps:          0

S-10-821-670A-30 (1-329) x MMU19841 (1-1080)

Y        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        646 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 705

Y        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        706 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 762

ESULT 36
?595965
LCUS       AR595965                 921 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 52 from patent US 6818444.
CCESSION   AR595965
ERSION     AR595965.1  GI:56646946
YWORDS     .
URCE       Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 921)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 52 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES              Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
?IGIN

lignment Scores:
ted. No.:              1.56e-34       Length:        921
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.2%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-30 (1-329) x AR595965 (1-921)

Y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
c        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651
```

```
RESULT 37
AR595966/c
LOCUS       AR595966                 921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 54 from patent US 6818444.
ACCESSION   AR595966
VERSION     AR595966.1  GI:56646947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 54 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:             1.56e-34       Length:        921
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           11.2%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-30 (1-329) x AR595966 (1-921)

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 38
BD171282
LOCUS       BD171282                 924 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171282
VERSION     BD171282.1  GI:28412572
KEYWORDS    JP 2002241398-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 924)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 2 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/2
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .924
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
```

```
ed. No.:              1.57e-34        Length:         924
core:                 37.00           Matches:        37
ercent Similarity:    100.0%          Conservative:   0
est Local Similarity: 100.0%          Mismatches:     0
uery Match:           11.2%           Indels:         0
B:                    2               Gaps:           0

S-10-821-670A-30 (1-329) x BD171282 (1-924)

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        544 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 603

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        604 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 654

ESULT 39
R595969
OCUS        AR595969                 987 bp    DNA     linear   PAT 15-DEC-2004
EFINITION   Sequence 58 from patent US 6818444.
CCESSION    AR595969
ERSION      AR595969.1  GI:56646950
EYWORDS     .
OURCE       Unknown.
  ORGANISM  Unknown.
            Unclassified.
EFERENCE    1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 58 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
     source         1. .987
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
ed. No.:              1.68e-34        Length:         987
core:                 37.00           Matches:        37
ercent Similarity:    100.0%          Conservative:   0
est Local Similarity: 100.0%          Mismatches:     0
uery Match:           11.2%           Indels:         0
B:                    2               Gaps:           0

S-10-821-670A-30 (1-329) x AR595969 (1-987)

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 40
R595970/c
OCUS        AR595970                 987 bp    DNA     linear   PAT 15-DEC-2004
EFINITION   Sequence 60 from patent US 6818444.
CCESSION    AR595970
ERSION      AR595970.1  GI:56646951
EYWORDS     .
OURCE       Unknown.
  ORGANISM  Unknown.
            Unclassified.
EFERENCE    1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 60 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
     source         1. .987
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:            1.68e-34        Length:         987
Score:                37.00           Matches:        37
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          11.2%           Indels:         0
DB:                   2               Gaps:           0

US-10-821-670A-30 (1-329) x AR595970 (1-987)

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 41
AR151061
LOCUS       AR151061                 990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6231850.
ACCESSION   AR151061
VERSION     AR151061.1  GI:15117111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
FEATURES            Location/Qualifiers
     source         1. .990
                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:            1.68e-34        Length:         990
Score:                37.00           Matches:        37
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          11.2%           Indels:         0
DB:                   2               Gaps:           0

US-10-821-670A-30 (1-329) x AR151061 (1-990)

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 42
AR151071
LOCUS       AR151071                 990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6231850.
ACCESSION   AR151071
VERSION     AR151071.1  GI:15117121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
```

```
 JOURNAL   Patent: US 6231850-A 11 15-MAY-2001;
EATURES             Location/Qualifiers
    source          1. .990
                    /organism="unknown"
                    /mol_type="unassigned DNA"
?IGIN

lignment Scores:
red. No.:               1.68e-34        Length:         990
core:                   37.00           Matches:        37
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             11.2%           Indels:         0
B:                      2               Gaps:           0

5-10-821-670A-30 (1-329) x AR151071 (1-990)

Y       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
D       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Y       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
D       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 43
'014653
'CUS        BD014653                  990 bp    DNA     linear   PAT 27-AUG-2002
EFINITION   Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
CCESSION    BD014653
ERSION      BD014653.1  GI:22555436
EYWORDS     JP 2001161378-A/1.
OURCE       Canis sp.
 ORGANISM   Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
EFERENCE    1  (bases 1 to 990)
 AUTHORS    Okano,F.
 TITLE      Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
 JOURNAL    Patent: JP 2001161378-A 1 19-JUN-2001;
            TORAY INDUSTRIES INC
OMMENT      OS   Canis sp. (dog)
            PN   JP 2001161378-A/1
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
            FT   mat_peptide     (67). .(987).
EATURES             Location/Qualifiers
    source          1. .990
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
?IGIN

lignment Scores:
red. No.:               1.68e-34        Length:         990
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x BD014653 (1-990)

Qy      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 44
BD014663
LOCUS       BD014663                  990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014663
VERSION     BD014663.1  GI:22555446
KEYWORDS    JP 2001161378-A/11.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 11 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/11
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
            FT   mat_peptide     (67). .(987).
FEATURES            Location/Qualifiers
     source         1. .990
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:              1.68e-34        Length:         990
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x BD014663 (1-990)

Qy      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 45
E15017
LOCUS       E15017                  990 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 40kDa subunit,complete cds.
ACCESSION   E15017
VERSION     E15017.1  GI:5709700
KEYWORDS    JP 1998036397-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 1 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/1
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .990
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .990
            FT                   /product='interleukin 12 40kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"

ORIGIN

Alignment Scores:
Pred. No.:              1.68e-34        Length:         990
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x E15017 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 46
AR316460
LOCUS       AR316460                990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6562334.
ACCESSION   AR316460
VERSION     AR316460.1  GI:33695288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 1 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.68e-34        Length:         990
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x AR316460 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 47
AR316470
LOCUS       AR316470                990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6562334.
ACCESSION   AR316470
VERSION     AR316470.1  GI:33695298
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 11 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.68e-34        Length:         990
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x AR316470 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

```
ESULT 48
FU49100
:CUS        CFU49100                1015 bp    mRNA    linear   MAM 13-MAR-1996
EFINITION   Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
:CESSION    U49100
ERSION      U49100.1  GI:1223907
EYWORDS     .
URCE        Canis familiaris (dog)
 ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
EFERENCE    1  (bases 1 to 1015)
 AUTHORS    Belke-Louis,G.F. and Buettner,M.
 TITLE      Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
 JOURNAL    Unpublished
EFERENCE    2  (bases 1 to 1015)
 AUTHORS    Belke-Louis,G.F.
 TITLE      Direct Submission
 JOURNAL    Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
EATURES             Location/Qualifiers
     source         1. .1015
                    /organism="Canis familiaris"
                    /mol_type="mRNA"
                    /db_xref="taxon:9615"
     CDS            1. .990
                    /codon_start=1
                    /product="interleukin-12 p40 subunit"
                    /protein_id="AAA92059.1"
                    /db_xref="GI:1223908"
                    /translation="MHPQQLVISWFSLVLLASSLMTIWELEKDVYVVELDWHPDAPGE
                    MVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLL
                    LIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                    GFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHK
                    LKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCV
                    QAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCS"
IGIN

lignment Scores:
ed. No.:              1.73e-34       Length:        1015
core:                 37.00          Matches:       37
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            11.2%          Indels:        0
:                     14             Gaps:          0

-10-821-670A-30 (1-329) x CFU49100 (1-1015)

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
c        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 49
R595973
:CUS        AR595973                1533 bp    DNA     linear   PAT 15-DEC-2004
EFINITION   Sequence 66 from patent US 6818444.
:CESSION    AR595973
ERSION      AR595973.1  GI:56646954
EYWORDS     .
:URCE       Unknown.
 ORGANISM   Unknown.
            Unclassified.
EFERENCE    1  (bases 1 to 1533)
 AUTHORS    Wonderling,R.S. and Boroughs,K.L.
 TITLE      Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL    Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.65e-34       Length:        1533
Score:                  37.00          Matches:       37
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.2%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x AR595973 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 50
AR595974/c
LOCUS       AR595974                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.65e-34       Length:        1533
Score:                  37.00          Matches:       37
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.2%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x AR595974 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 51
AR595971
LOCUS       AR595971                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

```
           Unclassified.
EFERENCE   1  (bases 1 to 1599)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
     source         1. .1599
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
red. No.:              2.76e-34      Length:        1599
core:                  37.00         Matches:       37
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            11.2%         Indels:        0
B:                     2             Gaps:          0

S-10-821-670A-30 (1-329) x AR595971 (1-1599)

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 52
R595972/c
OCUS       AR595972               1599 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 63 from patent US 6818444.
CCESSION   AR595972
ERSION     AR595972.1  GI:56646953
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 1599)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
     source         1. .1599
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
red. No.:              2.76e-34      Length:        1599
core:                  37.00         Matches:       37
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            11.2%         Indels:        0
B:                     2             Gaps:          0

S-10-821-670A-30 (1-329) x AR595972 (1-1599)

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

ESULT 53
D171281
OCUS       BD171281               2154 bp    DNA     linear   PAT 18-FEB-2003
EFINITION  Novel canine cytokine protein.
ACCESSION  BD171281
VERSION    BD171281.1  GI:28412571
KEYWORDS   JP 2002241398-A/1.
SOURCE     unidentified
  ORGANISM unidentified
           unclassified sequences.
REFERENCE  1  (bases 1 to 2154)
  AUTHORS  Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE    Novel canine cytokine protein
  JOURNAL  Patent: JP 2002241398-A 1 28-AUG-2002;
           CHEMO SERO THERAPEUT RES INST
COMMENT    OS   Canine splenocyte
           PN   JP 2002241398-A/1
           PD   28-AUG-2002
           PF   03-JUN-1997 JP 1997161936
           PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
             C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
           C12P21/02//
           PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
             Strandedness: Double;
           CC   Topology: Linear;
           FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .2154
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:             3.76e-34      Length:        2154
Score:                 37.00         Matches:       37
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           11.2%         Indels:        0
DB:                    2             Gaps:          0

US-10-821-670A-30 (1-329) x BD171281 (1-2154)

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 720

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 771

RESULT 54
AR596011
LOCUS      AR596011               2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION Sequence 107 from patent US 6818444.
ACCESSION  AR596011
VERSION    AR596011.1  GI:56646992
KEYWORDS   .
SOURCE     Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 2267)
  AUTHORS  Wonderling,R.S. and Boroughs,K.L.
  TITLE    Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL  Patent: US 6818444-A 107 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .2267
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:             3.96e-34      Length:        2267
Score:                 37.00         Matches:       37
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
```

```
uery Match:            11.2%          Indels:        0
:                      2              Gaps:          0

S-10-821-670A-30 (1-329) x AR596011 (1-2267)

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
c        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

ESULT 55
R596012/c
OCUS       AR596012               2267 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 109 from patent US 6818444.
CCESSION   AR596012
ERSION     AR596012.1  GI:56646993
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 2267)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 109 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
    source          1. .2267
                    /organism="unknown"
                    /mol_type="genomic DNA"
IGIN

lignment Scores:
red. No.:              3.96e-34       Length:        2267
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.2%          Indels:        0
:                      2              Gaps:          0

S-10-821-670A-30 (1-329) x AR596012 (1-2267)

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
c       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

ESULT 56
F091134
OCUS       AF091134               446 bp    mRNA    linear   MAM 04-AUG-1999
EFINITION  Canis familiaris interleukin-12 p40 mRNA, partial cds.
CCESSION   AF091134
ERSION     AF091134.1  GI:5690205
EYWORDS    .
OURCE      Canis familiaris (dog)
 ORGANISM  Canis familiaris
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
           Canis.
EFERENCE   1  (bases 1 to 446)
 AUTHORS   German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J.
 TITLE     Cloning and sequencing of canine IL-12 p40 mRNA
 JOURNAL   Unpublished
EFERENCE   2  (bases 1 to 446)
 AUTHORS   German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J.
 TITLE     Direct Submission
 JOURNAL   Submitted (12-SEP-1998) Department of Clinical Veterinary Science,
           University of Bristol, Langford House, Langford, Bristol, North
           Somerset BS40 5DU, United Kingdom
FEATURES             Location/Qualifiers
     source          1. .446
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             <1. .>446
                     /note="Il-12 p40"
                     /codon_start=1
                     /product="interleukin-12 p40"
                     /protein_id="AAD46992.1"
                     /db_xref="GI:5690206"
                     /translation="LGAGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIW
                     STDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTC
                     GAVTLSAERVRVDNRDYNKYTVECQEGSACPSAEESLPIEVVVDAIP"
ORIGIN

Alignment Scores:
Pred. No.:             1.26e-33       Length:        446
Score:                 36.00          Matches:       36
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           10.9%          Indels:        0
DB:                    14             Gaps:          0

US-10-821-670A-30 (1-329) x AF091134 (1-446)

Qy       119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       151 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 210

Qy       139 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db       211 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 258

RESULT 57
AF333121
LOCUS       AF333121               452 bp    mRNA    linear   MAM 06-FEB-2001
DEFINITION  Canis familiaris interleukin 12 subunit p40 mRNA, partial cds.
ACCESSION   AF333121
VERSION     AF333121.1  GI:12667429
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Expression of canine interleukin-12 subunit p40 mRNA in a
            continuous macrophage cell line
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JAN-2001) Department of Veterinary Pathology,
            Justus-Liebig-University of Giessen, Frankfurter Strasse 96,
            Giessen 35392, Germany
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /cell_line="DH 82"
                     /cell_type="macrophage"
                     /note="amplified using primer pair p77s/p34as"
     CDS             <1. .>452
                     /codon_start=2
                     /product="interleukin 12 subunit p40"
                     /protein_id="AAK01441.1"
                     /db_xref="GI:12667430"
                     /translation="TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK
                     GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST
```

DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
ORIGIN

Alignment Scores:
Pred. No.: 1.28e-33 Length: 452
Score: 36.00 Matches: 36
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.9% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-30 (1-329) x AF333121 (1-452)

Qy 119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 212 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 271

Qy 139 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 272 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 319

RESULT 58
AF349536
LOCUS AF349536 588 bp mRNA linear MAM 17-MAY-2001
DEFINITION Canis familiaris interleukin-12 subunit p40 mRNA, partial cds.
ACCESSION AF349536
VERSION AF349536.1 GI:14133584
KEYWORDS .
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 588)
AUTHORS Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
TITLE Sequence of canine interleukin-12-p40 mRNA in DH82-cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 588)
AUTHORS Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2001) Institute of Pathology,
Justus-Liebig-University, Frankfurter Str. 96, Giessen 35392,
Germany
FEATURES Location/Qualifiers
source 1. .588
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/cell_line="DH82"
CDS <1. .>588
/codon_start=3
/product="interleukin-12 subunit p40"
/protein_id="AAK54070.1"
/db_xref="GI:14133585"
/translation="QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVV
LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIH
KKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFS
DPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
ORIGIN

Alignment Scores:
Pred. No.: 1.68e-33 Length: 588
Score: 36.00 Matches: 36
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.9% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-30 (1-329) x AF349536 (1-588)

Qy 119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 348 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 407

Qy 139 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 408 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 455

RESULT 59
BD021808
LOCUS BD021808 906 bp DNA linear PAT 27-AUG-2002
DEFINITION Natural killer stimulatory factor.
ACCESSION BD021808
VERSION BD021808.1 GI:22563031
KEYWORDS JP 2001245678-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 906)
AUTHORS Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
Hewick,R.M.
TITLE Natural killer stimulatory factor
JOURNAL Patent: JP 2001245678-A 1 11-SEP-2001;
GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT OS Unidentified
PN JP 2001245678-A/1
PD 11-SEP-2001
PF 10-JAN-2001 JP 2001002839
PR 10-NOV-1988 US 269945,07-FEB-1989 US 307817 PI
GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C PI
CLARK,
PI GORDON G WONG,RODNEY M HEWICK
PC C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
PC A61P43/00,
PC C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
Natural killer stimulatory factor
FH Key Location/Qualifiers
FT source 1. .906
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1. .906
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.: 4.47e-32 Length: 906
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-30 (1-329) x BD021808 (1-906)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 60
BD021809
LOCUS BD021809 906 bp DNA linear PAT 27-AUG-2002
DEFINITION Natural killer stimulatory factor.
ACCESSION BD021809
VERSION BD021809.1 GI:22563032
KEYWORDS JP 2001245678-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 906)
AUTHORS Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and

```
          Hewick,R.M.
 TITLE    Natural killer stimulatory factor
 JOURNAL  Patent: JP 2001245678-A 2 11-SEP-2001;
          GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
:MMENT    OS   Unidentified
          PN   JP 2001245678-A/2
          PD   11-SEP-2001
          PF   10-JAN-2001 JP 2001002839
          PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
          GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
          CLARK,
          PI   GORDON G WONG,RODNEY M HEWICK
          PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
          PC   A61P43/00,
          PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
          Natural killer stimulatory factor
          FH   Key             Location/Qualifiers
          FT   source          1. .906
          FT                   /organism='Unidentified'.
EATURES              Location/Qualifiers
    source           1. .906
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
RIGIN

lignment Scores:
red. No.:              4.47e-32       Length:        906
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            10.6%          Indels:        0
B:                     2              Gaps:          0

3-10-821-670A-30 (1-329) x BD021809 (1-906)

y        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

y        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
         738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

:SULT 61
·154602
 CUS       AX154602                975 bp    DNA     linear   PAT 22-JUN-2001
EFINITION  Sequence 6 from Patent WO0140257.
:CESSION   AX154602
ERSION     AX154602.1  GI:14536185
EYWORDS    .
URCE       synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
EFERENCE   1
 AUTHORS   Leong,S.R. and Punnonen,J.
 TITLE     Cytokine polypeptides and nucleic acids
 JOURNAL   Patent: WO 0140257-A 6 07-JUN-2001;
           Maxygen, Inc. (US)
EATURES              Location/Qualifiers
    source           1. .975
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
RIGIN

lignment Scores:
red. No.:              4.82e-32       Length:        975
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            10.6%          Indels:        0
```

```
DB:                    2              Gaps:          0

US-10-821-670A-30 (1-329) x AX154602 (1-975)

Qy       128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       382 TTTCTAAAGTGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGGTGGCTGACGGCA 441

Qy       148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
             |||||||||||||||||||||||||||||||||||||||||||||
Db       442 ATCAGTACTGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

RESULT 62
AR008950
LOCUS       AR008950                987 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5756085.
ACCESSION   AR008950
VERSION     AR008950.1  GI:3967755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 1 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:             4.88e-32       Length:        987
Score:                 35.00          Matches:       35
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           10.6%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-30 (1-329) x AR008950 (1-987)

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 63
BD007070
LOCUS       BD007070                987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007070
VERSION     BD007070.1  GI:18635441
KEYWORDS    JP 2001503257-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 1 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
```

```
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
EATURES             Location/Qualifiers
     source         1. .987
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
RIGIN

lignment Scores:
ed. No.:              4.88e-32       Length:        987
core:                 35.00          Matches:       35
ercent Similarity:    100.0%         Conservative:  0
est Local Similarity: 100.0%         Mismatches:    0
uery Match:           10.6%          Indels:        0
B:                    2              Gaps:          0

S-10-821-670A-30 (1-329) x BD007070 (1-987)

Y        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Y        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||||
b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 64
0007076
OCUS       BD007076                 987 bp    DNA     linear   PAT 31-JAN-2002
EFINITION  Gene expression and delivery systems and uses.
CCESSION   BD007076
ERSION     BD007076.1  GI:18635447
EYWORDS    JP 2001503258-A/1.
OURCE      unidentified
 ORGANISM  unidentified
           unclassified sequences.
EFERENCE   1  (bases 1 to 987)
  AUTHORS  Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE    Gene expression and delivery systems and uses
  JOURNAL  Patent: JP 2001503258-A 1 13-MAR-2001;
           BARENTISU INC
OMMENT     OS   Unidentified
           PN   JP 2001503258-A/1
           PD   13-MAR-2001
           PF   10-OCT-1997 JP 1998519520
           PR   18-OCT-1996 US    60/028687
           PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
           C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
           C12N15/00
           CC   Strandedness: Single;
           CC   Topology: Linear;
           FH   Key             Location/Qualifiers
           FT   source          1. .987
           FT                   /organism='Unidentified'.
EATURES             Location/Qualifiers
     source         1. .987
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
RIGIN

lignment Scores:
ed. No.:              4.88e-32       Length:        987
core:                 35.00          Matches:       35
ercent Similarity:    100.0%         Conservative:  0
est Local Similarity: 100.0%         Mismatches:    0
uery Match:           10.6%          Indels:        0
B:                    2              Gaps:          0
```

```
US-10-821-670A-30 (1-329) x BD007076 (1-987)

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 65
BD007077
LOCUS       BD007077                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007077
VERSION     BD007077.1  GI:18635448
KEYWORDS    JP 2001503258-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 2 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/2
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              4.88e-32       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x BD007077 (1-987)

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 66
BD007078
LOCUS       BD007078                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007078
VERSION     BD007078.1  GI:18635449
KEYWORDS    JP 2001503258-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
```

```
            unclassified sequences.
EFERENCE    1  (bases 1 to 987)
 AUTHORS    Nodosutoromu,J., Freemark,B. and Dishupande,D.
 TITLE      Gene expression and delivery systems and uses
 JOURNAL    Patent: JP 2001503258-A 3 13-MAR-2001;
            BARENTISU INC
:MMENT      OS   Unidentified
            PN   JP 2001503258-A/3
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
:ATURES             Location/Qualifiers
    source          1. .987
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
:IGIN

lignment Scores:
ted. No.:               4.88e-32        Length:         987
core:                   35.00           Matches:        35
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             10.6%           Indels:         0
B:                      2               Gaps:           0

3-10-821-670A-30 (1-329) x BD007078 (1-987)

y       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

y       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
c       706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

ESULT 67
:136034
:CUS        BD136034                987 bp    DNA     linear   PAT 18-SEP-2002
EFINITION   Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
:CESSION    BD136034
ERSION      BD136034.1  GI:23230979
EYWORDS     JP 2002506647-A/1.
:URCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
FERENCE     1  (bases 1 to 987)
 AUTHORS    Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
 TITLE      Interferon alpha plasmid and delivery system and method of
            preparing and using the same
 JOURNAL    Patent: JP 2002506647-A 1 05-MAR-2002;
            VALENTIS INC
:MMENT      OS   Homo sapiens (human)
            PN   JP 2002506647-A/1
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                 preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Homo sapiens (human)'.
FEATURES            Location/Qualifiers
     source         1. .987
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              4.88e-32        Length:         987
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x BD136034 (1-987)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 68
BD136035
LOCUS       BD136035                987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136035
VERSION     BD136035.1  GI:23230980
KEYWORDS    JP 2002506647-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 2 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/2
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: all codons optimized
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .987
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              4.88e-32        Length:         987
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
```

```
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            10.6%           Indels:        0
B:                     2               Gaps:          0

S-10-821-670A-30 (1-329) x BD136035 (1-987)

y        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

y        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
b        706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

ESULT 69
D136036
OCUS       BD136036                 987 bp    DNA     linear   PAT 18-SEP-2002
EFINITION  Interferon alpha plasmid and delivery system and method of
           preparing and using the same.
CCESSION   BD136036
ERSION     BD136036.1  GI:23230981
EYWORDS    JP 2002506647-A/3.
OURCE      synthetic construct
  ORGANISM synthetic construct
           other sequences; artificial sequences.
EFERENCE   1  (bases 1 to 987)
  AUTHORS  Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE    Interferon alpha plasmid and delivery system and method of
           preparing and using the same
  JOURNAL  Patent: JP 2002506647-A 3 05-MAR-2002;
           VALENTIS INC
OMMENT     OS   Artificial Sequence
           PN   JP 2002506647-A/3
           PD   05-MAR-2002
           PF   12-MAR-1999 JP 2000536861
           PR   19-MAR-1998 US    60/078654
           PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
           PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
           PC   C12N1/15,
           PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
            C12N5/00
           CC   Sequence source: most codons optimized
           FH   Key             Location/Qualifiers
           FT   source          1. .987
           FT                   /organism='Artificial Sequence'.
EATURES              Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
RIGIN

lignment Scores:
red. No.:              4.88e-32        Length:        987
core:                  35.00           Matches:       35
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            10.6%           Indels:        0
B:                     2               Gaps:          0

S-10-821-670A-30 (1-329) x BD136036 (1-987)

y        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

y        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
b        706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

ESULT 70
Q803342
OCUS       CQ803342                 987 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 2 from Patent WO2004035799.
ACCESSION   CQ803342
VERSION     CQ803342.1  GI:47110208
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 2 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:             4.88e-32        Length:        987
Score:                 35.00           Matches:       35
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           10.6%           Indels:        0
DB:                    2               Gaps:          0

US-10-821-670A-30 (1-329) x CQ803342 (1-987)

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 71
CS131491
LOCUS       CS131491                 987 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 10 from Patent WO2005066348.
ACCESSION   CS131491
VERSION     CS131491.1  GI:71794159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 10 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HuIL12 p40 subunit"
ORIGIN

Alignment Scores:
Pred. No.:             4.88e-32        Length:        987
Score:                 35.00           Matches:       35
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           10.6%           Indels:        0
DB:                    2               Gaps:          0

US-10-821-670A-30 (1-329) x CS131491 (1-987)

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
                ||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 72
28591
:CUS        I28591                    987 bp    DNA     linear   PAT 06-FEB-1997
EFINITION   Sequence 1 from patent US 5573764.
:CESSION    I28591
ERSION      I28591.1  GI:1819367
EYWORDS     .
:URCE       Unknown.
 ORGANISM   Unknown.
            Unclassified.
EFERENCE    1  (bases 1 to 987)
 AUTHORS    Sykes,M. and Wolf,S.F.
 TITLE      Use of interleukin-12 to prevent graft versus host disease
 JOURNAL    Patent: US 5573764-A 1 12-NOV-1996;
EATURES             Location/Qualifiers
     source         1. .987
                    /organism="unknown"
                    /mol_type="unassigned DNA"
:IGIN

lignment Scores:
:ed. No.:               4.88e-32        Length:         987
:ore:                   35.00           Matches:        35
:rcent Similarity:      100.0%          Conservative:   0
:st Local Similarity:   100.0%          Mismatches:     0
:ery Match:             10.6%           Indels:         0
:B:                     2               Gaps:           0

:-10-821-670A-30 (1-329) x I28591 (1-987)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
                ||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 73
X154633
:CUS        AX154633                  987 bp    DNA     linear   PAT 22-JUN-2001
EFINITION   Sequence 37 from Patent WO0140257.
:CESSION    AX154633
ERSION      AX154633.1  GI:14536197
EYWORDS     .
:URCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1
 AUTHORS    Leong,S.R. and Punnonen,J.
 TITLE      Cytokine polypeptides and nucleic acids
 JOURNAL    Patent: WO 0140257-A 37 07-JUN-2001;
            Maxygen, Inc. (US)
EATURES             Location/Qualifiers
     source         1. .987
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
:IGIN

lignment Scores:
:ed. No.:               4.88e-32        Length:         987
:ore:                   35.00           Matches:        35
:rcent Similarity:      100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x AX154633 (1-987)

Qy          217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy          237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
                ||||||||||||||||||||||||||||||||||||||||||||
Db          706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 74
AF180563
LOCUS       AF180563                1007 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P40 mRNA, complete cds.
ACCESSION   AF180563
VERSION     AF180563.1  GI:5923854
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
     source          1. .1007
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="peripheral mononuclear"
     CDS             7. .993
                     /note="NKSF/CLMF; IL12p40; 40kD"
                     /codon_start=1
                     /product="interleukin 12, P40"
                     /protein_id="AAD56386.1"
                     /db_xref="GI:5923855"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:              4.98e-32        Length:         1007
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-30 (1-329) x AF180563 (1-1007)

Qy          217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

Qy          237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
                ||||||||||||||||||||||||||||||||||||||||||||
Db          712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756
```

```
ESULT 75
B246353
OCUS       AB246353               1008 bp    mRNA    linear   MAM 13-JAN-2006
EFINITION  Bubalus bubalis IL-12p40 mRNA for interleukin-12p40, complete cds.
CCESSION   AB246353
ERSION     AB246353.1  GI:84871717
EYWORDS    .
OURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
EFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
EFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
EATURES             Location/Qualifiers
     source         1. .1008
                    /organism="Bubalus bubalis"
                    /mol_type="mRNA"
                    /db_xref="taxon:89462"
                    /sex="female"
                    /cell_type="PBMC"
                    /note="Bulgarian Murrah buffalo - crossbreed between
                    Mediterranean and Indian buffalo both are Riverine type
                    water buffalo"
     gene           1. .1008
                    /gene="IL-12p40"
     CDS            1. .984
                    /gene="IL-12p40"
                    /codon_start=1
                    /product="interleukin-12p40"
                    /protein_id="BAE75858.1"
                    /db_xref="GI:84871718"
                    /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
                    TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                    LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                    GSSDPRGVTCEAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                    LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                    QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
RIGIN

lignment Scores:
red. No.:              4.99e-32       Length:        1008
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            10.6%          Indels:        0
B:                     14             Gaps:          0

S-10-821-670A-30 (1-329) x AB246353 (1-1008)

y        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        649 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCA 708

y        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
b        709 GACCCACCCAAGAACCTGCAACTGAAACCATTAAAGAATTCTCGG 753

ESULT 76
198121
OCUS       AY198121               1012 bp    mRNA    linear   MAM 09-JUN-2005
DEFINITION  Bubalus bubalis interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
ACCESSION   AY198121
VERSION     AY198121.1  GI:28192687
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
  TITLE     Interleukin-12 subunits p35 and p40 of Indian water buffalo
            (Bubalus bubalis) maintain high sequence homology with those of
            other ruminants
  JOURNAL   Eur. J. Immunogenet. 32 (3), 179-186 (2005)
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E. and Rasool,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-2002) Animal Biotechnology, Rajiv Gandhi Center
            for Biotechnology, Jagathy, Thycaud PO, Trivandrum, Kerala 695014,
            India
FEATURES             Location/Qualifiers
     source         1. .1012
                    /organism="Bubalus bubalis"
                    /mol_type="mRNA"
                    /db_xref="taxon:89462"
     CDS            1. .984
                    /note="cytokine; 40 kDa subunit"
                    /codon_start=1
                    /product="interleukin 12 p40 subunit precursor"
                    /protein_id="AAO25629.1"
                    /db_xref="GI:28192688"
                    /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                    TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                    LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                    GSADPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                    LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                    QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:              5.01e-32       Length:        1012
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     14             Gaps:          0

US-10-821-670A-30 (1-329) x AY198121 (1-1012)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCA 708

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        709 GACCCACCCAAGAACCTGCAACTGAAACCATTAAAGAATTCTCGG 753

RESULT 77
AR052857
LOCUS       AR052857               1018 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 194 from patent US 5833975.
ACCESSION   AR052857
VERSION     AR052857.1  GI:5977719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
```

```
 JOURNAL   Patent: US 5833975-A 194 10-NOV-1998;
EATURES             Location/Qualifiers
    source          1. .1018
                    /organism="unknown"
                    /mol_type="unassigned DNA"
?IGIN

lignment Scores:
ted. No.:              5.04e-32       Length:        1018
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
ery Match:             10.6%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-30 (1-329) x AR052857 (1-1018)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

ESULT 78
R288169
OCUS       AR288169               1018 bp    mRNA    linear   PAT 12-JUN-2003
EFINITION  Sequence 194 from patent US 6537594.
CCESSION   AR288169
ERSION     AR288169.1  GI:31675448
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 1018)
 AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
 TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
           genes
 JOURNAL   Patent: US 6537594-A 194 25-MAR-2003;
           Virogenetics Corporation; Troy, NY
EATURES             Location/Qualifiers
    source          1. .1018
                    /organism="unknown"
                    /mol_type="mRNA"
?IGIN

lignment Scores:
ted. No.:              5.04e-32       Length:        1018
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
ery Match:             10.6%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-30 (1-329) x AR288169 (1-1018)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

ESULT 79
P567156
OCUS       AR567156               1018 bp    mRNA    linear   PAT 08-OCT-2004
EFINITION  Sequence 194 from patent US 6780407.
CCESSION   AR567156
ERSION     AR567156.1  GI:53984798
EYWORDS    .
OURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 194 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.04e-32       Length:        1018
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x AR567156 (1-1018)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 80
CQ829448
LOCUS       CQ829448               1029 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 7 from Patent WO2004052929.
ACCESSION   CQ829448
VERSION     CQ829448.1  GI:49732784
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 7 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES             Location/Qualifiers
     source          1. .1029
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="cDNA for beta chain of IL-12"
ORIGIN

Alignment Scores:
Pred. No.:              5.09e-32       Length:        1029
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x CQ829448 (1-1029)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 720

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 765

RESULT 81
```

```
C074723
OCUS        BC074723                1046 bp    mRNA    linear   PRI 28-JUL-2005
EFINITION   Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:103792 IMAGE:30915173), complete cds.
CCESSION    BC074723
ERSION      BC074723.2  GI:50960609
EYWORDS     MGC.
OURCE       Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 1046)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
    PUBMED  12477932
EFERENCE    2  (bases 1 to 1046)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
OMMENT      On Aug 4, 2004 this sequence version replaced gi:49901500.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
            Center
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBU Plate: 1 Row: A Column: 6.
EATURES                 Location/Qualifiers
     source             1. .1046
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="MGC:103792 IMAGE:30915173"
                        /tissue_type="Brain, PCR rescued clones"
                        /clone_lib="NIH_MGC_272"
                        /lab_host="DH10B"
                        /note="Vector: pCR4 Topo TA with reversed insert"
     gene               1. .1046
                        /gene="IL12B"
                        /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                        /db_xref="GeneID:3593"
                        /db_xref="MIM:161561"
     CDS                32. .1018
                        /gene="IL12B"
                        /codon_start=1
                        /product="interleukin 12B, precursor"
                        /protein_id="AAH74723.1"
                        /db_xref="GI:50960610"
                        /db_xref="GeneID:3593"
                        /db_xref="MIM:161561"
                        /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                        MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                        LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                        GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                        KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                        VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:                5.18e-32        Length:         1046
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              10.6%           Indels:         0
DB:                       5               Gaps:           0

US-10-821-670A-30 (1-329) x BC074723 (1-1046)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 82
BC067498
LOCUS       BC067498                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79355 IMAGE:6971868), complete cds.
ACCESSION   BC067498
VERSION     BC067498.1  GI:45768642
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
```

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
EFERENCE 2 (bases 1 to 1073)
AUTHORS .
CONSRTM NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
:MMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497437.

FEATURES Location/Qualifiers
source 1. .1073
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:79355 IMAGE:6971868"
/tissue_type="PCR rescued clones"
/clone_lib="NIH_MGC_195"
/lab_host="DH10B"
/note="Vector: pDNR-Dual"
gene 1. .1073
/gene="IL12B"
/note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
/db_xref="GeneID:3593"
/db_xref="MIM:161561"
CDS 5. .991
/gene="IL12B"
/codon_start=1
/product="interleukin 12B, precursor"
/protein_id="AAH67498.1"
/db_xref="GI:45768643"
/db_xref="GeneID:3593"
/db_xref="MIM:161561"
/translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"

RIGIN

lignment Scores:
red. No.: 5.32e-32 Length: 1073
core: 35.00 Matches: 35
ercent Similarity: 100.0% Conservative: 0
est Local Similarity: 100.0% Mismatches: 0
uery Match: 10.6% Indels: 0
2: 5 Gaps: 0

-10-821-670A-30 (1-329) x BC067498 (1-1073)

```
Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||||
Db      710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754
```

RESULT 83
BC067499
LOCUS BC067499 1073 bp mRNA linear PRI 28-JUL-2005
DEFINITION Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA (cDNA clone MGC:79356 IMAGE:6971869), complete cds.
ACCESSION BC067499
VERSION BC067499.1 GI:45768645
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1073)
AUTHORS .
CONSRTM NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497437.

FEATURES Location/Qualifiers
source 1. .1073
/organism="Homo sapiens"

```
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79356 IMAGE:6971869"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67499.1"
                     /db_xref="GI:45768646"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:                5.32e-32        Length:         1073
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              10.6%           Indels:         0
DB:                       5               Gaps:           0

US-10-821-670A-30 (1-329) x BC067499 (1-1073)

QY        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

QY        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 84
BC067500
LOCUS       BC067500                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79358 IMAGE:6971872), complete cds.
ACCESSION   BC067500
VERSION     BC067500.1  GI:45768649
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79358 IMAGE:6971872"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67500.1"
                     /db_xref="GI:45768650"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:                5.32e-32        Length:         1073
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              10.6%           Indels:         0
DB:                       5               Gaps:           0
```

```
S-10-821-670A-30 (1-329) x BC067500 (1-1073)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 85
BC067501
LOCUS       BC067501                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79359 IMAGE:6971873), complete cds.
ACCESSION   BC067501
VERSION     BC067501.1  GI:45767736
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
    PUBMED  12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.

FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79359 IMAGE:6971873"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67501.1"
                     /db_xref="GI:45767737"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:                  5.32e-32        Length:          1073
Score:                      35.00           Matches:         35
Percent Similarity:         100.0%          Conservative:    0
Best Local Similarity:      100.0%          Mismatches:      0
Query Match:                10.6%           Indels:          0
DB:                         5               Gaps:            0

US-10-821-670A-30 (1-329) x BC067501 (1-1073)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 86
BC067502
LOCUS       BC067502                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79360 IMAGE:6971874), complete cds.
ACCESSION   BC067502
VERSION     BC067502.1  GI:45768652
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
```

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRTM Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

EFERENCE 2 (bases 1 to 1073)

AUTHORS .

CONSRTM NIH MGC Project

TITLE Direct Submission

JOURNAL Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

OMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497437.

EATURES Location/Qualifiers

source 1. .1073
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:79360 IMAGE:6971874"
/tissue_type="PCR rescued clones"
/clone_lib="NIH_MGC_195"
/lab_host="DH10B"
/note="Vector: pDNR-Dual"

gene 1. .1073
/gene="IL12B"
/note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
/db_xref="GeneID:3593"
/db_xref="MIM:161561"

CDS 5. .991
/gene="IL12B"
/codon_start=1
/product="interleukin 12B, precursor"
/protein_id="AAH67502.1"
/db_xref="GI:45768653"
/db_xref="GeneID:3593"
/db_xref="MIM:161561"
/translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"

RIGIN

lignment Scores:
ed. No.: 5.32e-32 Length: 1073
core: 35.00 Matches: 35
ercent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 5 Gaps: 0

US-10-821-670A-30 (1-329) x BC067502 (1-1073)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 87
AR393788
LOCUS AR393788 1389 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6617135.
ACCESSION AR393788
VERSION AR393788.1 GI:40120790
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1389)
AUTHORS Gillies,S.D. and Lo,K.-M.
TITLE Multiple cytokine protein complexes
JOURNAL Patent: US 6617135-A 4 09-SEP-2003;
EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES Location/Qualifiers
source 1. .1389
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 6.95e-32 Length: 1389
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-30 (1-329) x AR393788 (1-1389)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 88
AX084106
LOCUS AX084106 1389 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 4 from Patent WO0110912.
ACCESSION AX084106
VERSION AX084106.1 GI:13185656
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gillies,S.D. and Lo,K.M.
TITLE Multiple cytokine-antibody complexes
JOURNAL Patent: WO 0110912-A 4 15-FEB-2001;
Lexigen Pharmaceuticals Corp. (US)
FEATURES Location/Qualifiers
source 1. .1389
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

```
                     /note="human p40-IL-2 fusion protein coding sequence"
RIGIN

lignment Scores:
red. No.:                6.95e-32        Length:         1389
core:                    35.00           Matches:        35
ercent Similarity:       100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              10.6%           Indels:         0
B:                       2               Gaps:           0

S-10-821-670A-30 (1-329) x AX084106 (1-1389)

y        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
c        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 89
D165800
.CUS        BD165800                1397 bp    DNA     linear   PAT 17-JAN-2003
EFINITION   Antibody against cytotoxic lymphocyte maturing factors.
.CESSION    BD165800
ERSION      BD165800.1  GI:27871612
EYWORDS     JP 2002167400-A/1.
 URCE       unidentified
 ORGANISM   unidentified
            unclassified sequences.
EFERENCE    1  (bases 1 to 1397)
 AUTHORS    Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
 TITLE      Antibody against cytotoxic lymphocyte maturing factors
 JOURNAL    Patent: JP 2002167400-A 1 11-JUN-2002;
            PROTEIN DESIGN LABS INC
OMMENT      OS   Homo sapiens (human)
            PN   JP 2002167400-A/1
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
            PI   GUBLER,
            PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
            PI   ALVIN SETH STERN
            PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
              Antibody against cytotoxic lymphocyte maturing factors FH   Key
                    Location/Qualifiers
            FT   CDS             (41). .(1024).
EATURES             Location/Qualifiers
    source          1. .1397
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
RIGIN

lignment Scores:
red. No.:                6.99e-32        Length:         1397
core:                    35.00           Matches:        35
rcent Similarity:        100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              10.6%           Indels:         0
:                        2               Gaps:           0

-10-821-670A-30 (1-329) x BD165800 (1-1397)

         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

y        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
Db       746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 90
AR091391
LOCUS       AR091391                1399 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from patent US 5994104.
ACCESSION   AR091391
VERSION     AR091391.1  GI:10018146
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1399)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 3 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1399
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:               7e-32           Length:         1399
Score:                   35.00           Matches:        35
Percent Similarity:      100.0%          Conservative:   0
Best Local Similarity:   100.0%          Mismatches:     0
Query Match:             10.6%           Indels:         0
DB:                      2               Gaps:           0

US-10-821-670A-30 (1-329) x AR091391 (1-1399)

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
Db       748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 91
HUMCLMF40
LOCUS       HUMCLMF40               1399 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human cytotoxic lymphocyte maturation factor 40 kDa subunit mRNA,
            complete cds.
ACCESSION   M65272 M38443 M38444
VERSION     M65272.1  GI:180625
KEYWORDS    cytotoxic lymphocyte maturation factor 40 kDa subunit; interleukin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1399)
  AUTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
            Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
            and Gately,M.K.
  TITLE     Coexpression of two distinct genes is required to generate secreted
            bioactive cytotoxic lymphocyte maturation factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
   PUBMED   1674604
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .1399
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             43. .1029
                     /codon_start=1
                     /product="cytotoxic lymphocyte maturation factor 40 kDa
                     subunit"
                     /protein_id="AAA35695.1"
```

```
                     /db_xref="GI:180626"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:                7e-32          Length:        1399
Score:                    35.00          Matches:       35
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              10.6%          Indels:        0
DB:                       5              Gaps:          0

US-10-821-670A-30 (1-329) x HUMCLMF40 (1-1399)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 92
AR091395
LOCUS       AR091395                1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                7.83e-32       Length:        1560
Score:                    35.00          Matches:       35
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              10.6%          Indels:        0
DB:                       2              Gaps:          0

US-10-821-670A-30 (1-329) x AR091395 (1-1560)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 642

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 687

RESULT 93
AR091394
LOCUS       AR091394                1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1623
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                8.16e-32       Length:        1623
Score:                    35.00          Matches:       35
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              10.6%          Indels:        0
DB:                       2              Gaps:          0

US-10-821-670A-30 (1-329) x AR091394 (1-1623)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 94
CQ715179
LOCUS       CQ715179                2307 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 1113 from Patent WO02068579.
ACCESSION   CQ715179
VERSION     CQ715179.1  GI:42276036
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 1113 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .2307
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.17e-31       Length:        2307
Score:                    35.00          Matches:       35
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              10.6%          Indels:        0
DB:                       2              Gaps:          0

US-10-821-670A-30 (1-329) x CQ715179 (1-2307)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 707

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        708 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 752
```

```
SULT 95
082684
CUS       AR082684                2362 bp    DNA     linear   PAT 01-SEP-2000
FINITION  Sequence 1 from patent US 5976539.
CESSION   AR082684
RSION     AR082684.1  GI:10009474
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 2362)
AUTHORS   Scott,P. and Trinchieri,G.
TITLE     Compositions and methods for use of IL-12 as an adjuvant
JOURNAL   Patent: US 5976539-A 1 02-NOV-1999;
EATURES             Location/Qualifiers
    source          1. .2362
                    /organism="unknown"
                    /mol_type="unassigned DNA"
RIGIN

lignment Scores:
red. No.:              1.2e-31        Length:        2362
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
st Local Similarity:   100.0%         Mismatches:    0
uery Match:            10.6%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-30 (1-329) x AR082684 (1-2362)

y       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

y       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

SULT 96
122960
CUS       AR122960                2362 bp    DNA     linear   PAT 16-MAY-2001
FINITION  Sequence 1 from patent US 6168923.
CESSION   AR122960
RSION     AR122960.1  GI:14107926
YWORDS    .
URCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 2362)
AUTHORS   Scott,P. and Trinchieri,G.
TITLE     Compositions and methods for use of IL-12 as an adjuvant
JOURNAL   Patent: US 6168923-A 1 02-JAN-2001;
EATURES             Location/Qualifiers
    source          1. .2362
                    /organism="unknown"
                    /mol_type="unassigned DNA"
RIGIN

lignment Scores:
red. No.:              1.2e-31        Length:        2362
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
st Local Similarity:   100.0%         Mismatches:    0
uery Match:            10.6%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-30 (1-329) x AR122960 (1-2362)

y       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 97
I28325
LOCUS       I28325                  2362 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5571515.
ACCESSION   I28325
VERSION     I28325.1  GI:1819101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2362)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5571515-A 1 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .2362
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.2e-31        Length:        2362
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x I28325 (1-2362)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 98
AR309636
LOCUS       AR309636                2362 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6555658.
ACCESSION   AR309636
VERSION     AR309636.1  GI:31701687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2362)
  AUTHORS   Trinchieri,G., Perussia,B., Clark,S.C., Wong,G.G., Hewick,R. and
            Kobayashi,M.
  TITLE     Antibodies to natural killer stimulatory factor
  JOURNAL   Patent: US 6555658-A 3 29-APR-2003;
            Wyeth and The Wistar Institute; Madison, NJ
FEATURES             Location/Qualifiers
     source          1. .2362
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.2e-31        Length:        2362
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x AR309636 (1-2362)
```

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 99
I89770
LOCUS       I89770                  2362 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 1 from patent US 5723127.
ACCESSION   I89770
VERSION     I89770.1  GI:3409710
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2362)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5723127-A 1 03-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .2362
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.2e-31       Length:         2362
Score:                  35.00         Matches:        35
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            10.6%         Indels:         0
DB:                     2             Gaps:           0

US-10-821-670A-30 (1-329) x I89770 (1-2362)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 100
BD136048
LOCUS       BD136048                5686 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136048
VERSION     BD136048.1  GI:23230993
KEYWORDS    JP 2002506647-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 5686)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 15 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/15
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
            C12N5/00
            CC   Sequence source: synthetic construct
            FH   Key             Location/Qualifiers
            FT   source          1. .5686
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .5686
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              2.98e-31      Length:         5686
Score:                  35.00         Matches:        35
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            10.6%         Indels:         0
DB:                     2             Gaps:           0

US-10-821-670A-30 (1-329) x BD136048 (1-5686)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3864 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3923

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db       3924 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3968


Search completed: June 10, 2006, 12:08:33
Job time : 7510.33 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioccelleration Ltd.

M protein - nucleic search, using frame_plus_p2n model

un on: June 10, 2006, 01:23:11 ; Search time 797.144 Seconds
(without alignments)
4316.416 Million cell updates/sec

itle: US-10-821-670A-30
erfect score: 329
equence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

coring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

earched: 5244920 seqs, 3486124231 residues

ord size: 1

otal number of hits satisfying chosen parameters: 10484873

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Listing first 200 summaries

ommand line parameters:
MODEL=frame+_p2n.model -DEV=xlh
Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110446_27507/app_query.fasta_1
DB=N_Geneseq -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rng -MINMATCH=0.1
LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
MAXLEN=2000000000 -HOST=abss05h
USER=US10821670_@CGN_1_1_1666_@runat_07062006_110446_27507 -NCPU=6 -ICPU=3
NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

atabase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
1	329	100.0	987	6	ABK98944	Abk98944 Feline in
c 2	329	100.0	987	6	ABK98945	Abk98945 Feline in
3	329	100.0	987	14	ADV34682	Adv34682 Feline si
c 4	329	100.0	987	14	ADV34684	Adv34684 Feline si
5	329	100.0	990	4	AAF26082	Aaf26082 Feline IL
6	329	100.0	990	4	AAF26085	Aaf26085 Feline IL
7	329	100.0	4522	4	AAF26076	Aaf26076 Feline IL
8	329	100.0	4522	4	AAF26094	Aaf26094 Plasmid p
c 9	328	99.7	985	6	ABK98962	Abk98962 Feline in
10	328	99.7	985	6	ABK98961	Abk98961 Feline in
11	328	99.7	985	14	ADV34707	Adv34707 Feline N-
c 12	328	99.7	985	14	ADV34709	Adv34709 Feline N-
13	317	96.4	2193	2	AAV56625	Aav56625 Feline FL
14	307	93.3	921	2	AAV56627	Aav56627 Feline FL
15	307	93.3	921	2	AAV56626	Aav56626 Feline FL
16	217	66.0	1599	6	ABK98950	Abk98950 Feline in
c 17	217	66.0	1599	6	ABK98951	Abk98951 Feline in
18	217	66.0	1599	14	ADV34691	Adv34691 Feline si
c 19	217	66.0	1599	14	ADV34693	Adv34693 Feline si
20	206	62.6	921	6	ABK98942	Abk98942 Feline in
c 21	206	62.6	921	6	ABK98943	Abk98943 Feline in
c 22	206	62.6	921	14	ADV34681	Adv34681 Feline si
23	206	62.6	921	14	ADV34679	Adv34679 Feline si
c 24	206	62.6	1533	6	ABK98954	Abk98954 Feline in
25	206	62.6	1533	6	ABK98953	Abk98953 Feline in
c 26	206	62.6	1533	14	ADV34697	Adv34697 Feline si
27	206	62.6	1533	14	ADV34695	Adv34695 Feline si
28	52	15.8	990	5	AAD15209	Aad15209 Modified
29	49	14.9	984	5	AAD15206	Aad15206 Modified
30	42	12.8	984	5	AAD15205	Aad15205 Modified
31	41	12.5	975	5	AAD15203	Aad15203 Modified
32	37	11.2	921	6	ABK98959	Abk98959 Canine in
c 33	37	11.2	921	6	ABK98960	Abk98960 Canine in
c 34	37	11.2	921	14	ADV34706	Adv34706 Canine si
35	37	11.2	921	14	ADV34704	Adv34704 Canine si
36	37	11.2	924	2	AAX18177	Aax18177 Canine ma
37	37	11.2	987	6	ABK98963	Abk98963 Canine in
c 38	37	11.2	987	6	ABK98964	Abk98964 Canine in
c 39	37	11.2	987	14	ADV34712	Adv34712 Canine si
40	37	11.2	987	14	ADV34710	Adv34710 Canine si
41	37	11.2	990	2	AAV13816	Aav13816 Canine IL
42	37	11.2	990	2	AAV13817	Aav13817 Canine IL
43	37	11.2	990	2	AAX03162	Aax03162 Nucleic a
44	37	11.2	990	2	AAX03152	Aax03152 Nucleic a
45	37	11.2	990	2	AAX35625	Aax35625 Nucleic a
46	37	11.2	990	2	AAX35615	Aax35615 Nucleic a
47	37	11.2	990	4	AAI64378	Aai64378 Canine co
48	37	11.2	990	4	AAI64388	Aai64388 Canine co
49	37	11.2	990	11	ADZ25698	Adz25698 Canine in
50	37	11.2	1015	13	ADT04849	Adt04849 Canine in
51	37	11.2	1533	6	ABK98967	Abk98967 Canine in
c 52	37	11.2	1533	6	ABK98968	Abk98968 Canine in
c 53	37	11.2	1533	14	ADV34718	Adv34718 Canine si
54	37	11.2	1533	14	ADV34716	Adv34716 Canine si
55	37	11.2	1599	6	ABK98965	Abk98965 Canine in
c 56	37	11.2	1599	6	ABK98966	Abk98966 Canine in
c 57	37	11.2	1599	14	ADV34715	Adv34715 Canine si
58	37	11.2	1599	14	ADV34713	Adv34713 Canine si
59	37	11.2	2154	2	AAX18176	Aax18176 Canine fu
c 60	37	11.2	2267	6	ABK99006	Abk99006 Canine in
61	37	11.2	2267	6	ABK99005	Abk99005 Canine in
62	37	11.2	2267	14	ADV34757	Adv34757 Canine si
c 63	37	11.2	2267	14	ADV34759	Adv34759 Canine si
64	35	10.6	906	2	AAQ04701	Aaq04701 Sequence
65	35	10.6	975	5	AAD15208	Aad15208 Modified
66	35	10.6	979	2	AAQ12149	Aaq12149 Cytotoxic
67	35	10.6	984	12	ADG39430	Adg39430 Human CLM
68	35	10.6	987	2	AAQ97484	Aaq97484 Human int
69	35	10.6	987	2	AAV07273	Aav07273 Human Int
70	35	10.6	987	2	AAV07217	Aav07217 DNA encod
71	35	10.6	987	2	AAZ40406	Aaz40406 Human int
72	35	10.6	987	2	AAZ40404	Aaz40404 Human int
73	35	10.6	987	2	AAZ40405	Aaz40405 Human int
74	35	10.6	987	5	AAD15210	Aad15210 Human cyt
75	35	10.6	987	12	ADF77278	Adf77278 Human IL-

76	35	10.6	987	12	ADF77263	Adf77263 Human IL-
77	35	10.6	987	12	ADF77277	Adf77277 Human IL-
78	35	10.6	987	12	ADF77276	Adf77276 Human IL-
79	35	10.6	987	12	ADO07653	Ado07653 Human int
80	35	10.6	987	13	ADS00006	Ads00006 Human int
81	35	10.6	987	14	ADV42753	Adv42753 Human psy
82	35	10.6	987	14	ADW97242	Adw97242 Human p40
83	35	10.6	987	14	AEB48822	Aeb48822 Human int
84	35	10.6	1007	5	AAD18585	Aad18585 Human int
85	35	10.6	1018	2	AAQ67879	Aaq67879 EPV 42 kD
86	35	10.6	1018	2	AAZ08510	Aaz08510 EPV 42 kD
87	35	10.6	1018	13	ADR21886	Adr21886 EPV 42kDa
88	35	10.6	1029	12	ADP88402	Adp88402 Human int
89	35	10.6	1389	4	AAF76880	Aaf76880 Human p40
90	35	10.6	1397	2	AAT77849	Aat77849 40 kDa su
91	35	10.6	1397	2	AAT97969	Aat97969 40 kDa su
92	35	10.6	1397	2	AAV00401	Aav00401 40 kDa su
93	35	10.6	1397	2	AAV37767	Aav37767 Cytotoxic
94	35	10.6	1397	12	ADG39387	Adg39387 Human cyt
95	35	10.6	1397	12	ADO03758	Ado03758 Human CLM
96	35	10.6	1399	3	AAZ40021	Aaz40021 Human p40
97	35	10.6	1399	14	ADY86632	Ady86632 Human int
98	35	10.6	2300	3	AAA92406	Aaa92406 Human int
99	35	10.6	2336	14	AEE03207	Aee03207 Human int
100	35	10.6	2347	12	ACF57534	Acf57534 Human IL1
101	35	10.6	2347	12	ADJ62892	Adj62892 Human int
102	35	10.6	2347	14	ADZ26728	Adz26728 Human IL1
103	35	10.6	2362	2	AAQ23586	Aaq23586 Natural k
104	35	10.6	2362	2	AAT48098	Aat48098 Human int
105	35	10.6	2362	2	AAV42535	Aav42535 Human int
106	35	10.6	2362	2	AAV15227	Aav15227 Heterodim
107	35	10.6	2362	3	AAZ28862	Aaz28862 Human int
108	35	10.6	2362	4	AAF56280	Aaf56280 IL-12 vac
109	35	10.6	5686	2	AAZ40415	Aaz40415 Plasmid p
110	35	10.6	5686	12	ADF77239	Adf77239 Human IL-
111	35	10.6	6139	3	AAZ40023	Aaz40023 Interleuk
112	35	10.6	11569	10	ADG25150	Adg25150 Vector pA
113	34	10.3	945	12	ADF77264	Adf77264 Human IL-
114	32	9.7	985	10	ADK98707	Adk98707 Human int
115	28	8.5	969	5	AAD15207	Aad15207 Modified
116	28	8.5	984	2	AAT50759	Aat50759 Sequence
117	28	8.5	984	5	AAD15204	Aad15204 Modified
118	28	8.5	1019	3	AAA70709	Aaa70709 Bovine in
119	28	8.5	2390	12	ADM29103	Adm29103 Human int
120	23	7.0	987	2	AAV83199	Aav83199 Interleuk
121	23	7.0	987	6	ACC47592	Acc47592 Human int
122	23	7.0	1007	10	ACD26421	Acd26421 cDNA enco
123	23	7.0	1580	12	ADQ14472	Adq14472 DNA encod
124	23	7.0	2318	8	ACA61267	Aca61267 DNA encod
125	23	7.0	2318	10	ABX33940	Abx33940 Human cDN
126	23	7.0	4727	14	AEA40942	Aea40942 T-DNA reg
127	23	7.0	8578	6	AAD31546	Aad31546 pIRES-hB7
128	23	7.0	8578	6	AAD31545	Aad31545 pIRES-hB7
129	23	7.0	8608	6	AAD31548	Aad31548 pIRES-hB7
130	23	7.0	8623	6	AAD31547	Aad31547 pIRES-hB7
131	23	7.0	8629	6	AAD31552	Aad31552 pIRES-IL1
132	23	7.0	8638	6	AAD31549	Aad31549 pIRES-hB7
133	23	7.0	8644	6	AAD31551	Aad31551 pIRES-IL1
134	23	7.0	8659	6	AAD31550	Aad31550 pIRES-IL1
135	23	7.0	11453	10	ADG25152	Adg25152 Vector pS
136	22	6.7	18110	6	ABK15357	Abk15357 Human int
137	22	6.7	18340	5	AAD19368	Aad19368 Mammalian
138	20	6.1	270	12	ACH83638	Ach83638 Human gen
139	20	6.1	399	14	AEE14792	Aee14792 Hamster S
140	20	6.1	399	14	AEE11150	Aee11150 Hamster c
141	20	6.1	556	12	ACH69938	Ach69938 Human gen
142	19	5.8	948	12	ADI28579	Adi28579 Duck inte
143	19	5.8	948	12	ADI28581	Adi28581 Turkey in
144	19	5.8	948	12	ADI28576	Adi28576 Chicken i
145	17	5.2	73	4	AAS15322	Aas15322 Mouse IL-
146	17	5.2	600	2	AAX78397	Aax78397 IL-12p40
147	17	5.2	600	2	AAX25947	Aax25947 Interleuk
148	17	5.2	1008	13	ADS00008	Ads00008 Murine in
149	17	5.2	1008	14	ADW97243	Adw97243 Murine p4
150	17	5.2	1056	2	AAV28472	Aav28472 Murine in
151	17	5.2	1061	2	AAT35200	Aat35200 Mouse int
152	17	5.2	1409	4	AAF76879	Aaf76879 Murine p4
153	17	5.2	1472	4	AAF76878	Aaf76878 Murine p4
154	17	5.2	1569	4	AAF76888	Aaf76888 Single-ch
155	17	5.2	1610	12	ADQ14470	Adq14470 DNA encod
156	17	5.2	1840	8	ACA61265	Aca61265 DNA encod
157	17	5.2	2013	4	AAF76887	Aaf76887 Murine p3
158	17	5.2	2334	14	AEE03206	Aee03206 Murine in
159	17	5.2	2438	12	ADO43004	Ado43004 DNA encod
160	17	5.2	2709	4	AAF76889	Aaf76889 Coding se
161	17	5.2	5252	12	ADO07652	Ado07652 Tricistro
162	17	5.2	5966	2	AAZ40417	Aaz40417 Plasmid p
163	17	5.2	5966	12	ADF77241	Adf77241 Mouse IL-
164	17	5.2	5985	12	ADQ82718	Adq82718 Anticance
165	17	5.2	6295	2	AAV02043	Aav02043 Plasmid p
166	17	5.2	7287	2	AAV02042	Aav02042 Plasmid p
167	17	5.2	9049	12	ADO07661	Ado07661 Viral vec
168	17	5.2	10633	12	ADO07660	Ado07660 Viral vec
169	17	5.2	11458	10	ADG25151	Adg25151 Vector pA
170	17	5.2	11746	12	ADO07659	Ado07659 Viral vec
171	17	5.2	28191	14	AEE03204	Aee03204 Adenovira
172	17	5.2	28892	14	AEE03202	Aee03202 Adenovira
173	17	5.2	38246	12	ADO07662	Ado07662 Viral vec
174	13	4.0	987	2	AAV31480	Aav31480 Human int
175	13	4.0	987	2	AAZ40422	Aaz40422 Human int
176	13	4.0	987	12	ADF77256	Adf77256 Human IL-
177	12	3.6	38	2	AAV56630	Aav56630 Feline FL
178	12	3.6	200	2	AAV03357	Aav03357 Homo sapi
c 179	10	3.0	30	3	AAA48905	Aaa48905 Probe 12.
180	10	3.0	21925	10	ADC87602	Adc87602 Human GPC
181	10	3.0	26184	10	ADC87236	Adc87236 Human GPC
182	9	2.7	28	6	ABK98985	Abk98985 Feline PC
183	9	2.7	28	14	ADV34735	Adv34735 Feline IL
184	9	2.7	30	5	AAD19247	Aad19247 Mammalian
185	9	2.7	31	14	ADW78364	Adw78364 Hybridizi
186	9	2.7	37	6	ABK98987	Abk98987 Feline PC
187	9	2.7	37	14	ADV34737	Adv34737 Feline IL
188	9	2.7	353	5	ABV07469	Abv07469 Human pro
189	9	2.7	419	5	AAD19240	Aad19240 Mammalian
190	9	2.7	419	5	AAD19239	Aad19239 Mammalian
191	9	2.7	426	5	ABV37403	Abv37403 Human pro
c 192	9	2.7	463	4	AAH08718	Aah08718 Human cDN
193	9	2.7	532	3	AAC04020	Aac04020 Human sec
c 194	9	2.7	664	4	AAL25132	Aal25132 Human bre
195	9	2.7	858	11	ACN88481	Acn88481 Breast ca
196	9	2.7	1974	4	AAH13637	Aah13637 Human cDN
197	9	2.7	2162	10	ADC30563	Adc30563 Human nov
198	9	2.7	2256	5	ABV22512	Abv22512 Human pro
199	9	2.7	2256	5	ABV28327	Abv28327 Human pro
200	9	2.7	2256	5	ABV24801	Abv24801 Human pro

ALIGNMENTS

RESULT 1
ABK98944
ID ABK98944 standard; cDNA; 987 BP.
XX
AC ABK98944;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.

XX
DT 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69303.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 51-53; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	0	Length:	987
Score:	329.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x ABK98944 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 2
ABK98945/c
ID ABK98945 standard; cDNA; 987 BP.
XX
AC ABK98945;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 3; Page 54; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

lignment Scores:

red. No.:	0	Length:	987
core:	329.00	Matches:	329
ercent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
uery Match:	100.0%	Indels:	0
s:	6	Gaps:	0

S-10-821-670A-30 (1-329) x ABK98945 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

RESULT 3
ADV34682
ID ADV34682 standard; cDNA; 987 BP.
XX
AC ADV34682;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a
FT /product= "PFeIL-12p40 329 protein "
FT /partial
FT /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34683.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 29; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40

CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p40 subunit protein
CC encoding full-length cDNA.
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	987
Score:	329.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-30 (1-329) x ADV34682 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 4
ADV34684/c
ID ADV34684 standard; DNA; 987 BP.
XX
AC ADV34684;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 31; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p40 subunit full-length
CC complementary DNA.
XX
SQ Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	987
Score:	329.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-30 (1-329) x ADV34684 (1-987)

```
          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

        321 SerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||
         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

```
ESULT 5
AF26082
   AAF26082 standard; DNA; 990 BP.
X
   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              0              Length:          990
Score:                  329.00         Matches:         329
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     4              Gaps:            0

US-10-821-670A-30 (1-329) x AAF26082 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
```

```
Qy          61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy          81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy         101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy         121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy         141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy         161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy         181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy         201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy         221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy         241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy         261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy         281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy         301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy         321 SerAsnTrpAlaSerValSerCysSer 329
               |||||||||||||||||||||||||
Db         961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 6
AAF26085
ID AAF26085 standard; DNA; 990 BP.
XX
AC AAF26085;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Felis sp.
XX

PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Claim 3; Page 30; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	990
Score:	329.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-30 (1-329) x AAF26085 (1-990)

```
Qy           1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy          21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy          41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy          61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy          81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
```

```
Db       241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

Db       301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

Db       361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160

Db       421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy       161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

Db       481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

Db       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db       601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

Db       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

Db       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

Db       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

Db       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy       321 SerAsnTrpAlaSerValSerCysSer 329

Db       961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

ESULT 7
AF26076

AAF26076 standard; DNA; 4522 BP.

AAF26076;

24-APR-2001 (first entry)

Feline IL-12p40 encoding DNA SEQ ID 2.

Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection; interleukin; antiviral; cytotoxic immune response; Th1 response; ds.

Felis sp.

WO200104280-A2.

18-JAN-2001.

08-JUL-2000; 2000WO-DE002262.

08-JUL-1999; 99CH-00001258.

XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Disclosure; Page 29-31; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	4522
Score:	329.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-30 (1-329) x AAF26076 (1-4522)

```
Qy         1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20

Db      3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy        21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40

Db      3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60

Db      3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

Db      3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100

Db      3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

Db      3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

Db      3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466
```

```
Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy       161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy       321 SerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||||
Db      4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
```

ESULT 8
AF26094
D AAF26094 standard; DNA; 4522 BP.
X
C AAF26094;
X
T 24-APR-2001 (first entry)
X
E Plasmid pMol-fil12p40 DNA SEQ ID 10.
X
W Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
W immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
W Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
X
S Synthetic.
X
N WO200104155-A2.
X
D 18-JAN-2001.
X
F 08-JUL-2000; 2000WO-DE002263.
X
R 08-JUL-1999; 99CH-00001259.
X
A (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
A (UYZU-) UNIV ZUERICH.
A (REGC) UNIV CALIFORNIA.
X
I Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
X
R WPI; 2001-147178/15.
X
T Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Example 1c; Page 33-35; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	4522
Score:	329.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-30 (1-329) x AAF26094 (1-4522)

```
Qy         1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy        21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy       161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
      3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

       321 SerAsnTrpAlaSerValSerCysSer 329
           |||||||||||||||||||||||||
      4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
```

SULT 9
K98962/c
ABK98962 standard; cDNA; 985 BP.

ABK98962;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12p40-N985 complementary strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins, useful for treating and preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Example 3; Page 75-76; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

XX
SQ Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	985
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.7%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x ABK98962 (1-985)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
                |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 10
ABK98961
ID ABK98961 standard; cDNA; 985 BP.
XX
AC ABK98961;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69311.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 73-74; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.:                0                 Length:              985
Score:                    328.00            Matches:             328
Percent Similarity:       100.0%            Conservative:        0
Best Local Similarity:    100.0%            Mismatches:          0
Query Match:              99.7%             Indels:              0
DB:                       6                 Gaps:                0

US-10-821-670A-30 (1-329) x ABK98961 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
```

```
Qy        321 SerAsnTrpAlaSerValSerCys 328
              ||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

SULT 11
V34707
   ADV34707 standard; cDNA; 985 BP.

   ADV34707;

   24-FEB-2005  (first entry)

   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; gene; ss.

   Felis catus.

   Key             Location/Qualifiers
   CDS             1. .984
                   /*tag= a
                   /product= "PCaIL-12P40-N328 protein"
                   /partial
                   /note= "No stop codon"

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.
   P-PSDB; ADV34708.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Claim 24; SEQ ID NO 55; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the feline N-terminal single chain IL-12p40 protein
   encoding cDNA.

   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

lignment Scores:
red. No.:               0           Length:         985
core:                   328.00      Matches:        328
ercent Similarity:      100.0%      Conservative:   0
st Local Similarity:    100.0%      Mismatches:     0
uery Match:             99.7%       Indels:         0
B:                      14          Gaps:           0

S-10-821-670A-30 (1-329) x ADV34707 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              ||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 12
ADV34709/c
ID   ADV34709 standard; DNA; 985 BP.
XX
AC   ADV34709;
XX
DT   24-FEB-2005  (first entry)
```

XX
DE Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 57; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline N-terminal single chain IL-12p40
CC complementary DNA.
XX
SQ Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:

Seed. No.:	0	Length:	985
Score:	328.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.7%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-30 (1-329) x ADV34709 (1-985)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 13
AAV56625
ID AAV56625 standard; cDNA; 2193 BP.
XX
AC AAV56625;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp40 cDNA.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX

FH	Key	Location/Qualifiers
FT	CDS	64. .1053
FT		/*tag= a
FT	sig_peptide	64. .129
FT		/*tag= b
FT	mat_peptide	130. .1050
FT		/*tag= c
FT		/product= "FLAFp40"
FT		/note= "feline cytokine"

XX
PN WO9746583-A1.
XX

11-DEC-1997.

29-MAY-1997; 97WO-JP001824.

04-JUN-1996; 96JP-00165249.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;

WPI; 1998-042118/04.
P-PSDB; AAW76173.

Novel feline cytokine protein - useful for treating feline auto:immune diseases, e.g. those caused by feline herpes virus or feline calcivirus.

Claim 19; Page 52-54; 94pp; Japanese.

This sequence encodes a novel feline cytokine protein, FLAFp40. This protein can be used in the production of a FLAFp35/FLAFp40 heterodimer which can potentiate the cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins are used for treatment of feline autoimmune diseases e.g. as caused by feline herpes virus or feline calcivirus

Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	3.08e-311	Length:	2193
Score:	317.00	Matches:	317
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	96.4%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AAV56625 (1-2193)

```
Qy         13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

Qy         33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy         53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy         73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

Qy         93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

Qy        113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

Qy        133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

Qy        153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

Qy        173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

Qy        193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

Qy        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

Qy        273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

Qy        293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

Qy        313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050
```

RESULT 14
AAV56627
ID AAV56627 standard; cDNA; 921 BP.
XX
AC AAV56627;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp40 cDNA mature transcript #2.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76174.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 21; Page 56-57; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC This protein can be used in the production of a FLAFp35/FLAFp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC feline autoimmune diseases e.g. as caused by feline herpes virus or
CC feline calcivirus
XX
SQ Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 U; 0 Other;

Alignment Scores:

;ed. No.:	1.89e-301	Length:	921
;core:	307.00	Matches:	307
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	93.3%	Indels:	0
B:	2	Gaps:	0

S-10-821-670A-30 (1-329) x AAV56627 (1-921)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
               |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 15
AAV56626
ID AAV56626 standard; cDNA; 921 BP.
XX
AC AAV56626;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp40 cDNA mature transcript #1.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76174.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 20; Page 55; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC This protein can be used in the production of a FLAFp35/FLAFp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC feline autoimmune diseases e.g. as caused by feline herpes virus or
CC feline calcivirus
XX
SQ Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1.89e-301	Length:	921
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	93.3%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AAV56626 (1-921)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
```

```
Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

SULT 16
BK98950

ABK98950 standard; cDNA; 1599 BP.

ABK98950;

21-OCT-2002 (first entry)

Feline interleukin-12 nFeIL-12-1599 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog; canine IL-12; autoimmune disease; allergic reaction; infectious disease; tumour development; inflammatory disease; graft rejection; gene; ss.

Felis catus.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69306.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 58-60; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.01e-210	Length:	1599
Score:	217.00	Matches:	317
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	66.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x ABK98950 (1-1599)

```
Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
```

```
                                                
```

```
y       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

y       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
        666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613

ESULT 18
'V34691
)   ADV34691 standard; cDNA; 1599 BP.
X
    ADV34691;
;
    24-FEB-2005  (first entry)
X
E   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
K
W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W   infectious disease; antimicrobial; gene; ss.
:
S   Felis catus.
X
H   Key             Location/Qualifiers
T   CDS             1. .1599
                    /*tag= a
T                   /product= "PFeIL-12p533 protein"
T                   /partial
T                   /note= "No stop codon"
:
    US2004248261-A1.
X
D   09-DEC-2004.
X
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
    (WOND/) WONDERLING R S.
    (BORO/) BOROUGHS K L.
K
I   Wonderling RS,  Boroughs KL;
X
    WPI; 2005-020565/02.
R   P-PSDB; ADV34692.
K
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
    vaccine against infectious diseases in feline animals.
X
    Claim 24; SEQ ID NO 38; 103pp; English.

    The present invention relates to the feline interleukin (IL)-12p35 or p40
    subunit protein and their encoding nucleic acid molecules and a nucleic
    acid linker. The invention also provides the feline caspase (casp)-1,
    feline IL-18 single chain and canine IL-12 single chain proteins and
    their nucleic acid molecules. The nucleic acid molecule is useful in
    preparing a vaccine against infectious diseases in feline animals. The
    present sequence is the feline single chain IL-12 protein encoding cDNA.
X
Q   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

'ignment Scores:
red. No.:               7.01e-210       Length:         1599
core:                   217.00          Matches:        317
ercent Similarity:      99.7%           Conservative:   0
st Local Similarity:    99.7%           Mismatches:     1
ery Match:              66.0%           Indels:         0
:                       14              Gaps:           0

3-10-821-670A-30 (1-329) x ADV34691 (1-1599)

Qy       12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy       32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy       52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy       72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy       92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy      112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy      132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy      152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy      172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy      192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy      212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy      232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy      252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy      272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy      292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

Qy      312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 19
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
```

XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 40; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:

Seed. No.:	7.01e-210	Length:	1599
Score:	217.00	Matches:	317
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	66.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-30 (1-329) x ADV34693 (1-1599)

```
Qy        12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

Qy        32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

Qy        52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

Qy        72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

Qy        92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

Qy       112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

Qy       132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

Qy       152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

Qy       172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy       192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy       212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy       232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy       252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy       272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

Qy       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613
```

RESULT 20
ABK98942
ID ABK98942 standard; cDNA; 921 BP.
XX
AC ABK98942;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-921 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69302.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and

preventing autoimmune diseases, inflammatory diseases and/or graft rejection in animals.

Claim 1; Page 49-50; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single chain and canine IL-12 single chain proteins. A composition comprising a feline IL-18, feline caspase-1, feline IL-12 single chain or canine IL-12 single chain proteins, a nucleic acid encoding these proteins, mimetopes of these proteins, multimeric forms of these proteins, an antibody against these proteins, or an inhibitor identified by its ability to inhibit the activity of these proteins, can be used to treat or prevent autoimmune diseases, allergic reactions, infectious diseases, tumour development, inflammatory diseases and/or graft rejection in animals. The present nucleic acid sequence represents a feline interleukin 12 DNA sequence, as described in the invention

Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

lignment Scores:
red. No.: 6.03e-199 Length: 921
core: 206.00 Matches: 306
ercent Similarity: 99.7% Conservative: 0
est Local Similarity: 99.7% Mismatches: 1
uery Match: 62.6% Indels: 0
B: 6 Gaps: 0

S-10-821-670A-30 (1-329) x ABK98942 (1-921)

```
        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy      243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy      323 TrpAlaSerValSerCysSer 329
            |||||||||||||||||||||
Db      901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 21
ABK98943/c
ID ABK98943 standard; cDNA; 921 BP.
XX
AC ABK98943;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-921 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 51; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

```
lignment Scores:
:ed. No.:              6.03e-199      Length:         921
:ore:                  206.00         Matches:        306
ercent Similarity:     99.7%          Conservative:   0
est Local Similarity:  99.7%          Mismatches:     1
uery Match:            62.6%          Indels:         0
B:                     6              Gaps:           0

S-10-821-670A-30 (1-329) x ABK98943 (1-921)

y         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

y         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

y         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

y         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

y        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

y        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

y        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

y        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
b        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

y        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

y        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

y        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

y        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

y        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

y        323 TrpAlaSerValSerCysSer 329
             |||||||||||||||||||||
```

```
Db        21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 22
ADV34681/c
ID   ADV34681 standard; DNA; 921 BP.
XX
AC   ADV34681;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 complementary DNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 28; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.03e-199      Length:         921
Score:                  206.00         Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            62.6%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-30 (1-329) x ADV34681 (1-921)

Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
```

```
                                                
```

```
                ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

```
ESULT 24
BK98954/c
D   ABK98954 standard; cDNA; 1533 BP.
X
C   ABK98954;
X
T   21-OCT-2002  (first entry)
X
E   Feline interleukin-12 nFeIL-12-1533 complementary strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; ss.
X
S   Felis catus.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
X
R   04-AUG-2000; 2000US-0223016P.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2002-573554/61.
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Claim 6; Page 66-67; 106pp; English.
X
```

```
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;
```

Alignment Scores:			
Pred. No.:	9.82e-199	Length:	1533
Score:	206.00	Matches:	306
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	62.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x ABK98954 (1-1533)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
                ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814
```

```
        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

        323 TrpAlaSerValSerCysSer 329
            |||||||||||||||||||||
        633 TGGGCATCCGTGTCCTGCAGT 613

SULT 25
K98953
   ABK98953 standard; cDNA; 1533 BP.

   ABK98953;

   21-OCT-2002  (first entry)

   Feline interleukin-12 nFeIL-12-1533 coding strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
   tumour development; inflammatory disease; graft rejection; gene; ss.

   Felis catus.

   US2002052030-A1.

   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.
   P-PSDB; ABG69307.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Claim 6; Page 63-64; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a feline interleukin 12 DNA sequence, as described in
   the invention

   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              9.82e-199      Length:        1533
ore:                  206.00         Matches:       306
Percent Similarity:     99.7%        Conservative:  0
Best Local Similarity:  99.7%        Mismatches:    1
Query Match:            62.6%        Indels:        0
DB:                     6            Gaps:          0

US-10-821-670A-30 (1-329) x ABK98953 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 26
ADV34697/c
```

```
D   ADV34697 standard; DNA; 1533 BP.
X
C   ADV34697;
X
T   24-FEB-2005  (first entry)
X
E   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
X
W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W   infectious disease; antimicrobial; ds.
X
S   Felis catus.
X
N   US2004248261-A1.
X
D   09-DEC-2004.
X
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
C
C   Wonderling RS,  Boroughs KL;
C
X   WPI; 2005-020565/02.
X
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
T   vaccine against infectious diseases in feline animals.
X
S   Example 3; SEQ ID NO 45; 103pp; English.
X
X   The present invention relates to the feline interleukin (IL)-12p35 or p40
X   subunit protein and their encoding nucleic acid molecules and a nucleic
X   acid linker. The invention also provides the feline caspase (casp)-1,
X   feline IL-18 single chain and canine IL-12 single chain proteins and
X   their nucleic acid molecules. The nucleic acid molecule is useful in
X   preparing a vaccine against infectious diseases in feline animals. The
X   present sequence is the feline single chain IL-12 complementary DNA.
X
SQ  Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

lignment Scores:
'ed. No.:              9.82e-199      Length:          1533
core:                  206.00         Matches:         306
ercent Similarity:     99.7%          Conservative:    0
est Local Similarity:  99.7%          Mismatches:      1
uery Match:            62.6%          Indels:          0
B:                     14             Gaps:            0

'S-10-821-670A-30 (1-329) x ADV34697 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 27
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag= a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
```

```
   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.
   P-PSDB; ADV34696.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Claim 24; SEQ ID NO 43; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the feline single chain IL-12 protein encoding cDNA.

   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              9.82e-199      Length:        1533
ore:                  206.00         Matches:       306
rcent Similarity:     99.7%          Conservative:  0
st Local Similarity:  99.7%          Mismatches:    1
ery Match:            62.6%          Indels:        0
:                     14             Gaps:          0

-10-821-670A-30 (1-329) x ADV34695 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 28
AAD15209
ID   AAD15209 standard; DNA; 990 BP.
XX
AC   AAD15209;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone R16-51.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08602.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
```

```
P   and p35 polypeptides), useful for treating various diseases e.g. diabetic
P   retinopathy and cancer.
X
S   Claim 1; Page 137-138; 223pp; English.
X
C   The invention relates to nucleic acids encoding modified cytokine
C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
C   gamma induction activities. The polypeptides and polynucleotides of the
C   invention are useful for treating various diseases e.g. bacterial
C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
C   vaccinated host's cell-mediated immunity for protective response to a
C   pathogen. The present sequence is a modified human p40 protein encoding
C   DNA
X
S   Sequence 990 BP; 270 A; 250 C; 254 G; 216 T; 0 U; 0 Other;

lignment Scores:
:ed. No.:              1.27e-42      Length:         990
core:                  52.00         Matches:        52
ercent Similarity:     100.0%        Conservative:   0
est Local Similarity:  100.0%        Mismatches:     0
uery Match:            15.8%         Indels:         0
B:                     5             Gaps:           0

S-10-821-670A-30 (1-329) x AAD15209 (1-990)

Y       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Y       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCTGACCCACCCAAGAACTTG 726

/       243 GlnLeuLysProLeuLysAsnSerArgHisValGlu 254
            ||||||||||||||||||||||||||||||||||||
b       727 CAGCTGAAGCCATTAAAGAATTCTCGACACGTGGAG 762

ESULT 29
AD15206
D   AAD15206 standard; DNA; 984 BP.
X
C   AAD15206;
X
T   01-NOV-2001  (first entry)
X
E   Modified human cytokine p40 encoding DNA from clone B1-81.
X
W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
W   p40; mutant; ds.
X
S   Homo sapiens.
S   Synthetic.
X
H   Key             Location/Qualifiers
T   CDS             1. .984
T                   /*tag=  a
T                   /product= "Modified p40 protein precursor"
T   sig_peptide     1. .66
T                   /*tag=  b
T   mat_peptide     67. .981
T                   /*tag=  c
T                   /product= "Mature modified p40 protein"
X
N   WO200140257-A2.
X
D   07-JUN-2001.
X
P   30-NOV-2000; 2000WO-US032664.
X
```

```
PR  02-DEC-1999;  99US-0169035P.
PR  28-NOV-2000; 2000US-00725324.
XX
PA  (MAXY-) MAXYGEN INC.
XX
PI  Leong SR,  Punnonen J;
XX
DR  WPI; 2001-502381/55.
DR  P-PSDB; AAE08599.
XX
PT  Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT  and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT  retinopathy and cancer.
XX
PS  Claim 1; Page 137; 223pp; English.
XX
CC  The invention relates to nucleic acids encoding modified cytokine
CC  polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC  cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC  gamma induction activities. The polypeptides and polynucleotides of the
CC  invention are useful for treating various diseases e.g. bacterial
CC  infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC  polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC  vaccinated host's cell-mediated immunity for protective response to a
CC  pathogen. The present sequence is a modified human p40 protein encoding
CC  DNA
XX
SQ  Sequence 984 BP; 272 A; 254 C; 247 G; 211 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.4e-39       Length:         984
Score:                  49.00         Matches:        49
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            14.9%         Indels:         0
DB:                     5             Gaps:           0

US-10-821-670A-30 (1-329) x AAD15206 (1-984)

Qy      124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      370 AAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGG 429

Qy      144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      430 TGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCT 489

Qy      164 AspProGlnGlyValThrCysGlyAla 172
            |||||||||||||||||||||||||||
Db      490 GACCCCCAAGGGGTGACTTGTGGAGCC 516

RESULT 30
AAD15205
ID  AAD15205 standard; DNA; 984 BP.
XX
AC  AAD15205;
XX
DT  01-NOV-2001  (first entry)
XX
DE  Modified human cytokine p40 encoding DNA from clone B2-52.
XX
KW  Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW  diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW  p40; mutant; ds.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .984
FT                  /*tag=  a
FT                  /product= "Modified p40 protein precursor"
FT  sig_peptide     1. .66
```

```
                /*tag=  b
mat_peptide     67. .981
                /*tag=  c
                /product= "Mature modified p40 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999;   99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR,  Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08598.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
and p35 polypeptides), useful for treating various diseases e.g. diabetic
retinopathy and cancer.

Claim 1; Page 136-137; 223pp; English.

The invention relates to nucleic acids encoding modified cytokine
polypeptides (i.e. modified p40 and p35 polypeptides). The modified
cytokine polypeptides have T-cell proliferative and interferon (IFN)-
gamma induction activities. The polypeptides and polynucleotides of the
invention are useful for treating various diseases e.g. bacterial
infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
polynucleotide may also be useful as a vaccine adjuvant, to enhance a
vaccinated host's cell-mediated immunity for protective response to a
pathogen. The present sequence is a modified human p40 protein encoding
DNA

Sequence 984 BP; 267 A; 246 C; 254 G; 217 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              1.78e-32      Length:        984
ore:                  42.00         Matches:       42
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            12.8%         Indels:        0
:                     5             Gaps:          0

-10-821-670A-30 (1-329) x AAD15205 (1-984)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACTTG 726

       243 GlnLeu 244
           ||||||
       727 CAGCTG 732

SULT 31
D15203
   AAD15203 standard; DNA; 975 BP.

   AAD15203;

   01-NOV-2001  (first entry)

   Modified human cytokine p40 encoding DNA from clone C2-22.

   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
```

```
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .975
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .972
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08596.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 975 BP; 269 A; 252 C; 250 G; 204 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.82e-31      Length:        975
Score:                  41.00         Matches:       41
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            12.5%         Indels:        0
DB:                     5             Gaps:          0

US-10-821-670A-30 (1-329) x AAD15203 (1-975)

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

Qy       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

Qy       257 Trp 257
             |||
Db       754 TGG 756
```

ESULT 32
BK98959
D ABK98959 standard; cDNA; 921 BP.
C
C ABK98959;
C
T 21-OCT-2002 (first entry)
C
E Canine interleukin-12 nCaIL-12p40-921 coding strand.
C
W Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W tumour development; inflammatory disease; graft rejection; gene; ss.
C
S Canis familiaris.
C
N US2002052030-A1.
C
D 02-MAY-2002.
C
F 27-JUL-2001; 2001US-00917265.
C
R 04-AUG-2000; 2000US-0223016P.
C
A (WOND/) WONDERLING R S.
A (BORO/) BOROUGHS K L.
C
I Wonderling RS, Boroughs KL;
C
R WPI; 2002-573554/61.
R P-PSDB; ABG69310.
C
T Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T chain and canine IL-12 single chain proteins, useful for treating and
T preventing autoimmune diseases, inflammatory diseases and/or graft
T rejection in animals.
C
S Claim 1; Page 71; 106pp; English.
C
C The present invention discloses new feline interleukin 18 (IL-18), feline
C caspase-1, feline IL-12 single chain and canine IL-12 single chain
C proteins. A composition comprising a feline IL-18, feline caspase-1,
C feline IL-12 single chain or canine IL-12 single chain proteins, a
C nucleic acid encoding these proteins, mimetopes of these proteins,
C multimeric forms of these proteins, an antibody against these proteins,
C or an inhibitor identified by its ability to inhibit the activity of
C these proteins, can be used to treat or prevent autoimmune diseases,
C allergic reactions, infectious diseases, tumour development, inflammatory
C diseases and/or graft rejection in animals. The present nucleic acid
C sequence represents a canine interleukin 12 DNA sequence, as described in
C the invention
C
SQ Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

lignment Scores:
red. No.: 1.98e-27 Length: 921
core: 37.00 Matches: 37
ercent Similarity: 100.0% Conservative: 0
est Local Similarity: 100.0% Mismatches: 0
uery Match: 11.2% Indels: 0
B: 6 Gaps: 0

S-10-821-670A-30 (1-329) x ABK98959 (1-921)

Qy 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

ESULT 33

ABK98960/c
ID ABK98960 standard; cDNA; 921 BP.
XX
AC ABK98960;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p40-921 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 73; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.98e-27 Length: 921
Score: 37.00 Matches: 37
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.2% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-30 (1-329) x ABK98960 (1-921)

Qy 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 34
ADV34706/c
ID ADV34706 standard; DNA; 921 BP.

```
   ADV34706;

   24-FEB-2005  (first entry)

   Canine single chain mature IL-12p40 complementary DNA, nCaIL-12p40 921.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; ds.

   Canis familiaris.

   US2004248261-A1.

   09-DEC-2004.

   09-APR-2004; 2004US-00821670.

   04-AUG-2000; 2000US-0223016P.
   27-JUL-2001; 2001US-00917265.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2005-020565/02.

   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   p40 subunit protein and a nucleic acid linker, useful in preparing a
   vaccine against infectious diseases in feline animals.

   Disclosure; SEQ ID NO 54; 103pp; English.

   The present invention relates to the feline interleukin (IL)-12p35 or p40
   subunit protein and their encoding nucleic acid molecules and a nucleic
   acid linker. The invention also provides the feline caspase (casp)-1,
   feline IL-18 single chain and canine IL-12 single chain proteins and
   their nucleic acid molecules. The nucleic acid molecule is useful in
   preparing a vaccine against infectious diseases in feline animals. The
   present sequence is the canine single chain IL-12p40 subunit reverse
   complementary DNA.

   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              1.98e-27      Length:        921
ore:                  37.00         Matches:       37
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            11.2%         Indels:        0
:                     14            Gaps:          0

-10-821-670A-30 (1-329) x ADV34706 (1-921)

        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

SULT 35
V34704
   ADV34704 standard; cDNA; 921 BP.

   ADV34704;

   24-FEB-2005  (first entry)

   Canine single chain mature IL-12p40 protein cDNA, nCaIL-12p40 921.

   KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   KW   infectious disease; antimicrobial; gene; ss.
   XX
   OS   Canis familiaris.
   XX
   FH   Key             Location/Qualifiers
   FT   CDS             1. .921
   FT                   /*tag=  a
   FT                   /product= "PCaIL-12P40 307 protein"
   FT                   /partial
   FT                   /note= "No start and stop codon"
   XX
   PN   US2004248261-A1.
   XX
   PD   09-DEC-2004.
   XX
   PF   09-APR-2004; 2004US-00821670.
   XX
   PR   04-AUG-2000; 2000US-0223016P.
   PR   27-JUL-2001; 2001US-00917265.
   XX
   PA   (WOND/) WONDERLING R S.
   PA   (BORO/) BOROUGHS K L.
   XX
   PI   Wonderling RS,  Boroughs KL;
   XX
   DR   WPI; 2005-020565/02.
   DR   P-PSDB; ADV34705.
   XX
   PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
   PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
   PT   vaccine against infectious diseases in feline animals.
   XX
   PS   Example 4; SEQ ID NO 52; 103pp; English.
   XX
   CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
   CC   subunit protein and their encoding nucleic acid molecules and a nucleic
   CC   acid linker. The invention also provides the feline caspase (casp)-1,
   CC   feline IL-18 single chain and canine IL-12 single chain proteins and
   CC   their nucleic acid molecules. The nucleic acid molecule is useful in
   CC   preparing a vaccine against infectious diseases in feline animals. The
   CC   present sequence is the canine single chain IL-12p40 subunit protein
   CC   encoding cDNA.
   XX
   SQ   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.98e-27      Length:        921
Score:                  37.00         Matches:       37
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            11.2%         Indels:        0
DB:                     14            Gaps:          0

US-10-821-670A-30 (1-329) x ADV34704 (1-921)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 36
AAX18177
ID   AAX18177 standard; cDNA; 924 BP.
XX
AC   AAX18177;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p40 subunit coding sequence.
```

XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis; ds.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP002295.
XX
PR 03-JUN-1997; 97JP-00161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Tokiyoshi S, Eda Y;
XX
DR WPI; 1999-070260/06.
DR P-PSDB; AAW74323.
XX
PT Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS Claim 8; Page 32; 51pp; Japanese.
XX
CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs
XX
SQ Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.99e-27	Length:	924
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AAX18177 (1-924)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 603

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 654
```

RESULT 37
ABK98963
ID ABK98963 standard; cDNA; 987 BP.
XX
AC ABK98963;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p40-987 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69312.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 76-77; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.12e-27	Length:	987
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x ABK98963 (1-987)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

RESULT 38
ABK98964/c
ID ABK98964 standard; cDNA; 987 BP.
XX
AC ABK98964;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p40-987 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.

```
   02-MAY-2002.

   27-JUL-2001; 2001US-00917265.

   04-AUG-2000; 2000US-0223016P.

   (WOND/) WONDERLING R S.
   (BORO/) BOROUGHS K L.

   Wonderling RS,  Boroughs KL;

   WPI; 2002-573554/61.

   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
   chain and canine IL-12 single chain proteins, useful for treating and
   preventing autoimmune diseases, inflammatory diseases and/or graft
   rejection in animals.

   Example 4; Page 78; 106pp; English.

   The present invention discloses new feline interleukin 18 (IL-18), feline
   caspase-1, feline IL-12 single chain and canine IL-12 single chain
   proteins. A composition comprising a feline IL-18, feline caspase-1,
   feline IL-12 single chain or canine IL-12 single chain proteins, a
   nucleic acid encoding these proteins, mimetopes of these proteins,
   multimeric forms of these proteins, an antibody against these proteins,
   or an inhibitor identified by its ability to inhibit the activity of
   these proteins, can be used to treat or prevent autoimmune diseases,
   allergic reactions, infectious diseases, tumour development, inflammatory
   diseases and/or graft rejection in animals. The present nucleic acid
   sequence represents a canine interleukin 12 DNA sequence, as described in
   the invention

   Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              2.12e-27      Length:         987
ore:                  37.00         Matches:        37
rcent Similarity:     100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            11.2%         Indels:         0
:                     6             Gaps:           0

-10-821-670A-30 (1-329) x ABK98964 (1-987)

        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

SULT 39
V34712/c
   ADV34712 standard; DNA; 987 BP.

   ADV34712;

   24-FEB-2005  (first entry)

   Canine single chain IL-12p40 complementary DNA, nCaIL-12p40 987.

   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
   infectious disease; antimicrobial; ds.

   Canis familiaris.

   US2004248261-A1.

   09-DEC-2004.

PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 60; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.12e-27      Length:         987
Score:                  37.00         Matches:        37
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            11.2%         Indels:         0
DB:                     14            Gaps:           0

US-10-821-670A-30 (1-329) x ADV34712 (1-987)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 40
ADV34710
ID   ADV34710 standard; cDNA; 987 BP.
XX
AC   ADV34710;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 full-length cDNA, nCaIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-329 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
```

```
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
    Wonderling RS,  Boroughs KL;
X
    WPI; 2005-020565/02.
    P-PSDB; ADV34711.
X
    New nucleic acid molecule comprising a sequence encoding a feline p35 or
    p40 subunit protein and a nucleic acid linker, useful in preparing a
    vaccine against infectious diseases in feline animals.
X
    Example 4; SEQ ID NO 58; 103pp; English.
X
    The present invention relates to the feline interleukin (IL)-12p35 or p40
    subunit protein and their encoding nucleic acid molecules and a nucleic
    acid linker. The invention also provides the feline caspase (casp)-1,
    feline IL-18 single chain and canine IL-12 single chain proteins and
    their nucleic acid molecules. The nucleic acid molecule is useful in
    preparing a vaccine against infectious diseases in feline animals. The
    present sequence is the canine single chain IL-12p40 subunit protein
    encoding full-length cDNA.
X
Q   Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

lignment Scores:
ed. No.:                2.12e-27        Length:         987
core:                   37.00           Matches:        37
ercent Similarity:      100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
uery Match:             11.2%           Indels:         0
B:                      14              Gaps:           0

S-10-821-670A-30 (1-329) x ADV34710 (1-987)

y       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 41
AV13816
    AAV13816 standard; cDNA to mRNA; 990 BP.
X
    AAV13816;
X
T   14-MAY-1998  (first entry)
X
E   Canine IL-12 P40 subunit cDNA.
X
W   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
W   antiviral; vaccine adjuvant; ds.
X
S   Canis sp.
X
H   Key             Location/Qualifiers
T   CDS             1. .990
T                   /*tag=  a
T                   /product= "interleukin-12_P40_subunit"
X
W   JP10036397-A.
X
D   10-FEB-1998.
X
F   08-NOV-1996;   96JP-00296789.
X
R   08-NOV-1995;   95JP-00289729.
R   23-MAY-1996;   96JP-00128104.
X
A   (TORA ) TORAY IND INC.
X
R   WPI; 1998-174914/16.
R   P-PSDB; AAW41790.
X
T   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
T   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
T   activities are expected.
X
S   Claim 8; Page 8; 12pp; Japanese.
X
C   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
C   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
C   antiviral activating factor and the expression of class II MHC molecules
C   in canine tumour cells, stimulating proliferation of canine blastogenic
C   lymphocytes and activating canine leukocytes to inhibit canine tumour
C   cells. The canine IL-12 can be used in veterinary medicines, e.g.
C   antitumour, antivirus and vaccine adjuvant activities are expected
X
Q   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.12e-27        Length:         990
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x AAV13816 (1-990)

Qy      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 42
AAV13817
ID  AAV13817 standard; cDNA to mRNA; 990 BP.
XX
AC  AAV13817;
XX
DT  14-MAY-1998  (first entry)
XX
DE  Canine IL-12 P40 subunit cDNA.
XX
KW  Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW  antiviral; vaccine adjuvant; ds.
XX
OS  Canis sp.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .990
FT                  /*tag=  a
FT                  /product= "interleukin-12_P40_subunit"
XX
PN  JP10036397-A.
XX
PD  10-FEB-1998.
XX
PF  08-NOV-1996;   96JP-00296789.
XX
PR  08-NOV-1995;   95JP-00289729.
PR  23-MAY-1996;   96JP-00128104.
XX
PA  (TORA ) TORAY IND INC.
```

```
   WPI; 1998-174914/16.
   P-PSDB; AAW41791.

   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
   activities are expected.

   Claim 10; Page 10-11; 12pp; Japanese.

   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
   antiviral activating factor and the expression of class II MHC molecules
   in canine tumour cells, stimulating proliferation of canine blastogenic
   lymphocytes and activating canine leukocytes to inhibit canine tumour
   cells. The canine IL-12 can be used in veterinary medicines, e.g.
   antitumour, antivirus and vaccine adjuvant activities are expected

   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

ignment Scores:
ed. No.:               2.12e-27       Length:         990
ore:                   37.00          Matches:        37
rcent Similarity:      100.0%         Conservative:   0
st Local Similarity:   100.0%         Mismatches:     0
ery Match:             11.2%          Indels:         0
:                      2              Gaps:           0

-10-821-670A-30 (1-329) x AAV13817 (1-990)

        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

SULT 43
X03162
   AAX03162 standard; cDNA to mRNA; 990 BP.

   AAX03162;

   30-MAR-1999  (first entry)

   Nucleic acid encoding canine interleukin 12.

   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
   skin disease; viral infection; allergic disease; breast tumour;
   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
   dog Parvovirus infection; distemper virus; cat plaque virus infection;
   feline leukaemia; allergy; pollinosis; ds.

   Canis sp.

   Key             Location/Qualifiers
   CDS             1. .990
                   /*tag= a
                   /product= "interleukin_12"

   WO9851327-A1.

   19-NOV-1998.

   07-MAY-1998;   98WO-JP002031.

   16-MAY-1997;   97JP-00127690.

   (TORA ) TORAY IND INC.
```

```
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84373.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.12e-27       Length:         990
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            11.2%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-30 (1-329) x AAX03162 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 44
AAX03152
ID   AAX03152 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03152;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag= a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
```

```
D   19-NOV-1998.
X
F   07-MAY-1998;   98WO-JP002031.
X
R   16-MAY-1997;   97JP-00127690.
X
A   (TORA ) TORAY IND INC.
X
I   Okano F,  Satoh M,  Yamada K;
X
R   WPI; 1999-070100/06.
R   P-PSDB; AAW84371.
X
T   New therapeutic and prophylactic agents - comprise genetically-engineered
T   canine interleukin 12, used to treat, e.g. canine and feline
T   immunological diseases.
X
S   Claim 1; Page 23-25; 45pp; Japanese.
X
    The present sequence encodes a canine interleukin 12 (IL-12) protein. The
    IL-12 protein can be used in therapeutic or prophylactic agents. The
    agents can be used to prevent and treat canine and feline immunological
    diseases including dog and cat tumours, skin diseases, viral infections
    and allergic diseases, especially tumours, breast tumour, oesinophilic
    granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
    pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
    diseases, otitis externa, dermatitis, eczema, fungal diseases of the
    skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
    and hair loss; infections; dog Parvovirus infection and distemper virus,
    cat plaque virus infection and feline leukaemia, and allergic diseases,
    e.g. pollinosis
C
    Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

lignment Scores:
ed. No.:              2.12e-27      Length:         990
core:                 37.00         Matches:        37
ercent Similarity:    100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
uery Match:           11.2%         Indels:         0
B:                    2             Gaps:           0

S-10-821-670A-30 (1-329) x AAX03152 (1-990)

y        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 45
AX35625
D   AAX35625 standard; cDNA to mRNA; 990 BP.
C
C   AAX35625;
X
T   09-JUL-1999  (first entry)
X
E   Nucleic acid encoding canine Interleukin-12 (IL-12).
X
W   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
W   tumour; skin disease; infectious disease; allergic disease; ds.
C
S   Canis sp.
C
    Key             Location/Qualifiers
T   CDS             1. .990
T                   /*tag=  a
C
N   JP11106350-A.
C
```

```
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02342.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 14-15; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.12e-27      Length:         990
Score:                  37.00         Matches:        37
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            11.2%         Indels:         0
DB:                     2             Gaps:           0

US-10-821-670A-30 (1-329) x AAX35625 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 46
AAX35615
ID   AAX35615 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35615;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
```

WPI; 1999-308068/26.
P-PSDB; AAY02339.

A prevention and treating agent containing interleukin 12 (CaIL12) - for prevention and treatment of dog and cat immune diseases.

Claim 1; Page 12; 16pp; Japanese.

The present sequence encodes canine interleukin-12 (IL-12). The specification describes a method for the prevention and treatment of dog and cat immune diseases. The treatment used an agent comprising dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is useful for preventing and treating dog and cat immune diseases, including tumours, skin diseases, infectious diseases and allergic diseases

Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 2.12e-27 Length: 990
ore: 37.00 Matches: 37
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 11.2% Indels: 0
: 2 Gaps: 0

-10-821-670A-30 (1-329) x AAX35615 (1-990)

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
|||||||||||||||||||||||||||||||||||||||||||||||||
667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

SULT 47
I64378
AAI64378 standard; DNA; 990 BP.

AAI64378;

23-NOV-2001 (first entry)

Canine coding sequence #1.

Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.

Canis familiaris.

Key	Location/Qualifiers
CDS	1. .990
	/*tag= a
	/product= "Canine protein #1"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .987
	/*tag= c

JP2001161378-A.

19-JUN-2001.

26-SEP-2000; 2000JP-00292946.

01-OCT-1999; 99JP-00281234.

(TORA) TORAY IND INC.

WPI; 2001-592466/67.
P-PSDB; AAG66480.

Preparation of a highly pure protein, interleukin 12, a protein
PT inhibiting the activity of interleukin 12, and a treating agent and a
PT treating method for immunopathy of mammalian.
XX
PS Claim 6; Page 14; 21pp; Japanese.
XX
CC The present invention relates to a method for the preparation of a highly
CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC IL12. The protein is used as a preventive agent for dog immunopathy. The
CC present sequence was used in the method of the present invention
XX
SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.12e-27	Length:	990
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-30 (1-329) x AAI64378 (1-990)

Qy 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 48
AAI64388
ID AAI64388 standard; DNA; 990 BP.
XX
AC AAI64388;
XX
DT 23-NOV-2001 (first entry)
XX
DE Canine coding sequence #3.
XX
KW Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS Canis familiaris.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .990
FT		/*tag= a
FT		/product= "Canine protein #1"
FT	sig_peptide	1. .66
FT		/*tag= b
FT	mat_peptide	67. .987
FT		/*tag= c

XX
PN JP2001161378-A.
XX
PD 19-JUN-2001.
XX
PF 26-SEP-2000; 2000JP-00292946.
XX
PR 01-OCT-1999; 99JP-00281234.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 2001-592466/67.
DR P-PSDB; AAG66482.
XX
PT Preparation of a highly pure protein, interleukin 12, a protein
PT inhibiting the activity of interleukin 12, and a treating agent and a
PT treating method for immunopathy of mammalian.
XX
PS Claim 6; Page 16-17; 21pp; Japanese.

```
CC
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
CC
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.12e-27      Length:          990
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              11.2%         Indels:          0
DB:                       4             Gaps:            0

US-10-821-670A-30 (1-329) x AAI64388 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 49
ADZ25698
ID   ADZ25698 standard; cDNA; 990 BP.
XX
AC   ADZ25698;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Canine interleukin 12 P40 encoding cDNA SEQ ID NO:3.
XX
KW   interleukin-12; antiviral; gene; ss.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  b
FT                   /product= "interleukin-12 P40"
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "interleukin-12 P40"
XX
PN   JP2003284585-A.
XX
PD   07-OCT-2003.
XX
PF   28-MAR-2002; 2002JP-00090161.
XX
PR   28-MAR-2002; 2002JP-00090161.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2003-885430/82.
DR   P-PSDB; ADZ25702.
XX
PT   Large scale production of interleukin-12 for pharmaceutical applications,
PT   comprises infecting an insect cell with a recombinant virus containing
PT   gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT   of insect cell.
XX
PS   Example; SEQ ID NO 3; 8pp; Japanese.
XX
CC   The invention related to the large scale production of interleukin-12 (IL
CC   -12), which involves infecting an insect cell with a recombinant virus
CC   containing a gene encoding IL-12, and producing IL-12 by carrying out
CC   spinner culture of insect cell. The method is useful for producing IL-12,
CC   preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC   present sequence encodes canine IL-12 P40, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.12e-27      Length:          990
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              11.2%         Indels:          0
DB:                       11            Gaps:            0

US-10-821-670A-30 (1-329) x ADZ25698 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 50
ADT04849
ID   ADT04849 standard; DNA; 1015 BP.
XX
AC   ADT04849;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p40 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
PT   Novel gene vector for expression in insect useful for expression of
PT   foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
PS   Claim 4; SEQ ID NO 5; 13pp; Japanese.
XX
CC   The invention relates to a novel gene vector for expression in an insect
CC   comprising at least two promoters, particularly the polyhedrin promoter
CC   and p10 promoter. The vector contains at least two types of foreign
CC   protein expression gene and the gene product of the vector is produced
CC   using a gene recombinant baculovirus, particularly a recombinant silkworm
CC   nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC   silkworm. The vector of the invention may be useful for expression of a
CC   foreign gene, such as canine interleukin 12. Within the vector, two types
CC   of foreign protein expression genes are integrated simultaneously for
CC   their simultaneous expression. The current sequence is that of the canine
CC   interleukin-12 (IL-12) p40 DNA of the invention.
XX
SQ   Sequence 1015 BP; 285 A; 251 C; 254 G; 225 T; 0 U; 0 Other;

Alignment Scores:
```

ed. No.: 2.18e-27 Length: 1015
ore: 37.00 Matches: 37
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 11.2% Indels: 0
B: 13 Gaps: 0

-10-821-670A-30 (1-329) x ADT04849 (1-1015)

Qy 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 51
X98967
ABK98967 standard; cDNA; 1533 BP.

ABK98967;

21-OCT-2002 (first entry)

Canine interleukin-12 nCaIL-12-1533 coding strand.

Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
canine IL-12; autoimmune disease; allergic reaction; infectious disease;
tumour development; inflammatory disease; graft rejection; gene; ss.

Canis familiaris.

US2002052030-A1.

02-MAY-2002.

27-JUL-2001; 2001US-00917265.

04-AUG-2000; 2000US-0223016P.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2002-573554/61.
P-PSDB; ABG69314.

Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
chain and canine IL-12 single chain proteins, useful for treating and
preventing autoimmune diseases, inflammatory diseases and/or graft
rejection in animals.

Claim 6; Page 83-85; 106pp; English.

The present invention discloses new feline interleukin 18 (IL-18), feline
caspase-1, feline IL-12 single chain and canine IL-12 single chain
proteins. A composition comprising a feline IL-18, feline caspase-1,
feline IL-12 single chain or canine IL-12 single chain proteins, a
nucleic acid encoding these proteins, mimetopes of these proteins,
multimeric forms of these proteins, an antibody against these proteins,
or an inhibitor identified by its ability to inhibit the activity of
these proteins, can be used to treat or prevent autoimmune diseases,
allergic reactions, infectious diseases, tumour development, inflammatory
diseases and/or graft rejection in animals. The present nucleic acid
sequence represents a canine interleukin 12 DNA sequence, as described in
the invention

Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 3.23e-27 Length: 1533

Score: 37.00 Matches: 37
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.2% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-30 (1-329) x ABK98967 (1-1533)

Qy 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 52
ABK98968/c
ID ABK98968 standard; cDNA; 1533 BP.
XX
AC ABK98968;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 86-87; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.23e-27 Length: 1533
Score: 37.00 Matches: 37
Percent Similarity: 100.0% Conservative: 0

```
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            11.2%         Indels:        0
B:                    6             Gaps:          0

S-10-821-670A-30 (1-329) x ABK98968 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

ESULT 53
DV34718/c
D    ADV34718 standard; DNA; 1533 BP.
C
C    ADV34718;
C
C    24-FEB-2005  (first entry)
C
C    Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
C
C    DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
C    infectious disease; antimicrobial; ds.
C
C    Canine familiaris.
C
C    US2004248261-A1.
C
C    09-DEC-2004.
C
C    09-APR-2004; 2004US-00821670.
C
C    04-AUG-2000; 2000US-0223016P.
C    27-JUL-2001; 2001US-00917265.
C
C    (WOND/) WONDERLING R S.
C    (BORO/) BOROUGHS K L.
C
C    Wonderling RS,  Boroughs KL;
C
C    WPI; 2005-020565/02.
C
C    New nucleic acid molecule comprising a sequence encoding a feline p35 or
C    p40 subunit protein and a nucleic acid linker, useful in preparing a
C    vaccine against infectious diseases in feline animals.
C
C    Example 4; SEQ ID NO 68; 103pp; English.
C
C    The present invention relates to the feline interleukin (IL)-12p35 or p40
C    subunit protein and their encoding nucleic acid molecules and a nucleic
C    acid linker. The invention also provides the feline caspase (casp)-1,
C    feline IL-18 single chain and canine IL-12 single chain proteins and
C    their nucleic acid molecules. The nucleic acid molecule is useful in
C    preparing a vaccine against infectious diseases in feline animals. The
C    present sequence is the canine single chain IL-12 complementary DNA.
C
C    Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

lignment Scores:
red. No.:             3.23e-27      Length:        1533
core:                 37.00         Matches:       37
ercent Similarity:    100.0%        Conservative:  0
est Local Similarity: 100.0%        Mismatches:    0
uery Match:           11.2%         Indels:        0
B:                    14            Gaps:          0

S-10-821-670A-30 (1-329) x ADV34718 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 54
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:            3.23e-27      Length:        1533
Score:                37.00         Matches:       37
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          11.2%         Indels:        0
DB:                   14            Gaps:          0

US-10-821-670A-30 (1-329) x ADV34716 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 55
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69313.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 79-80; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.36e-27        Length:         1599
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-30 (1-329) x ABK98965 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 56
ABK98966/c
ID   ABK98966 standard; cDNA; 1599 BP.
XX
AC   ABK98966;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 82-83; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.36e-27        Length:         1599
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-30 (1-329) x ABK98966 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 57
ADV34715/c
ID   ADV34715 standard; DNA; 1599 BP.
XX
AC   ADV34715;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 63; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.36e-27      Length:          1599
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              11.2%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-30 (1-329) x ADV34715 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 58
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.36e-27      Length:          1599
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              11.2%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-30 (1-329) x ADV34713 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 59
AAX18176
ID   AAX18176 standard; cDNA; 2154 BP.
XX
AC   AAX18176;
```

```
07-MAY-1999  (first entry)

Canine full length CLAF p40 subunit coding sequence.

CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
viral disease; canine distemper; canine parvovirus; autoimmune disease;
canine infectious hepatitis; ds.

Canis sp.

WO9855511-A1.

10-DEC-1998.

26-MAY-1998;   98WO-JP002295.

03-JUN-1997;   97JP-00161936.

(KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.

Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;

WPI; 1999-070260/06.
P-PSDB; AAW74322.

Canine cytokine protein which activates canine cytotoxic T lymphocytes -
is useful for treatment of viral and autoimmune diseases in dogs.

Claim 8; Page 30-31; 51pp; Japanese.

This sequence encodes the canine lymphocyte activation factor (CLAF) of
the invention. CLAF activates lymphocytes, especially canine cytotoxic T
cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
recognising it may be used in the treatment of viral diseases in dogs
(such as canine distemper, canine parvovirus and canine infectious
hepatitis). The antibodies may also be used in isolation of CLAF from
culture of the transformant host cells by affinity chromatography. The
p40 homodimer can be used for the treatment of autoimmune diseases in
dogs

Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              4.47e-27      Length:        2154
ore:                  37.00         Matches:       37
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            11.2%         Indels:        0
:                     2             Gaps:          0

-10-821-670A-30 (1-329) x AAX18176 (1-2154)

        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        661 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 720

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        721 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 771

SULT 60
K99006/c
   ABK99006 standard; cDNA; 2267 BP.

   ABK99006;

   21-OCT-2002  (first entry)

   Canine interleukin-12 nCaIL-12p40-2267 complementary strand.

   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 99-100; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.69e-27      Length:        2267
Score:                  37.00         Matches:       37
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            11.2%         Indels:        0
DB:                     6             Gaps:          0

US-10-821-670A-30 (1-329) x ABK99006 (1-2267)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

RESULT 61
ABK99005
ID   ABK99005 standard; cDNA; 2267 BP.
XX
AC   ABK99005;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-2267 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
```

```
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS, Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69317.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 97-98; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.69e-27      Length:          2267
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              11.2%         Indels:          0
DB:                       6             Gaps:            0

US-10-821-670A-30 (1-329) x ABK99005 (1-2267)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 62
ADV34757
ID   ADV34757 standard; cDNA; 2267 BP.
XX
AC   ADV34757;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 protein cDNA, nCaIL-12p40 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             154. .1143
FT                   /*tag= a
FT                   /product= "PCaIL-12p40 329 protein"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS, Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34758.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 107; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.69e-27      Length:          2267
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              11.2%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-30 (1-329) x ADV34757 (1-2267)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 63
ADV34759/c
ID   ADV34759 standard; DNA; 2267 BP.
XX
AC   ADV34759;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 complementary DNA, nCaIL-12p35 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
```

09-DEC-2004.

09-APR-2004; 2004US-00821670.

04-AUG-2000; 2000US-0223016P.
27-JUL-2001; 2001US-00917265.

(WOND/) WONDERLING R S.
(BORO/) BOROUGHS K L.

Wonderling RS, Boroughs KL;

WPI; 2005-020565/02.

New nucleic acid molecule comprising a sequence encoding a feline p35 or p40 subunit protein and a nucleic acid linker, useful in preparing a vaccine against infectious diseases in feline animals.

Example 4; SEQ ID NO 109; 103pp; English.

The present invention relates to the feline interleukin (IL)-12p35 or p40 subunit protein and their encoding nucleic acid molecules and a nucleic acid linker. The invention also provides the feline caspase (casp)-1, feline IL-18 single chain and canine IL-12 single chain proteins and their nucleic acid molecules. The nucleic acid molecule is useful in preparing a vaccine against infectious diseases in feline animals. The present sequence is the canine single chain IL-12p40 subunit complementary DNA.

Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	4.69e-27	Length:	2267
ore:	37.00	Matches:	37
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	11.2%	Indels:	0
:	14	Gaps:	0

-10-821-670A-30 (1-329) x ADV34759 (1-2267)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398
```

SULT 64
Q04701
AAQ04701 standard; DNA; 906 BP.

AAQ04701;

25-MAR-2003 (revised)
11-OCT-1990 (first entry)

Sequence encoding natural killer cell stimulatory factor (NKSF).

Natural killer cell stimulatory factor; NKSF; cancer; leukopaenia; anaemia; radiation; bone marrow transplantation; ds.

Homo sapiens.

WO9005147-A.

17-MAY-1990.

10-NOV-1988; 88US-00269945.

10-NOV-1988; 88US-00269945.

PR 07-FEB-1989; 89US-00307817.
XX
PA (GEMY) GENETICS INST INC.
PA (WIST-) WISTAR INST.
XX
PI Trinchieri G, Perussia B, Kobayashi M, Clark SC, Wong GG;
XX
DR WPI; 1990-178800/23.
DR P-PSDB; AAR05171.
XX
PT New natural killer cell stimulatory factor - useful for treating cancer
PT and e.g. leukopenia, bacterial and viral infections, anaemia and B or T
PT cell deficiencies.
XX
PS Claim 16; Page 60; 69pp; English.
XX
CC Natural killer cell stimulatory factor (NKSF) is useful in treating
CC cancer and other disease states which respond to NK cell activity. Such
CC states may arise from immune or haematopoietic-cell deficiency following
CC a bone marrow translpantation, exposure to radiation and disease.
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 906 BP; 244 A; 220 C; 238 G; 204 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.09e-25	Length:	906
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AAQ04701 (1-906)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782
```

RESULT 65
AAD15208
ID AAD15208 standard; DNA; 975 BP.
XX
AC AAD15208;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p40 encoding DNA from clone A16-94.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p40; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .975
FT		/*tag= a
FT		/product= "Modified p40 protein precursor"
FT	sig_peptide	1. .66
FT		/*tag= b
FT	mat_peptide	67. .972
FT		/*tag= c
FT		/product= "Mature modified p40 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.

```
XX
PD   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08601.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 975 BP; 261 A; 250 C; 255 G; 209 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.24e-25      Length:          975
Score:                    35.00         Matches:         35
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              10.6%         Indels:          0
DB:                       5             Gaps:            0

US-10-821-670A-30 (1-329) x AAD15208 (1-975)

Qy        128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB        382 TTTCTAAAGTGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGGTGGCTGACGGCA 441

Qy        148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||
DB        442 ATCAGTACTGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

RESULT 66
AAQ12149
ID   AAQ12149 standard; DNA; 979 BP.
XX
AC   AAQ12149;
XX
DT   10-SEP-1991  (first entry)
XX
DE   Cytotoxic lymphocyte maturation factor (40 kD subunit) gene.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; probe; antitumour;
KW   monoclonal antibodies; T cell; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .979
FT                   /*tag=  a
FT                   /product= "CLMF"
FT   sig_peptide     41. .106
FT                   /*tag=  b
FT                   /note= "hydrophobic signal peptide"
FT   mat_peptide     107. .979
FT                   /*tag=  c
XX
PN   EP433827-A.
XX
PD   26-JUN-1991.
XX
PF   09-DEC-1990;   90EP-00123670.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YCE;
PI   Podlaski FJ,  Stern AS;
XX
DR   WPI; 1991-186715/26.
DR   P-PSDB; AAR12493.
XX
PT   New cytotoxic lymphocyte maturation factor - used as antitumour agent and
PT   monoclonal antibodies used in transplantation to block proliferation and
PT   activation of cytotoxic T cells.
XX
PS   Disclosure; Fig 25 (a-c); 90pp; English.
XX
CC   The natural CLMF protein is a 75 kD heterodimer comprising two
CC   polypeptide subunits, a 40 kD and a 35 kD subunit (AAQ12150). The
CC   subunits are bonded together via one or more disulfide bonds. The CLMF
CC   can interact with IL-2 to synergistically induce the cytolytic activity
CC   of Lymphokine Activated Killer (LAK) cells. It is also capable of
CC   stimulating T-cell growth. It can be used for the prepn. of LAK- and T-
CC   cell activator and antitumour compsns. and for stimulating Natural Killer
CC   (NK) cells
XX
SQ   Sequence 979 BP; 261 A; 245 C; 257 G; 216 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.25e-25      Length:          979
Score:                    35.00         Matches:         35
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              10.6%         Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-30 (1-329) x AAQ12149 (1-979)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
DB        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 67
ADG39430
ID   ADG39430 standard; DNA; 984 BP.
XX
AC   ADG39430;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CLMF 40 kDa subunit DNA.
XX
KW   human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67. .984
```

```
                     /*tag=  a
                     /partial
                     /product= "CLMF 40 kDa subunit"
                     /note= "No start or stop codon given"

   US2003204059-A1.

   30-OCT-2003.

   08-OCT-2002; 2002US-00267565.

   22-DEC-1989;   89US-00455708.
   09-MAY-1990;   90US-00520935.
   27-AUG-1990;   90US-00572284.
   24-MAR-1992;   92US-00857023.
   02-MAR-1994;   94US-00205011.
   02-JUN-1995;   95US-00459151.
   22-SEP-1999;   99US-00401839.

   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.

   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
   Chizzonite RA,  Pan YE;

   WPI; 2004-010534/01.
   P-PSDB; ADG39429.

   Novel protein comprising cytotoxic lymphocyte maturation factor in
   substantially pure form or protein which exhibits cytotoxic lymphocyte
   maturation factor activity, useful as antitumor and immunoenhancing
   agent.

   Claim 17; Page 28-29; 74pp; English.

   The invention relates to a protein which comprises a cytotoxic lymphocyte
   maturation factor (CLMF). The protein is useful for stimulating activated
   T-cells which involves treating T-cells with the protein. The method
   further involves treating the activated T-cells with IL2 or its
   biologically active fragment. The protein is useful for stimulating
   natural killer cells which involves treating the natural killer cells
   with the protein. The protein has immunoenhancing and antitumour effects
   when used as single therapeutic agent in vivo. The present sequence is
   used in the exemplification of the present invention.

   Sequence 984 BP; 263 A; 243 C; 258 G; 220 T; 0 U; 0 Other;

ignment Scores:
ed. No.:               2.26e-25      Length:         984
ore:                   35.00         Matches:        35
rcent Similarity:      100.0%        Conservative:   0
st Local Similarity:   100.0%        Mismatches:     0
ery Match:             10.6%         Indels:         0
:                      12            Gaps:           0

-10-821-670A-30 (1-329) x ADG39430 (1-984)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

SULT 68
Q97484
   AAQ97484 standard; cDNA; 987 BP.

   AAQ97484;

   25-MAR-2003  (revised)
   22-DEC-1995  (first entry)

DE   Human interleukin-12 40 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Wolf SF,  Sykes M;
XX
DR   WPI; 1995-269273/35.
DR   P-PSDB; AAR79186.
XX
PT   Control of graft versus host disease using interleukin 12 - partic.
PT   admin. at the time of bone marrow transplant.
XX
PS   Disclosure; Page 21-22; 32pp; English.
XX
CC   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC   12 is a heterodimeric cytokine which was originally identified as a
CC   factor which induces gamma-interferon from T cells and natural killer
CC   cells as set forth in PCT/US91/06332, published April 2 1992, and
CC   incorporated by reference. EP 433827, published June 26 1991, disclosed
CC   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC   is defined as a heterodimeric glycoprotein comprised of two covalently
CC   linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC   subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             2.27e-25      Length:         987
Score:                 35.00         Matches:        35
Percent Similarity:    100.0%        Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:           10.6%         Indels:         0
DB:                    2             Gaps:           0

US-10-821-670A-30 (1-329) x AAQ97484 (1-987)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 69
AAV07273
ID   AAV07273 standard; cDNA; 987 BP.
XX
AC   AAV07273;
XX
DT   25-SEP-1998  (first entry)
```

Human Interleukin-12 p40 gene.

IL-12 subunit; expression construct; treatment; asthma;
microbial infection; viral infection; cancer; Human; Interleukin; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .987
	/*tag= a
	/product= "IL-12 p40"

WO9817689-A2.

30-APR-1998.

10-OCT-1997; 97WO-US018779.

18-OCT-1996; 96US-0028676P.

(GENE-) GENEMEDICINE INC.

Nordstrom J, Freimark B, Deshpande D;

WPI; 1998-261428/23.
P-PSDB; AAW51311.

Constructs for expression of interleukin-12 sub-units - are used for delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral infections and certain cancers.

Claim 1; Page 34; 80pp; English.

The IL-12 subunits AAV07273 and AAV07274 can be expressed using an appropriate expression construct engineered into a plasmid. The plasmids can provide for efficient expression of IL-12 subunits. The products can be used for the treatment of asthma, microbial and viral infections and certain cancers

Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	2.27e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AAV07273 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 70
AAV07217
AAV07217 standard; DNA; 987 BP.

AAV07217;

12-AUG-1998 (first entry)

DNA encoding human interleukin-12 40kDa subunit.

Interleukin-12; IL-12; graft-versus-host disease;
GVHD. bone marrow transplantation; graft-versus-leukemia; ss.

OS Homo sapiens.

Key	Location/Qualifiers
CDS	1. .987
	/*tag= a
	/product= "Interleukin-12_40kDa_subunit"

US5756085-A.

26-MAY-1998.

30-APR-1996; 96US-00640386.

21-JAN-1994; 94US-00186529.

(GEMY) GENETICS INST INC.
(GEHO) GEN HOSPITAL CORP.

Sykes M, Wolf SF;

WPI; 1998-321459/28.
P-PSDB; AAW51221.

Therapy of graft-versus-host disease - by administration of interleukin-12 to maintain and/or promote graft-versus-leukaemia effects.

Disclosure; Col 17-20; 20pp; English.

The invention relates to a method for the treatment or prevention of graft-versus-host disease (GVHD) which comprises the administration of interleukin-12 (IL-12) at the time of bone-marrow transplantation to maintain or promote graft-versus-leukaemia effects. Preferably, dosage is 0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of the bone marrow transplant. IL-12 is administered daily until there is an improvement in the condition. Administration is oral, cutaneous, subcutaneous, intravenous or by inhalation preferably subcutaneous, or intravenous. The present sequence encodes the human interleukin-12 40kDa subunit

Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	2.27e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AAV07217 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 71
AAZ40406
AAZ40406 standard; DNA; 987 BP.

AAZ40406;

15-FEB-2000 (first entry)

Human interleukin 12 p40 subunit semi-optimised coding sequence.

Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
promoter; growth hormone; untranslated region; UTR; mammal; disease;
cancer; ss.

Homo sapiens.

WO9947678-A2.

23-SEP-1999.

12-MAR-1999; 99WO-US005394.

19-MAR-1998; 98US-0078654P.

(GENE-) GENEMEDICINE INC.

Nordstrom J, Pericle F, Rolland A, Ralston R;

WPI; 1999-562116/47.
P-PSDB; AAY42487.

New plasmids containing an interferon-alpha coding sequence, used for the treatment of a mammalian condition or disease, particularly cancer.

Claim 11; Page 43-45; 137pp; English.

This sequence represents a semi-optimised coding region for the human interleukin 12 p40 subunit. The invention relates to a novel plasmid comprising a cytomegalovirus (CMV) promoter transcriptionally linked with an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-untranslated region (UTR). The plasmids can be used for treating a mammalian condition or disease, particularly cancer

Sequence 987 BP; 216 A; 330 C; 296 G; 145 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 2.27e-25 Length: 987
ore: 35.00 Matches: 35
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 10.6% Indels: 0
: 2 Gaps: 0

-10-821-670A-30 (1-329) x AAZ40406 (1-987)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750
```

GULT 72
Z40404
AAZ40404 standard; DNA; 987 BP.

AAZ40404;

15-FEB-2000 (first entry)

Human interleukin 12 p40 subunit wild type coding sequence.

Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV; promoter; growth hormone; untranslated region; UTR; mammal; disease; cancer; ss.

Homo sapiens.

WO9947678-A2.

23-SEP-1999.

12-MAR-1999; 99WO-US005394.

19-MAR-1998; 98US-0078654P.

PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR P-PSDB; AAY42487.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX
PS Claim 11; Page 43-45; 137pp; English.
XX
CC This sequence represents the wild type coding region for the human
CC interleukin 12 p40 subunit. The invention relates to a novel plasmid
CC comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC untranslated region (UTR). The plasmids can be used for treating a
CC mammalian condition or disease, particularly cancer
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.27e-25 Length: 987
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-30 (1-329) x AAZ40404 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 73
AAZ40405
ID AAZ40405 standard; DNA; 987 BP.
XX
AC AAZ40405;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human interleukin 12 p40 subunit optimised coding sequence.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9947678-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005394.
XX
PR 19-MAR-1998; 98US-0078654P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR P-PSDB; AAY42487.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX

Claim 11; Page 43-45; 137pp; English.

This sequence represents an optimised coding region for the human interleukin 12 p40 subunit. The invention relates to a novel plasmid comprising a cytomegalovirus (CMV) promoter transcriptionally linked with an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-untranslated region (UTR). The plasmids can be used for treating a mammalian condition or disease, particularly cancer

Sequence 987 BP; 220 A; 324 C; 318 G; 125 T; 0 U; 0 Other;

Alignment Scores:

ed. No.:	2.27e-25	Length:	987
ore:	35.00	Matches:	35
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
B:	2	Gaps:	0

S-10-821-670A-30 (1-329) x AAZ40405 (1-987)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750
```

ESULT 74
AD15210
AAD15210 standard; DNA; 987 BP.

AAD15210;

01-NOV-2001 (first entry)

Human cytokine p40 DNA.

Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human; p40; ds.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .987
	/*tag= a
	/product= "p40 protein precursor"
sig_peptide	1. .66
	/*tag= b
mat_peptide	67. .984
	/*tag= c
	/product= "Mature p40 protein"

WO200140257-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032664.

02-DEC-1999; 99US-0169035P.
28-NOV-2000; 2000US-00725324.

(MAXY-) MAXYGEN INC.

Leong SR, Punnonen J;

WPI; 2001-502381/55.
P-PSDB; AAE08603.

Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides), useful for treating various diseases e.g. diabetic retinopathy and cancer.

Claim 5; Page 142; 223pp; English.

CC The invention relates to nucleic acids encoding modified cytokine polypeptides (i.e. modified p40 and p35 polypeptides). The modified cytokine polypeptides have T-cell proliferative and interferon (IFN)-gamma induction activities. The polypeptides and polynucleotides of the invention are useful for treating various diseases e.g. bacterial infections, AIDS, diabetic retinopathy and cancer. The polypeptide and polynucleotide may also be useful as a vaccine adjuvant, to enhance a vaccinated host's cell-mediated immunity for protective response to a pathogen. The present sequence is human p40 protein encoding DNA

SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.27e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-30 (1-329) x AAD15210 (1-987)

```
Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 75
ADF77278
ID ADF77278 standard; DNA; 987 BP.
XX
AC ADF77278;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p40 subunit optimised DNA #2.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; Page 14-15; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,

comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 987 BP; 216 A; 331 C; 294 G; 145 T; 0 U; 1 Other;

ignment Scores:
ed. No.: 2.27e-25 Length: 987
ore: 35.00 Matches: 35
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 10.6% Indels: 0
: 12 Gaps: 0

-10-821-670A-30 (1-329) x ADF77278 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750
```

SULT 76
F77263
ADF77263 standard; DNA; 987 BP.

ADF77263;

26-FEB-2004 (first entry)

Human IL-12 p40 subunit optimised DNA #4.

ds; human; interferon alpha expression plasmid; tumour; IL-12.

Synthetic.
Homo sapiens.

US2003181405-A1.

25-SEP-2003.

29-APR-2002; 2002US-00136837.

12-MAR-1999; 99US-00268135.

(NORD/) NORDSTROM J L.
(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

Nordstrom JL, Pericle F, Rolland A, Ralston RO;

WPI; 2004-020834/02.

A mammalian interferon alpha expression plasmid is useful in gene therapy to deliver interferon alpha to cells to modulate tumor activity in the treatment of cancer.

Disclosure; SEQ ID NO 32; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 987 BP; 272 A; 138 C; 164 G; 413 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.27e-25 Length: 987
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 12 Gaps: 0

US-10-821-670A-30 (1-329) x ADF77263 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CATAAATTAAAATATGAAAATTATACTTCTTCTTTTTTTATTCGTGATATTATTAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GATCCTCCTAAAAATTTACAATTAAAACCTTTAAAAAATTCTCGT 750
```

RESULT 77
ADF77277
ID ADF77277 standard; DNA; 987 BP.
XX
AC ADF77277;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p40 subunit optimised DNA #1.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; Page 14-15; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,
CC comprising a promoter and a synthetic 5' intron transcriptionally linked
CC with an interferon alpha coding sequence and a 3' untranslated region.
CC The mammalian interferon alpha expression plasmid is useful for treating
CC tumour growth. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 987 BP; 220 A; 325 C; 317 G; 125 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.27e-25 Length: 987
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 12 Gaps: 0

-10-821-670A-30 (1-329) x ADF77277 (1-987)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750
```

ESULT 78
DF77276
ADF77276 standard; DNA; 987 BP.

ADF77276;

26-FEB-2004 (first entry)

Human IL-12 p40 subunit DNA.

ds; human; interferon alpha expression plasmid; tumour; IL-12.

Homo sapiens.

US2003181405-A1.

25-SEP-2003.

29-APR-2002; 2002US-00136837.

12-MAR-1999; 99US-00268135.

(NORD/) NORDSTROM J L.
(PERI/) PERICLE F.
(ROLL/) ROLLAND A.
(RALS/) RALSTON R O.

Nordstrom JL, Pericle F, Rolland A, Ralston RO;

WPI; 2004-020834/02.

A mammalian interferon alpha expression plasmid is useful in gene therapy to deliver interferon alpha to cells to modulate tumor activity in the treatment of cancer.

Disclosure; Page 14-15; 65pp; English.

The invention relates to a mammalian interferon alpha expression plasmid, comprising a promoter and a synthetic 5' intron transcriptionally linked with an interferon alpha coding sequence and a 3' untranslated region. The mammalian interferon alpha expression plasmid is useful for treating tumour growth. The present sequence is used in the exemplification of the present invention.

Sequence 987 BP; 264 A; 243 C; 258 G; 221 T; 0 U; 1 Other;

lignment Scores:			
red. No.:	2.27e-25	Length:	987
core:	35.00	Matches:	35
ercent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
B:	12	Gaps:	0

-10-821-670A-30 (1-329) x ADF77276 (1-987)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 79
ADO07653
ID ADO07653 standard; DNA; 987 BP.
XX
AC ADO07653;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human interleukin-12 40kDa coding sequence.
XX
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS Homo sapiens.
XX
PN WO2004035799-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011252.
XX
PR 11-OCT-2002; 2002DE-01048141.
XX
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI Waehler R, Schnieders F;
XX
DR WPI; 2004-357221/33.
XX
PT Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
PS Claim 4; Fig 19; 129pp; German.
XX
CC The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a human interleukin-12 coding sequence used in the
CC exemplification of the invention.
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	2.27e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-30 (1-329) x ADO07653 (1-987)

```
Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 80
ADS00006
ID ADS00006 standard; DNA; 987 BP.
XX
AC ADS00006;
XX
DT 16-DEC-2004 (first entry)
XX

Human interleukin-23 (IL-23) p40 subunit DNA.

tumour; interleukin-23; IL-23; cytostatic; immunostimulant; cancer;
p40 subunit; ds; gene.

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .987
	/*tag= a
	/product= "Human interleukin-23 (IL-23) p40 subunit protein"

JP2004262797-A.

24-SEP-2004.

28-FEB-2003; 2003JP-00052999.

28-FEB-2003; 2003JP-00052999.

(CHIB-) CHIBA PREFECTURE.

WPI; 2004-665614/65.
P-PSDB; ADS00010.

Novel anti-tumor agent comprising interleukin-23 gene, or cell transduced with interleukin-23 gene, as active ingredient, useful for activating anti-tumor immune response and treating tumor.

Disclosure; SEQ ID NO 2; 23pp; Japanese.

The invention relates to a novel anti-tumour agent comprising an interleukin-23 (IL-23) gene, or a cell transduced with an IL-23 gene, as an active ingredient. The molecules of the invention demonstrate cytostatic and immunostimulant activities and may be useful within an anti-tumour agent which activates an anti-tumour immune response. The agent is safe when used in cancer treatment, may be combined with other treatments and induces tumour-specific acquired immunity. The current sequence is that of the human interleukin-23 (IL-23) p40 subunit DNA of the invention.

Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	2.27e-25	Length:	987
ore:	35.00	Matches:	35
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
:	13	Gaps:	0

-10-821-670A-30 (1-329) x ADS00006 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

SULT 81
V42753
ADV42753 standard; cDNA; 987 BP.

ADV42753;

10-MAR-2005 (first entry)

Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 381.

microarray; psychoneuroendocrinimmune; chronic fatigue;
non-insulin dependent diabetes; allergy; immune disorder; inflammation;
cancer; neoplasm; infection; expressed sequence tag; ss.

Homo sapiens.

WO2004108899-A2.

16-DEC-2004.

04-JUN-2004; 2004WO-US017686.

04-JUN-2003; 2003US-0475915P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Nicholson A, Vernon SD;

WPI; 2005-031682/03.

New microarray comprising probes for genes involved in psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a condition associated with PNI activity, e.g., inflammatory or infectious diseases.

Claim 1; SEQ ID NO 381; 254pp; English.

The invention relates to a new microarray which comprises probes for genes involved in psychoneuroendocrinimmune (PNI) activity. The microarray is useful in diagnosing a condition associated with PNI activity, such as CFS, type-2 diabetes, allergic condition, inflammation, cancer and infection. The present sequence represents a psychoneuroendocrinimmune gene expressed sequence tag. Note the specificatio mentions SEQ ID NO of up to 3314 but only sequences up to SEQ ID NO 1829 are provided.

Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.27e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-30 (1-329) x ADV42753 (1-987)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 82
ADW97242
ADW97242 standard; DNA; 987 BP.

ADW97242;

19-MAY-2005 (first entry)

Human p40 gene that inhibits IL-23 immune response Seq 1a.

immune inhibition; transplant rejection; immune disorder;
autoimmune disease; allergy; immunosuppressive; antiallergic; gene; ds.

Homo sapiens.

FH Key	Location/Qualifiers
FT CDS	1. .987
FT	/*tag= a

```
                     /product= "P40 protein"

   JP2005060313-A.

   10-MAR-2005.

   13-AUG-2003; 2003JP-00292937.

   13-AUG-2003; 2003JP-00292937.

   (CHIB-) CHIBA PREFECTURE.

   WPI; 2005-200132/21.
   P-PSDB; ADW97244.

   Pharmaceutical formulation for inhibiting immune response generated by
   interleukin-23 (IL-23) and treating e.g. autoimmune diseases, comprises
   p40 molecules or gene encoding p40 molecules.

   Claim 3; SEQ ID NO 1; 12pp; Japanese.

   This invention relates to a novel pharmaceutical formulation used for
   inhibiting the immune response generated by interleukin-23 (IL-23).
   Specifically, it refers to a formulation comprising the p40 protein or
   the gene encoding this protein thereof. The present invention describes
   the p40 gene contained in the form of a viral or non-viral vector that is
   capable of expressing and secreting the p40 protein. This vector can be
   introduced into a cell such that it can in turn inhibit the immune
   response generated by the production of IL-23. Accordingly, this method
   is useful for suppressing organ transplant rejection or treating
   immunological disorders associated with abnormal immune response with
   regard to IL-23. Furthermore, it can be used to treat autoimmune diseases
   and allergy. As such, compositions exhibit immunosuppressive and
   antiallergic activities. This polynucleotide sequence is the human p40
   gene of the invention.

   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

lignment Scores:
red. No.:                2.27e-25        Length:         987
core:                    35.00           Matches:        35
ercent Similarity:       100.0%          Conservative:   0
st Local Similarity:     100.0%          Mismatches:     0
ery Match:               10.6%           Indels:         0
:                        14              Gaps:           0

-10-821-670A-30 (1-329) x ADW97242 (1-987)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 83
EB48822
   AEB48822 standard; cDNA to mRNA; 987 BP.

   AEB48822;

   22-SEP-2005  (first entry)

   Human interleukin-12 p40 domain coding sequence.

   Interleukin-12; cytokine; lymphokine; cancer; tumor; glioblastoma;
   neoplasm; neurological disease; cytostatic; therapy; immunoconjugate;
   fusion protein; gene; ss.

   Homo sapiens.

   Key             Location/Qualifiers

FT   CDS             1. .987
FT                   /*tag=  b
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .984
FT                   /*tag=  c
FT                   /product= "Mature interleukin-12 p40 subunit"
XX
PN   WO2005066348-A2.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-GB000007.
XX
PR   05-JAN-2004; 2004US-0534307P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
PA   (ANTI-) ANTISOMA PLC.
XX
PI   Gillies S,  Lo K,  Lan Y,  Verma R;
XX
DR   WPI; 2005-512669/52.
XX
PT   Novel compound comprising target specific portion having monoclonal
PT   antibody having specificity for oncofetal fibronectin and effector
PT   portion having interleukin-12, useful for treating cancer e.g.
PT   glioblastoma.
XX
PS   Claim 36; SEQ ID NO 10; 83pp; English.
XX
CC   The invention provides a compound comprising a target specific portion
CC   and an effector portion, in which the target specific portion comprises
CC   or consists of a monoclonal antibody having specificity for oncofetal
CC   fibronectin, or its fragment or variant which retains the antigen binding
CC   specificity of the parent monoclonal antibody, and the effector portion
CC   comprises or consists of interleukin-12, or its functional fragment or
CC   variant. The monoclonal antibody binds to a region of oncofetal
CC   fibronectin other than the extra-domain B region. Preferably, the
CC   compound comprises a target specific portion that is capable of binding
CC   to an amino acid sequence present in fibronectin expressed in both fetal
CC   and normal adult tissue, especially the repeat 7 domain of fibronectin,
CC   and is preferably specific for human oncofetal fibronectin. The
CC   monoclonal antibody is preferably a BC1 antibody. The invention also
CC   provides nucleic acids encoding the compounds of the invention and
CC   methods of their use in the production of these compounds, as well as
CC   methods of using the compounds in medicine, especially for the treatment
CC   of cancer in a patient, where the patient is a mammal, preferably a
CC   human, and the patient has a solid tumor. The cancer is a glioblastoma
CC   (claimed) or ovarian, gastric, colorectal or pancreatic cancer. The
CC   present sequence is the coding sequence of the p40 domain of human
CC   interleukin-12. In a claimed compound, the effector portion consists of a
CC   single chain interleukin-12 comprising or consisting of an interleukin-12
CC   p40 domain conjugated to the interleukin-12 and p35 domain AEB48815 via a
CC   disulfide bond. A further claimed compound comprises the p40 sequence
CC   linked by disulfide bond to a fusion protein AEB48818 comprising the BC1
CC   heavy chain fused to human interleukin-12 p35.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.27e-25        Length:         987
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              10.6%           Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-30 (1-329) x AEB48822 (1-987)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705
```

```
        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            ||||||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

SULT 84
D18585
   AAD18585 standard; DNA; 1007 BP.

   AAD18585;

   18-DEC-2001  (first entry)

   Human interleukin-12 (IL-12) p40 subunit DNA.

   Human; interleukin-12; IL-12; p40 subunit; cytostatic; virucide; AIDS;
   Acquired Immune Deficiency Syndrome; immunisation; hepatitis; malaria;
   tuberculosis; vaccine; gene therapy; cancer; influenza; ds.

   Homo sapiens.

   Key             Location/Qualifiers
   CDS             7. .993
                   /*tag=  a
                   /product= "Human IL-12p40 subunit protein"

   WO200168802-A2.

   20-SEP-2001.

   15-MAR-2001; 2001WO-KR000408.

   15-MAR-2000; 2000KR-00013133.
   13-MAR-2001; 2001KR-00012987.

   (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
   (PROG-) PROGEN CO LTD.

   Sung YC,  Lee SH,  Ha SJ,  Song MK,  Chang J;

   WPI; 2001-596904/67.
   P-PSDB; AAE11198.

   Novel human or mouse interleukin (IL)-12p40 subunit mutant genes, that
   inhibit secretion of IL-12p40, but normally secrete IL-12p70, useful as
   adjuvant for DNA vaccination and gene therapy to AIDS, cancer, malaria.

   Claim 1; Page 89-90; 103pp; English.

   The invention relates to mutant interleukin (IL)-12p40 subunit genes
   which produces highly active human or mouse IL-12p40 sequence. IL-12p40
   DNA is useful for DNA immunisation or gene therapy for treating diseases
   such as cancer, AIDS, hepatitis C, hepatitis B or influenza, malaria or
   tuberculosis, as an therapeutic or prophylactic adjuvant. IL-12p40 DNA
   induces immune response by increasing the hydrolysis activity of
   cytotoxic T lymphocytes when IL-12p40 subunit gene is injected with the
   DNA vaccine, or increasing secretion of interferon (IFN)-gamma from T
   helper cells or CD8+ T cells when IL-12p40 subunit gene is injected with
   DNA vaccine. IL-12p40 DNA is useful in gene therapy and as a DNA vaccine.
   The present sequence is a DNA encoding human Interleukin (IL)-12p40
   subunit protein

   Sequence 1007 BP; 270 A; 247 C; 265 G; 225 T; 0 U; 0 Other;

ignment Scores:
ed. No.:              2.31e-25      Length:        1007
ore:                  35.00         Matches:       35
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            10.6%         Indels:        0
:                     5             Gaps:          0

-10-821-670A-30 (1-329) x AAD18585 (1-1007)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756

RESULT 85
AAQ67879
ID   AAQ67879 standard; DNA; 1018 BP.
XX
AC   AAQ67879;
XX
DT   25-MAR-2003  (revised)
DT   23-MAR-1995  (first entry)
XX
DE   EPV 42 kD promoter/Human IL-12 p40 subunit expression cassette.
XX
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW   polymerase chain reaction; poxvirus; pSD542; immunological response;
KW   pathogen; human; interferon; IFN; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        1. .31
FT                   /*tag=  a
FT                   /note= "EPV 42 kD promoter"
FT   CDS             32. .1018
FT                   /*tag=  b
FT                   /product= "Human IL-12 p40"
XX
PN   WO9416716-A1.
XX
PD   04-AUG-1994.
XX
PF   21-JAN-1994;   94WO-US000888.
XX
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 1994-263767/32.
XX
PT   Attenuated recombinant virus used for cancer therapy - comprises DNA
PT   encoding cytokine and/or tumour associated antigen.
XX
PS   Example 27; Fig 33; 232pp; English.
XX
CC   The sequences given in AAQ67879-80 are expression cassettes which contain
CC   the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC   control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC   promoter, respectively. These sequences were used in the construction of
CC   an ALVAC-based recombinant virus containing the genes for the two
CC   subunits of human IL-12. The p40 subunit was amplified using primers
CC   JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC   42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC   using primers JP186 and JP201 and placed under the control of the
CC   vaccinia E3L promoter using primers JP218 and JP220. The expression
CC   cassette was isolated and ligated with pBSSK+ generating plasmid
CC   PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC   assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC   cassettes are orientated head-to-head relative to each other. The
CC   combination casette containing the poxvirus promoted genes for both IL-12
CC   subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC   plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC   and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
```

contains both the human IL-12 genes in the C6 locus. The resulting virus may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

Alignment Scores:

ed. No.:	2.34e-25	Length:	1018
core:	35.00	Matches:	35
ercent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
B:	2	Gaps:	0

S-10-821-670A-30 (1-329) x AAQ67879 (1-1018)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781
```

ESULT 86
AZ08510
AAZ08510 standard; DNA; 1018 BP.

AAZ08510;

19-OCT-1999 (first entry)

EPV 42 kDa/human IL-12 P40 expression cassette.

Attenuated recombinant virus; cytokine; tumour associated antigen; NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies; cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF; interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen; carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza; immunological response; immunotherapy; vaccine; Newcastle Disease; ss.

Synthetic.
pox virus.
Homo sapiens.
Unidentified.

US5942235-A.

24-AUG-1999.

02-JUN-1995; 95US-00458356.

24-DEC-1981; 81US-00334456.
08-DEC-1982; 82US-00446824.
19-JUN-1984; 84US-00622135.
27-AUG-1987; 87US-00090209.
28-AUG-1987; 87US-00090711.
20-OCT-1987; 87US-00110335.
25-APR-1988; 88US-00186054.
23-AUG-1988; 88US-00234390.
14-JUN-1990; 90US-00537882.
14-JUN-1990; 90US-00537890.
16-DEC-1991; 91US-00805567.
03-MAR-1992; 92US-00847977.
06-MAR-1992; 92US-00847951.
04-MAY-1992; 92US-00881995.
22-JUL-1992; 92US-00918278.
20-JAN-1993; 93US-00007115.
19-JAN-1994; 94US-00184009.
14-APR-1994; 94US-00228926.
13-SEP-1994; 94US-00306259.

PA (HEAL-) HEALTH RES INC.
PI Paoletti E;
DR WPI; 1999-493494/41.
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
PS Example 27; Fig 33; 163pp; English.
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC EPV 42 kDa/human IL-12 P40 expression cassette used in the
CC exemplification of the present invention
SQ Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.34e-25	Length:	1018
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AAZ08510 (1-1018)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781
```

RESULT 87
ADR21886
ID ADR21886 standard; DNA; 1018 BP.
AC ADR21886;
DT 04-NOV-2004 (first entry)
DE EPV 42kDa/human IL-12 expression cassette.
KW Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW cancer therapy; ds; human; IL-12; EPV 42kDa; expression cassette.
OS Heliothis armigera entomopoxvirus.
OS Homo sapiens.
OS Synthetic.
PN US6780407-B1.
PD 24-AUG-2004.

15-SEP-2000; 2000US-00663667.

08-MAR-1989; 89US-00320471.
14-FEB-1990; 90US-00478179.
07-JAN-1991; 91US-00638080.
07-MAR-1991; 91US-00666056.
11-JUN-1991; 91US-00713967.
16-DEC-1991; 91US-00805567.
03-MAR-1992; 92US-00847977.
06-MAR-1992; 92US-00847951.
21-JAN-1993; 93US-00007115.
19-JAN-1994; 94US-00184009.
30-AUG-1995; 95US-00521016.

(AVET) AVENTIS PASTEUR.

Paoletti E, Tartaglia J, Cox WI;

WPI; 2004-601998/58.

New recombinant poxvirus which is an attenuated avipox Virus that expresses an exogenous DNA encoding carcinoembryonic antigen and an exogenous DNA encoding B7 protein, useful for cancer therapy.

Example 27; SEQ ID NO 194; 181pp; English.

The invention describes a recombinant poxvirus containing exogenous DNA in a nonessential region of the poxvirus, where the poxvirus is an attenuated avipox Virus that expresses an exogenous DNA encoding carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also described are: a composition comprising a poxvirus above in admixture with a carrier; and expressing carcinoembryonic antigen and B7 protein in vivo comprising administering to a mammal the composition above. Disclosed are: making recombinant poxvirus defined above; recombinant poxvirus vaccine having an increased level of safety compared to known recombinant poxvirus vaccines; and a modified vector for expressing a gene product in a host. The recombinant poxvirus is useful for providing a recombinant poxvirus vaccine having an increased level of safety compared to known recombinant poxvirus vaccines. The recombinant poxvirus is useful for cancer therapy. This sequence represents a human IL-12 expression cassette used in the creation of NYVAC rescue virus and canarypox virus vector ALVAC comprising the human IL-12 gene.

Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 2.34e-25 Length: 1018
ore: 35.00 Matches: 35
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 10.6% Indels: 0
: 13 Gaps: 0

-10-821-670A-30 (1-329) x ADR21886 (1-1018)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781
```

SULT 88
P88402
ADP88402 standard; cDNA; 1029 BP.

ADP88402;

09-SEP-2004 (first entry)

Human interleukin-12 beta chain coding sequence.

KW antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW antibacterial; protozoacide; gene therapy; expression vector;
KW interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004052929-A2.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2003; 2003WO-IB006404.
XX
PR 06-DEC-2002; 2002GB-00028465.
XX
PA (UYBE-) UNIV QUEENS BELFAST.
XX
PI Vandenbroeck K, Alloza I;
XX
DR WPI; 2004-487887/46.
XX
PT New expression vector comprising DNA encoding a subunit of a dimeric form
PT of interleukin under transcriptional control of an ecdysone-inducible
PT promoter, useful in preparing a composition for treating e.g.,
PT inflammatory disease.
XX
PS Disclosure; Page 86-87; 87pp; English.
XX
CC The present invention relates to an expression vector comprising DNA
CC encoding a subunit of a dimeric form of interleukin under transcriptional
CC control of an ecdysone-inducible promoter. The expression vector is
CC useful in preparing a composition for treating a disease having a
CC pathogenesis which includes endogenous production of cytokine IL-12, IL-
CC 23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
CC induced inflammation, epithelial airway inflammation such as asthma,
CC allergic disease, or autoimmune disease such as multiple sclerosis or
CC inflammatory bowel disease. The present sequence is the coding sequence
CC of the human interleukin-12 beta chain used in the exemplification of the
CC invention.
XX
SQ Sequence 1029 BP; 275 A; 261 C; 267 G; 226 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.36e-25 Length: 1029
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 12 Gaps: 0

US-10-821-670A-30 (1-329) x ADP88402 (1-1029)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 720

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 765
```

RESULT 89
AAF76880
ID AAF76880 standard; DNA; 1389 BP.
XX
AC AAF76880;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human p40-IL-2 coding sequence.
XX
KW Human; p40-IL-2; interleukin-2; IL-2; antiviral; antibacterial;
KW antifungal; cytostatic; antiparasitic; vaccine; gene therapy;
KW fusion protein; protein complex; cytokine; immunoglobulin; cancer;

infection; ds.

Homo sapiens.
Synthetic.

WO200110912-A1.

15-FEB-2001.

09-AUG-2000; 2000WO-US021715.

09-AUG-1999; 99US-0147924P.

(LEXI-) LEXIGEN PHARM CORP.

Gillies SD, Lo KM;

WPI; 2001-191523/19.

Novel multifunctional fusion protein or protein complexes useful for treating cancer and viral infections, comprise two different cytokine molecules and a targeting group.

Example 1; Page 75-76; 90pp; English.

The present sequence is given in a specification relating to multifunctional fusion proteins and protein complexes comprising at least two different cytokine molecules and a targeting group such as an immunoglobulin. The fusion proteins and protein complexes are useful for treating cancers, and bacterial, viral, fungal and parasitic infections. They are also useful in gene therapy and as vaccines to prevent or treat various diseases

Sequence 1389 BP; 413 A; 325 C; 327 G; 324 T; 0 U; 0 Other;

lignment Scores:
ed. No.: 3.14e-25 Length: 1389
core: 35.00 Matches: 35
ercent Similarity: 100.0% Conservative: 0
est Local Similarity: 100.0% Mismatches: 0
uery Match: 10.6% Indels: 0
B: 4 Gaps: 0

-10-821-670A-30 (1-329) x AAF76880 (1-1389)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 90
AT77849
AAT77849 standard; DNA; 1397 BP.

AAT77849;

25-MAR-2003 (revised)
18-MAR-1998 (first entry)

40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.

Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit; interleukin-2; T-cell growth; antibody; lymphokine activated killer cell; CLMF bioactivity inhibition; affinity ligand; transplantation; cytotoxic T cell proliferation; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 41. .1027

FT /*tag= a
XX
PN EP790255-A2.
XX
PD 20-AUG-1997.
XX
PF 09-DEC-1990; 97EP-00104656.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 09-DEC-1990; 90EP-00123670.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE;
PI Podlanski FJ, Stern AS;
XX
DR WPI; 1997-404698/38.
DR P-PSDB; AAW24235.
XX
PT Antibodies to cytotoxic lymphocyte maturation factor protein - useful as affinity ligands, assay reagents and medicaments.
XX
PS Disclosure; Fig 25; 80pp; English.
XX
CC The present DNA sequence encodes the 40 kDa subunit of cytotoxic lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is a 75 kDa heterodimer, where the 2 subunits (see AAT77850 for the 35 kDa subunit) are bonded together via one or more disulphide bonds. CLMF protein is produced by a human B lyphoblastoid cell line. CLMF synergistically induces, in the presence of interleukin-2, the cytolytic activity of lymphokine activated killer cells. CLMF is also capable of stimulating T-cell growth. A novel antibody directed against an epitope of CLMF protein (see AAW24237 for epitope) is capable of neutralising and/or inhibiting CLMF bioactivity. This antibody may be used as an affinity ligand for purifying the CLMF protein. The antibody can also be used as an assay reagent for detecting the CLMF protein, and as a medicament for selectively blocking the proliferation and activation of cytotoxic T cells, e.g. in transplantation. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.16e-25 Length: 1397
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-30 (1-329) x AAT77849 (1-1397)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 91
AAT97969
ID AAT97969 standard; DNA; 1397 BP.
XX
AC AAT97969;
XX
DT 25-MAR-2003 (revised)
DT 18-MAR-1998 (first entry)
XX
DE 40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX

Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
CLMF bioactivity inhibition; affinity ligand; transplantation;
cytotoxic T cell proliferation; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	41. .1027
	/*tag= a

EP790308-A1.

20-AUG-1997.

09-DEC-1990; 97EP-00104682.

22-DEC-1989; 89US-00455708.
09-MAY-1990; 90US-00520935.
27-AUG-1990; 90US-00572284.
09-DEC-1990; 90EP-00123670.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE;
Podlanski FJ, Stern AS;

WPI; 1997-404733/38.
P-PSDB; AAW36939.

Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for producing protein and as antitumour agent.

Disclosure; Fig 25; 83pp; English.

The present DNA sequence encodes a 40 kDa subunit of cytotoxic lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is a 75 kDa heterodimer, where the 2 subunits (see AAT97970 for the 35 kDa subunit) are bonded together via one or more disulphide bonds. CLMF protein is produced by a human B lyphoblastoid cell line. CLMF synergistically induces, in the presence of interleukin-2, the cytolytic activity of lymphokine activated killer cells. CLMF is also capable of stimulating T-cell growth. The subunits may be used for preparing the CLMF protein and for preparing medicants for antitumour therapy. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)

Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	3.16e-25	Length:	1397
ore:	35.00	Matches:	35
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
:	2	Gaps:	0

-10-821-670A-30 (1-329) x AAT97969 (1-1397)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

SULT 92
V00401
AAV00401 standard; DNA; 1397 BP.

AAV00401;

25-MAR-2003 (revised)

DT 18-MAR-1998 (first entry)
XX
DE 40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW CLMF bioactivity inhibition; affinity ligand; transplantation;
KW cytotoxic T cell proliferation; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	41. .1027
FT		/*tag= a

XX
PN EP790309-A1.
XX
PD 20-AUG-1997.
XX
PF 09-DEC-1990; 97EP-00104860.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 09-DEC-1990; 90EP-00123670.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Chizzonite RA, Gately MK, Gubler UA, Hulmes J, Pan YE;
PI Podlanski FJ, Stern AS, Witte H;
XX
DR WPI; 1997-404734/38.
DR P-PSDB; AAW36941.
XX
PT Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT producing CLMF protein and as an antitumour agent.
XX
PS Disclosure; Fig 25; 83pp; English.
XX
CC The present DNA sequence encodes a novel 40 kDa subunit of cytotoxic
CC lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC a 75 kDa heterodimer, where the 2 subunits (see AAV00402 for the 35 kDa
CC subunit) are bonded together via one or more disulphide bonds. CLMF
CC protein is produced by a human B lyphoblastoid cell line. CLMF
CC synergistically induces, in the presence of interleukin-2, the cytolytic
CC activity of lymphokine activated killer cells. CLMF is also capable of
CC stimulating T-cell growth. The subunits may be used for preparing the
CC CLMF protein and for preparing medicants for antitumour therapy. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.16e-25	Length:	1397
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AAV00401 (1-1397)

```
Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

RESULT 93
AAV37767

AAV37767 standard; cDNA; 1397 BP.

AAV37767;

17-SEP-1998 (first entry)

Cytotoxic lymphocyte maturation factor 40 kD subunit encoding cDNA.

Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize; interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying; proliferation; cytotoxic T cell; transplantation; antibody; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	41. .1027
	/*tag= a
	/product= "CLMF 40 kD subunit"

US5780597-A.

14-JUL-1998.

02-JUN-1995; 95US-00460061.

22-DEC-1989; 89US-00455708.
09-MAY-1990; 90US-00520935.
27-AUG-1990; 90US-00572284.
24-MAR-1992; 92US-00857023.
02-MAR-1994; 94US-00205011.

(HOFF) HOFFMANN LA ROCHE INC.

Podlaski FJ, Stern AS, Gately MK, Pan YE, Hulmes JD;
Chizzonite RA, Gubler UA;

WPI; 1998-413150/35.
P-PSDB; AAW58725.

New antibodies to cytotoxic lymphocyte maturation factor - useful for detecting, purifying, and/or blocking proliferation and activation of cytotoxic T cells, such as in transplantation(s).

Example 10; Fig 25; 71pp; English.

An isolated antibody has been developed which binds specifically to cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF induced proliferation by more than 50% in a CLMF dependent T cell growth assay and/or inhibits binding of at least 60% of the factor to phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL) blasts as determined in a CLMF receptor binding assay. CLMF is a heterodimeric protein having a molecular weight band of 75 kD, determined by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) under non-reducing and/or reducing conditions, providing a first subunit having a molecular weight band of 40 kD and a second subunit having a molecular weight of 35 kD. The present sequence encodes the CLMF 40 kD subunit, from an example of the present invention. The antibody can be used for the purification and/or detection of CLMF. It is also used in therapeutic treatments which require selective blocking of proliferation and activation of cytotoxic T cells (CTLs) such as in transplantation

Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

ignment Scores:			
ed. No.:	3.16e-25	Length:	1397
ore:	35.00	Matches:	35
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
:	2	Gaps:	0

-10-821-670A-30 (1-329) x AAV37767 (1-1397)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

RESULT 94
ADG39387
ID ADG39387 standard; DNA; 1397 BP.
XX
AC ADG39387;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human cytotoxic lymphocyte maturation factor, CLMF, 40 kDa subunit DNA.
XX
KW ds; gene; human; cytotoxic lymphocyte maturation factor; CLMF;
KW activated T-cell stimulator; natural killer cell stimulator;
KW immunoenhancer; antitumour; tumour; cancer.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	41. .1027
FT		/*tag= a
FT		/product= "CLMF 40 kDa subunit"

XX
PN US2003204059-A1.
XX
PD 30-OCT-2003.
XX
PF 08-OCT-2002; 2002US-00267565.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 24-MAR-1992; 92US-00857023.
PR 02-MAR-1994; 94US-00205011.
PR 02-JUN-1995; 95US-00459151.
PR 22-SEP-1999; 99US-00401839.
XX
PA (HOFF) HOFFMANN LA ROCHE & CIE SA F.
XX
PI Gately MK, Gubler UA, Hulmes JD, Podlaski FJ, Stern AS;
PI Chizzonite RA, Pan YE;
XX
DR WPI; 2004-010534/01.
DR P-PSDB; ADG39388.
XX
PT Novel protein comprising cytotoxic lymphocyte maturation factor in
PT substantially pure form or protein which exhibits cytotoxic lymphocyte
PT maturation factor activity, useful as antitumor and immunoenhancing
PT agent.
XX
PS Disclosure; Fig 25; 74pp; English.
XX
CC The invention relates to a protein which comprises a cytotoxic lymphocyte
CC maturation factor (CLMF). The protein is useful for stimulating activated
CC T-cells which involves treating T-cells with the protein. The method
CC further involves treating the activated T-cells with IL2 or its
CC biologically active fragment. The protein is useful for stimulating
CC natural killer cells which involves treating the natural killer cells
CC with the protein. The protein has immunoenhancing and antitumour effects
CC when used as single therapeutic agent in vivo. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	3.16e-25	Length:	1397
Score:	35.00	Matches:	35

```
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            10.6%           Indels:        0
:                     12              Gaps:          0

-10-821-670A-30 (1-329) x ADG39387 (1-1397)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

SULT 95
)03758
   ADO03758 standard; cDNA; 1397 BP.

   ADO03758;

   01-JUL-2004  (first entry)

   Human CLMF 40kDa subunit cDNA.

   pharmaceutical composition; T cell growth factor assay; cytokine;
   cytokine lymphocyte maturation factor; CLMF; interleukin-12; IL-12;
   NC-37 B lymphoblastoid cell; T-cell growth stimulator; human; gene; ss;
   40 kDa subunit.

   Homo sapiens.

   Key             Location/Qualifiers
   CDS             41. .1027
                   /*tag= b
                   /product= "CLMF 40 kDa subunit"
                   /note= "Cytotoxic Lymphocyte Maturation Factor"
   sig_peptide     41. .106
                   /*tag= a
   mat_peptide     107. .1024
                   /*tag= c
                   /note= "Mature CLMF 40 kDa subunit"

   US6683046-B1.

   27-JAN-2004.

   02-JUN-1995;   95US-00459151.

   22-DEC-1989;   89US-00455708.
   09-MAY-1990;   90US-00520935.
   27-AUG-1990;   90US-00572284.
   24-MAR-1992;   92US-00857023.
   02-MAR-1994;   94US-00205011.

   (HOFF ) HOFFMANN LA ROCHE INC.

   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
   Chizzonite RA,  Pan YE;

   WPI; 2004-118577/12.
   P-PSDB; ADO03759, ADO03795.

   Pharmaceutical composition useful for activating T cell growth factors in
   assays comprises heterodimeric protein comprising first and second
   subunits and carrier.

   Disclosure; Fig 25; 72pp; English.

   The invention describes a pharmaceutical composition active in a T cell
   growth factor assay. The pharmaceutical composition comprises a
   heterodimeric protein having a molecular weight of 75 kDa as determined
   by Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)
CC under non-reducing conditions, and under reducing conditions, providing a
CC first subunit having a molecular weight of 40 kDa as determined by (SDS-
CC PAGE), and having a fully defined sequence of 306 amino acids as given in
CC the specification, and second subunit having a molecular weight of 35 kDa
CC as determined by (SDS-PAGE). Also described are: a novel cytokine protein
CC called Cytokine lymphocyte maturation factor (CLMF) or interleukin-12 (IL
CC -12) synthesised by mammalian cells, particularly human NC-37 B
CC lymphoblastoid cells, and capable of stimulating T-cell growth; and
CC monoclonal antibodies directed against (CLMF). (I) is useful as a
CC pharmaceutical composition which is active in a T cell growth factor
CC assay. This sequence encodes human cytotoxic lymphocyte maturation factor
CC (CLMF) 40 kDa subunit.
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.16e-25        Length:        1397
Score:                  35.00           Matches:       35
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            10.6%           Indels:        0
DB:                     12              Gaps:          0

US-10-821-670A-30 (1-329) x ADO03758 (1-1397)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 96
AAZ40021
ID   AAZ40021 standard; DNA; 1399 BP.
XX
AC   AAZ40021;
XX
DT   14-FEB-2000  (first entry)
XX
DE   Human p40 coding sequence.
XX
KW   Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
KW   IL-12 p40 subunit; gene therapy; tumour; leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   US5994104-A.
XX
PD   30-NOV-1999.
XX
PF   08-NOV-1996;   96US-00751767.
XX
PR   08-NOV-1996;   96US-00751767.
XX
PA   (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI   Anderson RJ,  Prentice HG,  Macdonald ID;
XX
DR   WPI; 2000-038261/03.
DR   P-PSDB; AAY54919.
XX
PT   Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT   for treating leukemia and other cancers.
XX
PS   Example; Fig 9; 73pp; English.
XX
CC   This sequence encodes the human p40 protein sequence. The invention
CC   relates to an isolated nucleic acid construct (I) comprising a region
CC   encoding an interleukin-12 (IL-12) fusion protein (comprising an IL-12
CC   p35 subunit, an IL-12 p40 subunit and a linker peptide (joining the
CC   subunits)) and a region encoding a B7 protein. (I) may be used to produce
```

IL-12 fusion proteins according to standard recombinant DNA methodologies. The fusion proteins may be produced either in vitro in a fermentation culture or in vivo as part of a gene therapy protocol (in this case (I) is used to transform a patients cells, which then secrete the functional polypeptide to supplement the patients own production of IL-12 or to rectify mutations which lead to the expression of inactive polypeptides). The fusion proteins produced in this way may be used to treat any disease which responds to IL-12 such as tumours (both solid and dispersed of the kidney, breast, colon, ovarian and cervical tumours and melanomas) and in particular, tumours of the blood such as leukaemia. Alternatively, the polypeptides may be used as antigens in the production of antibodies to IL-12 and to assay for agonists and antagonists of its activity. The antibodies and antagonists may be used to inhibit the activity of IL-12. (I) may also be used diagnostically as a probe which hybridizes to sequences encoding IL-12 and the antibodies may be used to detect the presence of IL-12 polypeptides in samples. They may be used diagnostically to quantitate the expression of the polypeptide by patients and hence which subjects may be in need of restorative therapy

Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

lignment Scores:

ed. No.:	3.17e-25	Length:	1399
ore:	35.00	Matches:	35
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
:	3	Gaps:	0

-10-821-670A-30 (1-329) x AAZ40021 (1-1399)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

SULT 97
Y86632
ADY86632 standard; DNA; 1399 BP.

ADY86632;

02-JUN-2005 (first entry)

Human interleukin-12 40 kDa (IL-12 p40) subunit gene.

Gene expression; screening; multiple sclerosis; neuroprotective; immune disorder; neurological disease; DNA microarray; gene; ds; interleukin-12; lymphokine; cytokine.

Homo sapiens.

US2005064483-A1.

24-MAR-2005.

30-AUG-2004; 2004US-00929182.

28-AUG-2003; 2003US-0498731P.

(BAYU) BAYLOR COLLEGE MEDICINE.

Zang JZ, Hong J;

WPI; 2005-252668/26.
GENBANK; M65272.

Monitoring multiple sclerosis patient taking beta-interferon or glatiramer acetate to predict treatment response by determining expression profile of inflammatory nucleic acids using RNA of patient and comparing to control.

PT
XX
PS Claim 1; SEQ ID NO 22; 73pp; English.
XX
CC The present invention relates to gene expression profiling technology to
CC quantatively measure the expression profiles of genes selected based on
CC their role in inflammation and their susceptibility to regulation by
CC current multiple sclerosis (MS) treatment agents by isolating RNA from
CC peripheral blood mononuclear cells (PBMC) of patient. The invention is
CC particularly useful for monitoring a multiple sclerosis patient taking
CC interferon-beta (IFN-beta) or glatiramer acetate (GA) in order to predict
CC treatment response. The present sequence is human interleukin-12 40 kDa
CC (IL-12 p40) subunit gene. This gene is used to illustrate the evaluation
CC of PBMC responses to in Vitro treatment with IFN-beta or GA agents by
CC gene expression profiling technology.
XX
SQ Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.17e-25	Length:	1399
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-30 (1-329) x ADY86632 (1-1399)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

RESULT 98
AAA92406
ID AAA92406 standard; cDNA; 2300 BP.
XX
AC AAA92406;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human interleukin 2 encoding p35 and p40 proteins.
XX
KW Human; interleukin 2; IL-2; p35; p40; immune response; tumour;
KW infectious disease; bacteria; virus; parasite; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	19. .678
FT		/*tag= a
FT		/product= "p35"
FT	CDS	1304. .2290
FT		/*tag= b
FT		/product= "p40"

XX
PN CN1258740-A.
XX
PD 05-JUL-2000.
XX
PF 31-DEC-1998; 98CN-00126748.
XX
PR 31-DEC-1998; 98CN-00126748.
XX
PA (HUAC-) HUACHEN BIOLOGICAL TECHNOLOGY INST SHANG.
XX
PI Cao X, Zhang W, Ju D;
XX
DR WPI; 2000-558956/52.
DR P-PSDB; AAB23795, AAB23796.

Recombinant adenovirus expressing human interleukin-12 and its preparation and use.

Example 3; Fig 4; 27pp; Chinese.

The present invention describes a recombinant adenovirus and its preparation and use, as well as medicine composite containing the recombinant adenovirus. The recombinant adenovirus is used clinically, has the advantages of low cost, easy use and high efficiency and is especially suitable for immune treatment of tumour and infectious diseases caused by bacteria, virus and parasite. The present sequence represents human interleukin 2 (IL-2) cDNA which encodes the p35 and p40 proteins, which is used in an example from the present invention

Sequence 2300 BP; 598 A; 591 C; 571 G; 540 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 5.09e-25 Length: 2300
ore: 35.00 Matches: 35
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 10.6% Indels: 0
: 3 Gaps: 0

-10-821-670A-30 (1-329) x AAA92406 (1-2300)

217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
1949 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 2008

237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
2009 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 2053

SULT 99
303207
AEE03207 standard; DNA; 2336 BP.

AEE03207;

26-JAN-2006 (first entry)

Human interleukin-12 DNA, SEQ ID 13.

Cytostatic; gene therapy; tumor; immune stimulation; cancer; vector; ds.

Homo sapiens.

WO2005112541-A2.

01-DEC-2005.

18-MAY-2005; 2005WO-ES000277.

20-MAY-2004; 2004ES-00001219.

(PROY-) PROYECTO BIOMEDICINA CIMA SL.

Qian C, Guan M, Smerdou Picazo C, Prieto Valtuena J;

WPI; 2005-812033/82.

Hybrid adenoviral gene expression vector for treating cancer, comprises adenovirus liberation system, alpha virus derived vector and specific tumoral promoter.

Disclosure; SEQ ID NO 13; 149pp; Spanish.

The invention relates to a novel adenovirus/alphavirus hybrid vector used in the expression of therapeutic genes in tumor cells. The vector comprises: a first chain of adenoviral origin containing a first inverted terminal repeated sequence and a signal sequence for packing the

CC adenovirus; a first non-coding filler sequence; a sequence corresponding
CC to a specific tissue promoter; an alpha virus-derived cDNA chain, the
CC sequence of which is in part complementary to an alpha viral RNA,
CC comprising at least one sequence coding for at least one exogenous gene
CC of interest, a polyadenylation sequence and a second adenoviral ITR
CC sequence. The invention further includes pharmaceutical compositions
CC containing the vector. The novel vector is used to transfer genetic
CC material to a cell, preferably a tumoral cell, especially one which
CC expresses an alfa fetoprotein (AFP). The vector is used to prepare drugs
CC for treating tumors. The vector or pharmaceutical compositions containing
CC them can be used to induce an immune response against foreign antigens.
CC This gene therapy method can be used to treat cancer. This polynucleotide
CC represents a human interleukin-12 DNA sequence used in the construction
CC of a novel vector of the invention.
XX
SQ Sequence 2336 BP; 612 A; 602 C; 577 G; 545 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.17e-25 Length: 2336
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-30 (1-329) x AEE03207 (1-2336)

Qy 217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
Db 1964 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 2023

Qy 237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
Db 2024 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 2068

RESULT 100
ACF57534
ID ACF57534 standard; DNA; 2347 BP.
XX
AC ACF57534;
XX
DT 22-APR-2004 (first entry)
XX
DE Human IL12B DNA SEQ ID NO: 35.
XX
KW Protein targeting; angiogenesis inhibitor; fusion gene; cancer; gene; ds;
KW antiangiogenic; cytostatic; ophthalmological; antiarthritic;
KW antirheumatic; antiinflammatory; dermatological; immunosuppressive;
KW antipsoriatic; antidiabetic; neuroprotective; vasotropic; anorectic.
XX
OS Homo sapiens.
XX
PN WO2003093303-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-US014243.
XX
PR 06-MAY-2002; 2002US-0380063P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Hung M, Lan K, Ou-Yang F, Liu J, Lan K;
XX
DR WPI; 2004-053038/05.
XX
PT New polypeptide comprising an antiangiogenesis polypeptide region linked
PT to a therapeutic protein or a diagnostic protein, useful for diagnosing
PT or treating angiogenesis-dependent diseases e.g. cancer, lupus or
PT restenosis.
XX
PS Disclosure; Page 111-112; 0pp; English.
XX

The present invention relates to a polypeptide comprising an antiangiogenesis polypeptide region linked to a therapeutic protein or polypeptide region, or a diagnostic protein or polypeptide region. The polypeptide comprising an antiangiogenesis polypeptide region or the nucleic acid encoding the polypeptide comprising the antiangiogenesis polypeptide is useful for diagnosing or treating angiogenesis-dependent diseases or cancer. Angiogenesis-dependent diseases include age-related macular degeneration, artherosclerosis, angiofibroma, neovascular glaucoma, arteriovenous malformations, nonunion fractures, arthritis, rheumatoid arthritis, lupus, connective tissue disorders, Osler-Weber syndrome, psoriasis, corneal graft neovascularisation, pyogenic granuloma, delayed wound healing, retrolental fibroplasia, diabetic retinopathy, scleroderma, granulations, haemangioma, trachoma, haemophilic joints, vascular adhesions, hypertrophic scars, multiple sclerosis, restenosis or obesity. The present sequence is a coding sequence shown in the exemplification of the invention

Sequence 2347 BP; 695 A; 486 C; 543 G; 623 T; 0 U; 0 Other;

lignment Scores:

ed. No.:	5.19e-25	Length:	2347
ore:	35.00	Matches:	35
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
:	12	Gaps:	0

-10-821-670A-30 (1-329) x ACF57534 (1-2347)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

arch completed: June 10, 2006, 02:28:49
b time : 835.144 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 01:35:52 ; Search time 4558.64 Seconds
(without alignments)
6053.601 Million cell updates/sec

le: US-10-821-670A-30
fect score: 329
quence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 48236798 seqs, 27959665780 residues

d size: 1

al number of hits satisfying chosen parameters: 96471816

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlp
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110453_27580/app_query.fasta_1
B=EST -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rst -MINMATCH=0.1 -LOOPCL=0
OOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
IST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL
UTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
SER=US10821670_@CGN_1_1_22222_@runat_07062006_110453_27580 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	35	10.6	725	5	CD559454	CD559454 AGENCOURT
2	35	10.6	736	5	CD559453	CD559453 AGENCOURT
3	35	10.6	762	5	CD559451	CD559451 AGENCOURT
4	35	10.6	766	5	CD559449	CD559449 AGENCOURT
c 5	35	10.6	772	5	CD559450	CD559450 AGENCOURT
c 6	35	10.6	785	5	CD559448	CD559448 AGENCOURT
7	31	9.4	700	12	CE093997	CE093997 tigr-gss-
8	24	7.3	735	5	CD559605	CD559605 AGENCOURT
9	23	7.0	745	5	CD559602	CD559602 AGENCOURT
10	23	7.0	747	5	CD559607	CD559607 AGENCOURT
c 11	23	7.0	754	5	CD559452	CD559452 AGENCOURT
12	23	7.0	756	5	CK130264	CK130264 AGENCOURT
13	23	7.0	772	5	CD559604	CD559604 AGENCOURT
14	20	6.1	252	10	DV799576	DV799576 est_t_tru
15	20	6.1	724	5	CD559603	CD559603 AGENCOURT
16	20	6.1	1042	5	CD559606	CD559606 AGENCOURT
17	18	5.5	704	13	CZ422673	CZ422673 1018376 R
18	17	5.2	1839	6	AK162981	AK162981 Mus muscu
19	17	5.2	2908	6	AK155593	AK155593 Mus muscu
c 20	16	4.9	581	11	AQ394113	AQ394113 CITBI-E1-
21	13	4.0	346	4	BY164658	BY164658 BY164658
22	13	4.0	355	4	BY221814	BY221814 BY221814
23	13	4.0	375	4	BY222535	BY222535 BY222535
24	13	4.0	387	4	BY167742	BY167742 BY167742
25	13	4.0	417	8	CO949904	CO949904 UMC-pd12c
26	13	4.0	423	4	BY218447	BY218447 BY218447
27	13	4.0	432	4	BY154173	BY154173 BY154173
28	13	4.0	475	7	BF704417	BF704417 MI-P-E6-a
c 29	13	4.0	569	11	AZ853726	AZ853726 2M0157M01
30	13	4.0	649	5	CJ134671	CJ134671 CJ134671
31	13	4.0	666	4	BY749553	BY749553 BY749553
c 32	13	4.0	668	14	AG079702	AG079702 Pan trogl
33	12	3.6	535	11	AZ441303	AZ441303 1M0232M24
c 34	10	3.0	385	1	AA879565	AA879565 vx37c03.r
c 35	10	3.0	414	13	CW885638	CW885638 RPCI42_10
c 36	9	2.7	115	14	ATH521069	AJ521069 Arabidops
37	9	2.7	263	3	BQ356685	BQ356685 PM0-HT033
38	9	2.7	353	4	BY024612	BY024612 BY024612
39	9	2.7	354	4	BY024263	BY024263 BY024263
40	9	2.7	355	4	BY013557	BY013557 BY013557
41	9	2.7	361	10	W00972	W00972 za55d07.r1
42	9	2.7	382	4	BY204279	BY204279 BY204279
43	9	2.7	409	4	BY183786	BY183786 BY183786
c 44	9	2.7	415	11	AQ305003	AQ305003 HS_2012_A
c 45	9	2.7	423	7	AW382621	AW382621 PM0-HT033
c 46	9	2.7	435	7	BE153120	BE153120 PM0-HT033
c 47	9	2.7	442	5	CI330861	CI330861 CI330861
c 48	9	2.7	442	7	BE677126	BE677126 7d80f03.x
c 49	9	2.7	463	1	AU143811	AU143811 AU143811
c 50	9	2.7	477	1	AI754066	AI754066 cr19c06.x
51	9	2.7	479	1	AI683279	AI683279 tw50a03.x
52	9	2.7	479	4	CA699592	CA699592 wlk8.pk00
c 53	9	2.7	494	2	BI325004	BI325004 ic21a08.x
54	9	2.7	500	11	AQ300559	AQ300559 HS_3175_B
c 55	9	2.7	504	2	BM090808	BM090808 ig15e03.x
56	9	2.7	507	7	AW367597	AW367597 MR0-HT016
c 57	9	2.7	510	1	AI554405	AI554405 tq11a12.x
c 58	9	2.7	516	1	AV706519	AV706519 AV706519
c 59	9	2.7	546	9	DA098991	DA098991 DA098991
c 60	9	2.7	548	7	BE143328	BE143328 MR0-HT016
c 61	9	2.7	553	9	DB284546	DB284546 DB284546
c 62	9	2.7	561	9	DA102042	DA102042 DA102042
63	9	2.7	563	13	CW054731	CW054731 104_295_1
64	9	2.7	566	9	DB349096	DB349096 DB349096
65	9	2.7	572	3	BM907722	BM907722 AGENCOURT
c 66	9	2.7	593	5	CK818181	CK818181 ic21a08.y
c 67	9	2.7	624	13	CW136151	CW136151 104_521_1
c 68	9	2.7	631	3	BU813156	BU813156 N006A02 P
69	9	2.7	638	13	CW136150	CW136150 104_521_1
70	9	2.7	645	13	CL344654	CL344654 RPCI44_27
c 71	9	2.7	648	10	DT874689	DT874689 AGENCOURT
c 72	9	2.7	649	13	CW374083	CW374083 fsbb001f0
73	9	2.7	650	2	BG696339	BG696339 602658709
74	9	2.7	657	13	CL344592	CL344592 RPCI44_27
c 75	9	2.7	661	3	BU773963	BU773963 SJEGBC03
76	9	2.7	677	7	AW956339	AW956339 EST368409
77	9	2.7	683	10	DR724059	DR724059 AGENCOURT

78	9	2.7	688	4	CA413781	CA413781 UI-H-EZ0-
79	9	2.7	692	13	CW470377	CW470377 fsbb001f2
80	9	2.7	697	7	BE387304	BE387304 601275594
81	9	2.7	700	3	BQ009739	BQ009739 UI-H-ED0-
82	9	2.7	707	8	CN279085	CN279085 170004247
83	9	2.7	722	8	CN412356	CN412356 170005325
84	9	2.7	746	9	DN494937	DN494937 N006A02.5
85	9	2.7	757	3	BU633670	BU633670 UI-H-FL1-
86	9	2.7	763	3	BP446084	BP446084
87	9	2.7	780	3	BU375548	BU375548 603807808
88	9	2.7	796	11	BZ056171	BZ056171 l1b95f10.
89	9	2.7	798	11	BZ020584	BZ020584 oeg90c01.
90	9	2.7	798	14	CT202661	CT202661 Sus scrof
91	9	2.7	802	9	DN518405	DN518405 1259097 M
92	9	2.7	819	2	BG332928	BG332928 602430781
93	9	2.7	819	9	DN521145	DN521145 1263973 M
94	9	2.7	829	7	BF616281	BF616281 HVSMEc000
95	9	2.7	841	2	BG582789	BG582789 EST484535
96	9	2.7	864	8	CR551254	CR551254 CR551254
97	9	2.7	876	11	AQ895672	AQ895672 HS_4861_B
98	9	2.7	893	8	CX115638	CX115638 EI100A06
99	9	2.7	894	2	BI258748	BI258748 602970329
100	9	2.7	895	2	BI088766	BI088766 602851556
101	9	2.7	913	5	CF409178	CF409178 CH3#059_B
102	9	2.7	923	9	DN565372	DN565372 90930534
103	9	2.7	937	9	DN786150	DN786150 94044776
104	9	2.7	938	5	CF406341	CF406341 CH3#041_F
105	9	2.7	943	13	DU365640	DU365640 109831307
106	9	2.7	960	2	BG035474	BG035474 602325507
107	9	2.7	986	2	BG027599	BG027599 602294475
108	9	2.7	1029	13	CL493139	CL493139 SAIL_574_
109	9	2.7	1030	2	BG539271	BG539271 602567868
110	9	2.7	1037	1	AL539211	AL539211
111	9	2.7	1183	2	BG853175	BG853175 1024036D0
112	9	2.7	1315	14	AG430040	AG430040 Mus muscu
113	9	2.7	1340	14	AG448476	AG448476 Mus muscu
114	9	2.7	1447	10	DV783213	DV783213 HW_LIVER_
115	9	2.7	2562	6	CR592197	CR592197 full-leng
116	8	2.4	88	1	AA727638	AA727638 vv02c12.r
117	8	2.4	113	4	C00679	C00679 HUMGS000823
118	8	2.4	113	11	AQ282443	AQ282443 RPCI11-79
119	8	2.4	117	7	AW478729	AW478729 21097 MAR
120	8	2.4	123	7	BE721839	BE721839 189673 MA
121	8	2.4	141	1	AU260162	AU260162 AU260162
122	8	2.4	142	7	BE812604	BE812604 RC3-AN004
123	8	2.4	167	14	AG475481	AG475481 Mus muscu
124	8	2.4	168	11	B28469	B28469 F25I18TR IG
125	8	2.4	168	12	CE024998	CE024998 tigr-gss-
126	8	2.4	195	2	BG953233	BG953233 CM4-CT063
127	8	2.4	201	7	BE843494	BE843494 CM3-TN006
128	8	2.4	202	1	AI450727	AI450727 ms78g05.x
129	8	2.4	209	4	CD087249	CD087249 MC1-0036T
130	8	2.4	215	1	AA863462	AA863462 oh43c02.s
131	8	2.4	215	12	BZ949925	BZ949925 CH240_38B
132	8	2.4	217	5	CJ097946	CJ097946 CJ097946
133	8	2.4	221	2	BF950279	BF950279 CM3-NN021
134	8	2.4	223	13	CZ024046	CZ024046 CH240_184
135	8	2.4	232	2	BF767515	BF767515 CM4-CN009
136	8	2.4	235	1	AI639761	AI639761 ms78g05.y
137	8	2.4	235	1	AA174908	AA174908 ms78g05.r
138	8	2.4	235	3	BP888606	BP888606 BP888606
139	8	2.4	238	7	AW893763	AW893763 RC4-NN002
140	8	2.4	240	5	CK886537	CK886537 SGP166980
141	8	2.4	242	2	BJ656057	BJ656057 BJ656057
142	8	2.4	242	7	BE204318	BE204318 EST396994
143	8	2.4	243	14	TA90A03P	AL465275 T. brucei
144	8	2.4	244	12	CE767861	CE767861 tigr-gss-
145	8	2.4	249	7	BB481174	BB481174 BB481174
146	8	2.4	250	12	CE820902	CE820902 tigr-gss-
147	8	2.4	252	1	AI152063	AI152063 ud19c07.r
148	8	2.4	252	5	CD240364	CD240364 AREL5P2LH
149	8	2.4	258	4	BW840228	BW840228 BW840228
150	8	2.4	258	10	R95251	R95251 SWOvL3CA136
151	8	2.4	259	1	AI077000	AI077000 BSBmMFSZ1
c 152	8	2.4	264	8	CN801148	CN801148 DI8P00356
c 153	8	2.4	270	9	CX357606	CX357606 ssalrgb51
c 154	8	2.4	271	8	CN297233	CN297233 170005326
155	8	2.4	272	7	AW660342	AW660342 98331 MAR
c 156	8	2.4	275	10	DW181457	DW181457 SGP307413
157	8	2.4	276	7	AW383445	AW383445 PM0-HT034
c 158	8	2.4	277	8	CN635347	CN635347 114G02_54
c 159	8	2.4	279	10	DY126470	DY126470 001017BEM
c 160	8	2.4	285	14	FR0014280	AL005523 F.rubripe
c 161	8	2.4	290	7	BF053671	BF053671 EST438901
c 162	8	2.4	291	11	AQ422723	AQ422723 RPCI-11-1
c 163	8	2.4	293	7	BF283817	BF283817 EST448408
164	8	2.4	296	1	AA459674	AA459674 zx49c07.s
165	8	2.4	296	7	BB231764	BB231764 BB231764
166	8	2.4	297	2	BM002849	BM002849 1031107A0
c 167	8	2.4	298	1	AV144660	AV144660 AV144660
c 168	8	2.4	300	1	AA766328	AA766328 oa31b01.s
c 169	8	2.4	301	2	BI504009	BI504009 BB170026B
c 170	8	2.4	301	2	BI508512	BI508512 BB170008B
171	8	2.4	302	8	CV068923	CV068923 f2_new_ch
c 172	8	2.4	302	10	DY061950	DY061950 000308BSP
c 173	8	2.4	302	10	DY126242	DY126242 000910BEM
174	8	2.4	303	1	AJ670502	AJ670502 AJ670502
c 175	8	2.4	309	8	CX215577	CX215577 MNS25532
c 176	8	2.4	320	7	BB830723	BB830723 BB830723
177	8	2.4	321	12	CC988275	CC988275 ZUAFC89TV
c 178	8	2.4	324	11	AQ981401	AQ981401 RPCI-23-3
c 179	8	2.4	326	13	CZ811335	CZ811335 OC__Ba018
180	8	2.4	327	7	AW613780	AW613780 hh81b08.x
181	8	2.4	337	8	CO884451	CO884451 BovGen_12
c 182	8	2.4	338	3	BQ374466	BQ374466 RC0-TT000
183	8	2.4	340	3	BQ081130	BQ081130 san20b06.
184	8	2.4	342	12	CC507444	CC507444 CH240_349
185	8	2.4	346	1	AA894731	AA894731 oj28d02.s
c 186	8	2.4	346	7	AW388577	AW388577 MR2-ST012
c 187	8	2.4	346	8	CN999170	CN999170 UMC-bend_
188	8	2.4	347	4	BX638688	BX638688 BX638688
189	8	2.4	351	1	AA970176	AA970176 op60g06.s
190	8	2.4	351	1	AL385304	AL385304 MtBC27F11
c 191	8	2.4	353	7	BF515693	BF515693 UI-H-BW1-
c 192	8	2.4	355	11	BH257866	BH257866 CH230-283
c 193	8	2.4	355	13	CZ241047	CZ241047 AIAA-aah1
194	8	2.4	357	12	BZ934589	BZ934589 CH240_90J
c 195	8	2.4	358	14	CR300210	CR300210 mte1-18O1
c 196	8	2.4	361	7	BE109169	BE109169 UI-R-BS1-
c 197	8	2.4	369	2	BG788723	BG788723 SEAUMC008
198	8	2.4	369	2	BI191084	BI191084 j3b09fs.r
c 199	8	2.4	371	4	BY164446	BY164446 BY164446
c 200	8	2.4	374	4	BW924716	BW924716 BW924716

ALIGNMENTS

```
RESULT 1
CD559454/c
LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
```

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 11
High quality sequence start: 13
High quality sequence stop: 573.

ATURES Location/Qualifiers
source 1. .725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971868"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

IGIN

:gnment Scores:

ed. No.:	7.13e-24	Length:	725
ore:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
:	5	Gaps:	0

-10-821-670A-30 (1-329) x CD559454 (1-725)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        441 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 382

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        381 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 337
```

SULT 2
559453/c
CUS CD559453 736 bp mRNA linear EST 19-NOV-2003
FINITION AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
CESSION CD559453
RSION CD559453.2 GI:38453475
YWORDS EST.
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 736)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585521.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 683.

FEATURES Location/Qualifiers
source 1. .736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	7.23e-24	Length:	736
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-30 (1-329) x CD559453 (1-736)

```
Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      416 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 357

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      356 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 312
```

RESULT 3
CD559451/c
LOCUS CD559451 762 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CD559451
VERSION CD559451.2 GI:38453471
KEYWORDS EST.

```
:RCE       Homo sapiens (human)
:RGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
:ERENCE    1  (bases 1 to 762)
)UTHORS    NIH-MGC http://mgc.nci.nih.gov/.
:ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
)OURNAL    Unpublished (1999)
'MENT      On Jun 10, 2003 this sequence version replaced gi:31585519.
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 02
           High quality sequence start: 38
           High quality sequence stop: 761.
\TURES             Location/Qualifiers
   source          1. .762
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:6971871"
                   /tissue_type="mixed"
                   /lab_host="DH5A (T1 phage-resistant)"
                   /clone_lib="NIH_MGC_195"
                   /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                   loxP-HindIII; Clones from this library have been
                   PCR-amplified using gene-specific primers to contain the
                   complete open reading frame (based on known gene sequences
                   available from NCBI's RefSeq). Template for PCR is cDNA
                   derived from either pooled cytoplasmic polyA RNA from 30
                   cells lines or pooled total RNA from 10 different tissues
                   (from BD Biosciences/Clontech and Washington University).
                   PCR products are directionally cloned into the loxP sites
                   of the pDNR-Dual vector. Library constructed by Dr.
                   Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                   Expression Laboratory, Research Technology Program, SAIC
                   Frederick, NCI-Frederick, Frederick, MD 21702). For
                   information on which gene each clone represents, please
                   visit our anonymous ftp site at
                   ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                   a Note: this is a NIH_MGC Library."
:GIN

.gnment Scores:
:d. No.:              7.46e-24       Length:        762
:re:                  35.00          Matches:       35
:cent Similarity:     100.0%         Conservative:  0
:t Local Similarity:  100.0%         Mismatches:    0
:ry Match:            10.6%          Indels:        0
:                     5              Gaps:          0

·10-821-670A-30 (1-329) x CD559451 (1-762)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        437 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 378

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        377 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 333

:ULT 4
:59449/c
```

```
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
     source          1. .766
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              7.49e-24       Length:        766
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-30 (1-329) x CD559449 (1-766)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 370

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||
        369 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 325

SULT 5
559450/c
CUS       CD559450                 772 bp    mRNA    linear   EST 19-NOV-2003
FINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
          IMAGE:6971872 5', mRNA sequence.
CESSION   CD559450
RSION     CD559450.2  GI:38453469
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 772)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
MMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: h  column: 03
          High quality sequence start: 2
          High quality sequence stop: 753.
ATURES              Location/Qualifiers
   source           1. .772
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971872"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
IGIN

ignment Scores:
ed. No.:              7.54e-24        Length:         772
ore:                  35.00           Matches:        35
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            10.6%           Indels:         0
:                     5               Gaps:           0

-10-821-670A-30 (1-329) x CD559450 (1-772)
```

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 381

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        380 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 336

RESULT 6
CD559448/c
LOCUS       CD559448                 785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES              Location/Qualifiers
     source           1. .785
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971874"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              7.66e-24        Length:         785
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
```

```
:t Local Similarity:  100.0%        Mismatches:    0
:ry Match:            10.6%         Indels:        0
                      5             Gaps:          0

-10-821-670A-30 (1-329) x CD559448 (1-785)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        431 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 372

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            ||||||||||||||||||||||||||||||||||||||||||||||
        371 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 327

;ULT 7
)93997
:US       CE093997                700 bp    DNA     linear   GSS 24-SEP-2003
:INITION  tigr-gss-dog-17000359883851 Dog Library Canis familiaris genomic,
          genomic survey sequence.
:ESSION   CE093997
?SION     CE093997.1  GI:35160844
/WORDS    GSS.
:RCE      Canis familiaris (dog)
:RGANISM  Canis familiaris
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
          Canis.
:ERENCE   1  (bases 1 to 700)
)UTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
          Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
          Venter,J.C.
:ITLE     The dog genome: survey sequencing and comparative analysis
)OURNAL   Science 301 (5641), 1898-1903 (2003)
 PUBMED   14512627
/MENT     Contact: Kirkness EF
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0200
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.
'TURES              Location/Qualifiers
   source           1. .700
                    /organism="Canis familiaris"
                    /mol_type="genomic DNA"
                    /strain="Standard Poodle"
                    /db_xref="taxon:9615"
                    /clone_lib="Dog Library"
                    /note="Site_1: BstXI; Libraries were prepared from
                    peripheral blood"
:GIN

.gnment Scores:
:d. No.:              6.54e-20       Length:        700
:re:                  31.00          Matches:       31
:cent Similarity:     100.0%         Conservative:  0
:t Local Similarity:  100.0%         Mismatches:    0
:ry Match:            9.4%           Indels:        0
:                     12             Gaps:          0

-10-821-670A-30 (1-329) x CE093997 (1-700)

        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        430 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 489

        223 AsnTyrThrSerSerPhePheIleArgAspIle 233
            |||||||||||||||||||||||||||||||
        490 AACTACACCAGCAGCTTCTTCATCAGAGACATC 522

;ULT 8
;59605
```

```
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              6.21e-13       Length:        735
Score:                  24.00          Matches:       24
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            7.3%           Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-30 (1-329) x CD559605 (1-735)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 721

Qy        237 AspProProLys 240
```

```
              ||||||||||||
        722 GACCCACCCAAG 733

SULT 9
559602
CUS       CD559602                745 bp    mRNA    linear   EST 26-NOV-2003
FINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
          IMAGE:6971874 5', mRNA sequence.
CESSION   CD559602
RSION     CD559602.2  GI:38558930
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 745)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
MMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: h  column: 05
          High quality sequence start: 2
          High quality sequence stop: 644.
ATURES              Location/Qualifiers
   source           1. .745
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971874"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
IGIN

ignment Scores:
ed. No.:              6.2e-12        Length:        745
ore:                  23.00          Matches:       23
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            7.0%           Indels:        0
:                     5              Gaps:          0

-10-821-670A-30 (1-329) x CD559602 (1-745)
```

```
Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 530

Qy        176 SerAlaGlu 178
              |||||||||
Db        531 TCTGCAGAG 539

RESULT 10
CD559607
LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES              Location/Qualifiers
     source           1. .747
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971868"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              6.21e-12        Length:        747
Score:                  23.00           Matches:       23
```

```
:cent Similarity:     100.0%          Conservative:  0
:t Local Similarity:  100.0%          Mismatches:    0
:ry Match:            7.0%            Indels:        0
                      5               Gaps:          0

-10-821-670A-30 (1-329) x CD559607 (1-747)

        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        494 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 553

        176 SerAlaGlu 178
            |||||||||
        554 TCTGCAGAG 562

:ULT 11
:59452/c
:US       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
:INITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
          IMAGE:6971870 5', mRNA sequence.
:ESSION   CD559452
:SION     CD559452.2  GI:38453473
'WORDS    EST.
:RCE      Homo sapiens (human)
:RGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
:ERENCE   1  (bases 1 to 754)
:UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
:ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
)URNAL    Unpublished (1999)
'MENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: h  column: 01
          High quality sequence start: 130
          High quality sequence stop: 572.
:TURES              Location/Qualifiers
   source           1. .754
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971870"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              6.26e-12        Length:         754
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-30 (1-329) x CD559452 (1-754)

Qy        228 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TTTTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 344

Qy        248 LysAsnSer 250
              ||||||||
Db        343 AAGAATTCT 335

RESULT 12
CK130264
LOCUS       CK130264                756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES              Location/Qualifiers
     source           1. .756
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971871"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
```

Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

IGIN

ignment Scores:

ed. No.:	6.28e-12	Length:	756
ore:	23.00	Matches:	23
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	7.0%	Indels:	0
:	5	Gaps:	0

10-821-670A-30 (1-329) x CK130264 (1-756)

```
       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       499 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 558

       176 SerAlaGlu 178
           |||||||||
       559 TCTGCAGAG 567
```

SULT 13
559604
CUS CD559604 772 bp mRNA linear EST 26-NOV-2003
FINITION AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971872 5', mRNA sequence.
CESSION CD559604
RSION CD559604.2 GI:38558934
YWORDS EST.
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
FERENCE 1 (bases 1 to 772)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
MMENT On Jun 10, 2003 this sequence version replaced gi:31585672.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 03
High quality sequence start: 13
High quality sequence stop: 750.

ATURES Location/Qualifiers
source 1. .772
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971872"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	6.4e-12	Length:	772
Score:	23.00	Matches:	23
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.0%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-30 (1-329) x CD559604 (1-772)

```
Qy      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      503 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 562

Qy      176 SerAlaGlu 178
            |||||||||
Db      563 TCTGCAGAG 571
```

RESULT 14
DV799576
LOCUS DV799576 252 bp mRNA linear EST 23-NOV-2005
DEFINITION est_t_truncatus2262 HML_TuTr_IL-2_PBL Tursiops truncatus cDNA, mRNA sequence.
ACCESSION DV799576
VERSION DV799576.1 GI:82652485
KEYWORDS EST.
SOURCE Tursiops truncatus (bottlenosed dolphin)
ORGANISM Tursiops truncatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Tursiops.
REFERENCE 1 (bases 1 to 252)
AUTHORS Mancia,A., Gefroh,H.A., Lundqvist,M.L., Romano,T.A., Almeida,J.S., Chen,Y., McKillen,D.J., Trent,H.F., Wu,S. and Warr,G.W.
TITLE Construction and validation of T. truncatus immunospecific cDNA microarray at marinegenomics.org
JOURNAL Unpublished (2005)
COMMENT Contact: Annalaura Mancia
Hollings Marine Lab
Medical University of South Carolina
Hollings Marine Lab, 331 Ft. Johnson Rd., Charleston, SC 29412, USA
Tel: (843) 762 8962
Fax: (843) 762 8737
Email: mancia@musc.edu.

FEATURES Location/Qualifiers
source 1. .252
/organism="Tursiops truncatus"
/mol_type="mRNA"
/db_xref="taxon:9739"
/tissue_type="PBL"
/cell_type="PBL"
/clone_lib="HML_TuTr_IL-2_PBL"
/note="Vector: pCR2.1TOPO; Site_1: GAATTC"

ORIGIN

Alignment Scores:

Pred. No.:	2.26e-09	Length:	252
Score:	20.00	Matches:	20
Percent Similarity:	100.0%	Conservative:	0

```
;t Local Similarity:  100.0%          Mismatches:     0
;ry Match:            6.1%           Indels:         0
                      10             Gaps:           0

-10-821-670A-30 (1-329) x DV799576 (1-252)

       194 CysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValVal 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       143 TGTCAGGAGGGCAGCGCCTGCCCAGCCGCCGAGGAGAGCCTGCCCATTGAGGTCGTGGTG 202

;ULT 15
;59603
:US       CD559603                724 bp    mRNA    linear   EST 26-NOV-2003
:INITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
          IMAGE:6971873 5', mRNA sequence.
:ESSION   CD559603
:SION     CD559603.2  GI:38558932
:WORDS    EST.
JRCE      Homo sapiens (human)
)RGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
:ERENCE   1  (bases 1 to 724)
\UTHORS   NIH-MGC http://mgc.nci.nih.gov/.
:ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
)URNAL    Unpublished (1999)
:MENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: h  column: 04
          High quality sequence stop: 525.
)TURES              Location/Qualifiers
   source           1. .724
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971873"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
:GIN

.gnment Scores:
:d. No.:            5.8e-09        Length:         724
:re:                20.00          Matches:        20

Percent Similarity:     100.0%      Conservative:   0
Best Local Similarity:  100.0%      Mismatches:     0
Query Match:            6.1%        Indels:         0
DB:                     5           Gaps:           0

US-10-821-670A-30 (1-329) x CD559603 (1-724)

Qy          63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         200 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 259

RESULT 16
CD559606
LOCUS       CD559606               1042 bp    mRNA    linear   EST 11-JUN-2003
DEFINITION  AGENCOURT_14497125 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559606
VERSION     CD559606.1  GI:31585674
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1042)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 386.
FEATURES              Location/Qualifiers
     source           1. .1042
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971869"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:          8.02e-09       Length:         1042
Score:              20.00          Matches:        20
```

```
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            6.1%            Indels:        0
:                     5               Gaps:          0

-10-821-670A-30 (1-329) x CD559606 (1-1042)

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       190 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 249

SULT 17
422673
CUS       CZ422673                704 bp    DNA     linear   GSS 06-APR-2005
FINITION  1018376 RP42 Bos taurus genomic clone RP42-49A21, genomic survey
          sequence.
CESSION   CZ422673
RSION     CZ422673.1  GI:62309882
YWORDS    GSS.
URCE      Bos taurus (cattle)
ORGANISM  Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bos.
FERENCE   1  (bases 1 to 704)
AUTHORS   Sonstegard,T.S., Van Tassell,C.P., Capuco,A.V., de Jong,P.,
          Matukumalli,L.K., Shade,L.S., Bosak,S., Rubenfield,M. and
          Gasbarre,L.C.
TITLE     Bovine BAC End Sequences from Library RPCI-42
JOURNAL   Unpublished (2005)
MMENT     Contact: Tad S. Sonstegard
          Bovine Functional Genomics Laboratory
          Animal and Natural Resources Institute
          Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
          Tel: 3015048416
          Fax: 3015048414
          Email: tads@anri.barc.usda.gov
          Clones are derived from the bovine BAC library RPCI-42
          (http://bacpac.chori.org/mbovine42.htm). For BAC library
          availability, please contact Pieter de Jong (pdejong@mail.cho.org).
          Clones may be purchased from BACPAC Resources
          (http://www.chori.org/bacpac/ordering_information.htm). This work
          was undertaken as part of the International Bovine BAC Mapping
          Consortium (IBBMC) by USDA-ARS-BFGL.
          Plate: 49  row: A  column: 21
          Seq primer: TAATACGACTCACTATAGGG
          Class: BAC ends.
ATURES              Location/Qualifiers
   source           1. .704
                    /organism="Bos taurus"
                    /mol_type="genomic DNA"
                    /strain="Holstein"
                    /db_xref="taxon:9913"
                    /clone="RP42-49A21"
                    /sex="male"
                    /cell_type="Blood"
                    /clone_lib="RP42"
                    /note="Vector: pBACe3.6; Site_1: MboI; Site_2: MboI;
                    RPCI-42 Bovine BAC library (Male Holstein) produced by
                    Pieter de Jong"
IGIN

ignment Scores:
ed. No.:              5.5e-07         Length:        704
ore:                  18.00           Matches:       18
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            5.5%            Indels:        0
:                     13              Gaps:          0

-10-821-670A-30 (1-329) x CZ422673 (1-704)

       257 TrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPhe 274
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TGGGAGTACCCTGACACGTGGAGCACCCCGCATTCCTACTTCTCCCTGACGTTT 57

RESULT 18
AK162981
LOCUS       AK162981                1839 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A430014H12 product:interleukin 12b, full insert
            sequence.
ACCESSION   AK162981
VERSION     AK162981.1  GI:74188061
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
```

Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

:ONSRTM FANTOM Consortium

:ITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

!OURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

:ERENCE 6

!UTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

:ONSRTM FANTOM Consortium

:ITLE The transcriptional landscape of the mammalian genome

!OURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

:ERENCE 7

!UTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .1839
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A430014H12"
/db_xref="taxon:10090"
/clone="A430014H12"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"

CDS 58. .1065
/note="unnamed protein product; interleukin 12b (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%, match=1816)
putative"
/codon_start=1
/protein_id="BAE37146.1"
/db_xref="GI:74188062"
/translation="MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVRS"

ORIGIN

Alignment Scores:

Pred. No.:	1.28e-05	Length:	1839
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.2%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x AK162981 (1-1839)

Qy 227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 727 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 777

RESULT 19

155593
CUS AK155593 2908 bp mRNA linear HTC 21-SEP-2005
FINITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730005O03 product:interleukin 12b, full insert sequence.
CESSION AK155593
RSION AK155593.1 GI:74212721
WORDS HTC; CAP trapper.
URCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
FERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
FERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
FERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
FERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group

```
ITLE     Antisense transcription in the mammalian transcriptome
OURNAL   Science 309 (5740), 1564-1566 (2005)
 PUBMED  16141073
ERENCE   8  (bases 1 to 2908)
UTHORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
         Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
         Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
         Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
         Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
         Muramatsu,M. and Hayashizaki,Y.
ITLE     Direct Submission
OURNAL   Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
         Physical and Chemical Research (RIKEN), Laboratory for Genome
         Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
         RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
         Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
         URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
         Fax:81-45-503-9216)
MENT     cDNA library was prepared and sequenced in Mouse Genome
         Encyclopedia Project of Genome Exploration Research Group in Riken
         Genomic Sciences Center and Genome Science Laboratory in RIKEN.
         Division of Experimental Animal Research in Riken contributed to
         prepare mouse tissues.
         Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
         Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
         Trust/MRC building Addenbrookes Hospital Cambridge) whose
         assistance we gratefully acknowledge.
         Please visit our web site for further details.
         URL:http://genome.gsc.riken.jp/
         URL:http://fantom.gsc.riken.jp/.
TURES                Location/Qualifiers
   source            1. .2908
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:F730005O03"
                     /db_xref="taxon:10090"
                     /clone="F730005O03"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
   misc_feature      1. .2908
                     /note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence:
                     BLASTN, 99%, match=1807)
                     putative"
GIN

gnment Scores:
d. No.:              1.92e-05        Length:         2908
re:                  17.00           Matches:        17
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            5.2%            Indels:         0
                     6               Gaps:           0

10-821-670A-30 (1-329) x AK155593 (1-2908)

       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1131 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1181

ULT 20
94113/c
US       AQ394113                581 bp    DNA     linear   GSS 06-MAR-1999
INITION  CITBI-E1-2542F7.TF CITBI-E1 Homo sapiens genomic clone 2542F7,
         genomic survey sequence.
ESSION   AQ394113
SION     AQ394113.1  GI:4365136
WORDS    GSS.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.

REFERENCE   1  (bases 1 to 581)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2542F7.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2542F7"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

Alignment Scores:
Pred. No.:              4.51e-05        Length:         581
Score:                  16.00           Matches:        16
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.9%            Indels:         0
DB:                     11              Gaps:           0

US-10-821-670A-30 (1-329) x AQ394113 (1-581)

Qy        235 LysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 AAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCG 1

RESULT 21
BY164658
LOCUS       BY164658                346 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY164658 RIKEN full-length enriched, bone marrow macrophage Mus
            musculus cDNA clone I830052P21 5', mRNA sequence.
ACCESSION   BY164658
VERSION     BY164658.1  GI:26301304
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
```

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

PUBMED 12466851

MMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

ATURES Location/Qualifiers

source 1. .346
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I830052P21"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"

GIN

ignment Scores:

ed. No.:	0.0273	Length:	346
ore:	13.00	Matches:	13
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	4.0%	Indels:	0

DB: 4 Gaps: 0

US-10-821-670A-30 (1-329) x BY164658 (1-346)

```
Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
              ||||||||||||||||||||||||||||||||||||||||
Db        211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249
```

RESULT 22
BY221814
LOCUS BY221814 355 bp mRNA linear EST 10-DEC-2002
DEFINITION BY221814 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830223O08 5', mRNA sequence.
ACCESSION BY221814
VERSION BY221814.1 GI:26402917
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 355)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
TURES             Location/Qualifiers
  source          1. .355
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="NOD"
                  /db_xref="taxon:10090"
                  /clone="F830223O08"
                  /tissue_type="activated spleen"
                  /clone_lib="RIKEN full-length enriched, activated spleen"
IGIN

gnment Scores:
d. No.:              0.0279          Length:         355
re:                  13.00           Matches:        13
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            4.0%            Indels:         0
                     4               Gaps:           0

10-821-670A-30 (1-329) x BY221814 (1-355)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
       210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248

ULT 23
22535
US       BY222535                 375 bp    mRNA    linear   EST 10-DEC-2002
INITION  BY222535 RIKEN full-length enriched, activated spleen Mus musculus
         cDNA clone F830228K06 5', mRNA sequence.
ESSION   BY222535
SION     BY222535.1  GI:26403638
WORDS    EST.
RCE      Mus musculus (house mouse)
RGANISM  Mus musculus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
         Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE   1  (bases 1 to 375)
UTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
         Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
         Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
         Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
         Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
         Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
         Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
         Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
         Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
         Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
         Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
         Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
         Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
         Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
         Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
         Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
         Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
         Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
         Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
         Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
         Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
         Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
         Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
         Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
         Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
         Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
         Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE    Analysis of the mouse transcriptome based on functional annotation
         of 60,770 full-length cDNAs
JOURNAL  Nature 420, 563-573 (2002)
PUBMED   12466851
COMMENT  Contact: Yoshihide Hayashizaki
         Laboratory for Genome Exploration Research Group, RIKEN Genomic
         Sciences Center(GSC), Yokohama Institute
         The Institute of Physical and Chemical Research (RIKEN)
         1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
         Tel: 81-45-503-9222
         Fax: 81-45-503-9216
         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
         Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
         Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
         Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
         Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
         Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
         Hayashizaki,Y. Direct Submission
         Computational Analysis of Full-Length Mouse cDNAs Compared with
         Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
         Normalization and subtraction of cap-trapper-selected cDNAs to
         prepare full-length cDNA libraries for rapid discovery of new
         genes. Genome Res. 10 (10), 1617-1630 (2000)
         RIKEN integrated sequence analysis (RISA) system--384-format
         sequencing pipeline with 384 multicapillary sequencer. Genome Res.
         10 (11), 1757-1771 (2000)
         Computer-based methods for the mouse full-length cDNA
         encyclopedia: real-time sequence clustering for construction of a
         nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
         cDNA library was prepared and sequenced in Mouse Genome
         Encyclopedia Project of Genome Exploration Research Group in Riken
         Genomic Sciences Center and Genome Science Laboratory in RIKEN.
         Division of Experimental Animal Research in Riken contributed to
         prepare mouse tissues.
         Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
         Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
         Trust/MRC building Addenbrookes Hospital Cambridge) whose
         assistance we gratefully acknowledge.
         Please visit our web site (http://genome.gsc.riken.go.jp) for
         further details.
FEATURES           Location/Qualifiers
     source        1. .375
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="NOD"
                   /db_xref="taxon:10090"
                   /clone="F830228K06"
                   /tissue_type="activated spleen"
                   /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

Alignment Scores:
Pred. No.:              0.0293          Length:         375
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.0%            Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-30 (1-329) x BY222535 (1-375)

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
              ||||||||||||||||||||||||||||||||||||||||
Db        210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248
```

```
SULT 24
167742
CUS         BY167742                 387 bp    mRNA    linear   EST 10-DEC-2002
FINITION    BY167742 RIKEN full-length enriched, bone marrow macrophage Mus
            musculus cDNA clone I830068I17 5', mRNA sequence.
CESSION     BY167742
RSION       BY167742.1  GI:26304388
YWORDS      EST.
URCE        Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE     1  (bases 1 to 387)
AUTHORS     Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
  PUBMED    12466851
MMENT       Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by David A. Hume ( Depts. of Biochemistry
            and Microbiology/Parasitology Institute for Molecular Bioscience
            University of Queensland Brisbane,Q 4072 Australia ) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES                Location/Qualifiers
     source             1. .387
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="I830068I17"
                        /tissue_type="bone marrow"
                        /cell_type="macrophage"
                        /clone_lib="RIKEN full-length enriched, bone marrow
                        macrophage"
ORIGIN

Alignment Scores:
Pred. No.:                0.0301          Length:          387
Score:                    13.00           Matches:         13
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              4.0%            Indels:          0
DB:                       4               Gaps:            0

US-10-821-670A-30 (1-329) x BY167742 (1-387)

Qy          52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
               ||||||||||||||||||||||||||||||||||||||||
Db         211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

RESULT 25
CO949904
LOCUS       CO949904                 417 bp    mRNA    linear   EST 09-SEP-2004
DEFINITION  UMC-pd12cl-003-b07 Day 12 Corpus Luteum pd12cl Sus scrofa cDNA 3',
            mRNA sequence.
ACCESSION   CO949904
VERSION     CO949904.1  GI:51326849
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 417)
  AUTHORS   Jiang,H., Whitworth,K.M., Bivens,N.J., Ries,J.E., Woods,R.J.,
            Forrester,L.J., Springer,G.K., Mathialagan,N., Agca,C.,
            Prather,R.S. and Lucy,M.C.
  TITLE     Large-scale Generation and Analysis of Expressed Sequence Tags from
            Porcine Ovary
  JOURNAL   Unpublished (2004)
COMMENT     Contact: DNA Core Facility (Swine Project)
            Animal Science - RS Prather
            University of Missouri-Columbia
            M616 Medical Sciences Bldg., Columbia, MO 65212, USA
            Tel: (573)882-0428
            Fax: (573)884-5552
            Email: porcine@rnet.missouri.edu
            POLYA=No.
FEATURES                Location/Qualifiers
     source             1. .417
                        /organism="Sus scrofa"
                        /mol_type="mRNA"
                        /db_xref="taxon:9823"
                        /dev_stage="Day 12 Corpus Luteum"
                        /clone_lib="pd12cl"
                        /note="Vector: T3T7PAC; Funding: A grant from the Monsanto
                        Company to the University of Missouri. Genetic Source:
```

Ovarian tissue (whole ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea; Day 12 corpora lutea and Day 12 follicles. More information regarding the methods can be found at:
http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mg of poly(A)+ RNA will be annealed at 37 degrees Celsius with 10mg of NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs was ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pSPORT1 vector (Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. 2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.

TAG_TISSUE=Day 12 Corpus Luteum
TAG_SEQ=Not found"
ORIGIN

Alignment Scores:

Pred. No.:	0.0322	Length:	417
Score:	13.00	Matches:	13
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.0%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-30 (1-329) x CO949904 (1-417)

```
Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
              |||||||||||||||||||||||||||||||||||||||
Db        198 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 236
```

RESULT 26
BY218447
LOCUS BY218447 423 bp mRNA linear EST 10-DEC-2002
DEFINITION BY218447 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830107N16 5', mRNA sequence.
ACCESSION BY218447
VERSION BY218447.1 GI:26399344
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,

Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
ATURES             Location/Qualifiers
   source          1. .423
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="NOD"
                   /db_xref="taxon:10090"
                   /clone="F830107N16"
                   /tissue_type="activated spleen"
                   /clone_lib="RIKEN full-length enriched, activated spleen"
IGIN

ignment Scores:
ed. No.:              0.0326          Length:         423
ore:                  13.00           Matches:        13
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            4.0%            Indels:         0
:                     4               Gaps:           0

-10-821-670A-30 (1-329) x BY218447 (1-423)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
       210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248

SULT 27
154173
CUS        BY154173                 432 bp    mRNA    linear   EST 10-DEC-2002
FINITION   BY154173 RIKEN full-length enriched, bone marrow macrophage Mus
           musculus cDNA clone G530005B20 5', mRNA sequence.
CESSION    BY154173
RSION      BY154173.1  GI:26290747
YWORDS     EST.
URCE       Mus musculus (house mouse)
ORGANISM   Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE    1  (bases 1 to 432)
AUTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
           Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
           Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
           Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
           Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
           Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
           Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
           Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
           Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
           Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
           Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
           Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
           Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
           Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
           Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
           Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
           Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
           Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
           Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
           Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
           Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
           Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
           Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
           Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
           Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
           Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
           Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE      Analysis of the mouse transcriptome based on functional annotation
           of 60,770 full-length cDNAs
JOURNAL    Nature 420, 563-573 (2002)
PUBMED     12466851
COMMENT    Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
           Sciences Center(GSC), Yokohama Institute
           The Institute of Physical and Chemical Research (RIKEN)
           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
           Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
           Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
           Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
           Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
           Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
           Hayashizaki,Y. Direct Submission
           Computational Analysis of Full-Length Mouse cDNAs Compared with
           Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
           Normalization and subtraction of cap-trapper-selected cDNAs to
           prepare full-length cDNA libraries for rapid discovery of new
           genes. Genome Res. 10 (10), 1617-1630 (2000)
           RIKEN integrated sequence analysis (RISA) system--384-format
           sequencing pipeline with 384 multicapillary sequencer. Genome Res.
           10 (11), 1757-1771 (2000)
           Computer-based methods for the mouse full-length cDNA
           encyclopedia: real-time sequence clustering for construction of a
           nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
           cDNA library was prepared and sequenced in Mouse Genome
           Encyclopedia Project of Genome Exploration Research Group in Riken
           Genomic Sciences Center and Genome Science Laboratory in RIKEN.
           Division of Experimental Animal Research in Riken contributed to
           prepare mouse tissues.
           Tissues were provided by David A. Hume ( Depts. of Biochemistry
           and Microbiology/Parasitology Institute for Molecular Bioscience
           University of Queensland Brisbane,Q 4072 Australia ) whose
           assistance we gratefully acknowledge.
           Please visit our web site (http://genome.gsc.riken.go.jp) for
           further details.
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G530005B20"
                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched, bone marrow
                     macrophage"
ORIGIN

Alignment Scores:
```

```
:d. No.:              0.0332          Length:         432
:re:                  13.00           Matches:        13
:cent Similarity:     100.0%          Conservative:   0
:t Local Similarity:  100.0%          Mismatches:     0
:ry Match:            4.0%            Indels:         0
                      4               Gaps:           0

10-821-670A-30 (1-329) x BY154173 (1-432)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
       211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

ULT 28
04417
US       BF704417                 475 bp    mRNA    linear   EST 22-DEC-2000
INITION  MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
         MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
ESSION   BF704417
SION     BF704417.1  GI:11989825
WORDS    EST.
RCE      Sus scrofa (pig)
RGANISM  Sus scrofa
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
         Sus.
ERENCE   1  (bases 1 to 475)
UTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
ITLE     Normalization and subtraction: two approaches to facilitate gene
         discovery
OURNAL   Genome Res. 6 (9), 791-806 (1996)
PUBMED   8889548
MENT     Contact: Tuggle CK
         Molecular Genetics Laboratory, Department of Animal Science
         Iowa State University
         201 Kildee Hall, Ames, IA 50011-3150, USA
         Tel: 5152944252
         Fax: 5152942401
         Email: cktuggle@iastate.edu
         Oligo-dT track not found, Not I site shown in beginning of sequence
         is likely internal to the message. cDNA Library Preparation: RJ
         Woods, JA Green, RS Prather S142 Animal Science Research Center,
         Department of Animal Science, University of Missouri-Columbia,
         65211 Clone distribution: clones will be available through Research
         Genetics (www.resgen.com)
         Seq primer: M13 Forward
         POLYA=No.
TURES                Location/Qualifiers
  source             1. .475
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-E6-acc-g-09-1-UM"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="MI-P-E6"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: EcoRI;
                     The MI-P-E6 library is derived from fetus at gestational
                     day 20.  For a detailed description of the  library from
                     which this clone was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/.
                     TAG_SEQ=None found"
IGIN

gnment Scores:
d. No.:              0.0362          Length:         475
re:                  13.00           Matches:        13
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            4.0%            Indels:         0
                     7               Gaps:           0

10-821-670A-30 (1-329) x BF704417 (1-475)
```

```
Qy        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
             ||||||||||||||||||||||||||||||||||||||||
Db       199 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 237

RESULT 29
AZ853726/c
LOCUS       AZ853726                 569 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157M01 F, genomic survey sequence.
ACCESSION   AZ853726
VERSION     AZ853726.1  GI:13042136
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: M  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157M01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Alignment Scores:
Pred. No.:           0.0425          Length:         569
Score:               13.00           Matches:        13
```

```
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            4.0%            Indels:        0
:                     11              Gaps:          0

-10-821-670A-30 (1-329) x AZ853726 (1-569)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
       217 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 179

SULT 30
134671
CUS       CJ134671                649 bp    mRNA    linear   EST 23-SEP-2005
FINITION  CJ134671 RIKEN full-length enriched mouse cDNA library, C57BL/6J
          bone marrow macrophage Mus musculus cDNA clone G530135F14 5', mRNA
          sequence.
CESSION   CJ134671
RSION     CJ134671.1  GI:76234999
YWORDS    EST.
URCE      Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE   1  (bases 1 to 649)
AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
          and Genome Science Group (Genome Network Project Core Group).
ITLE      The transcriptional landscape of the mammalian genome
OURNAL    Science 309 (5740), 1559-1563 (2005)
 PUBMED   16141072
MMENT     Contact: Yoshihide Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center(GSC), Yokohama Institute
          The Institute of Physical and Chemical Research (RIKEN)
          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel: 81-45-503-9222
          Fax: 81-45-503-9216
          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
          cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues. Tissues were provided by David A. Hume (
          Depts. of Biochemistry and Microbiology/Parasitology Institute for
          Molecular Bioscience University of Queensland Brisbane,Q 4072
          Australia ) whose assistance we gratefully acknowledge.
          Please visit our web site for further details.
          URL:http://genome.gsc.riken.jp/.
ATURES              Location/Qualifiers
   source           1. .649
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="G530135F14"
                    /tissue_type="bone marrow"
                    /cell_type="macrophage"
                    /clone_lib="RIKEN full-length enriched mouse cDNA library,
                    C57BL/6J bone marrow macrophage"
IGIN

ignment Scores:
ed. No.:              0.0477          Length:        649
ore:                  13.00           Matches:       13
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            4.0%            Indels:        0
:                     5               Gaps:          0

-10-821-670A-30 (1-329) x CJ134671 (1-649)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
Db     211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

RESULT 31
BY749553
LOCUS       BY749553                666 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY749553 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730005O03 5', mRNA sequence.
ACCESSION   BY749553
VERSION     BY749553.1  GI:27179008
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
```

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
TURES             Location/Qualifiers
  source          1. .666
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="F730005O03"
                  /cell_type="B6-derived CD11 +ve dendritic cells"
                  /clone_lib="RIKEN full-length enriched, B6-derived CD11
                  +ve dendritic cells"
GIN

gnment Scores:
d. No.:              0.0489          Length:         666
re:                  13.00           Matches:        13
cent Similarity:     100.0%          Conservative:   0
t Local Similarity:  100.0%          Mismatches:     0
ry Match:            4.0%            Indels:         0
                     4               Gaps:           0

10-821-670A-30 (1-329) x BY749553 (1-666)

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGln 64
           ||||||||||||||||||||||||||||||||||||||||
       611 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 649

ULT 32
79702/c
US        AG079702                668 bp    DNA     linear   GSS 03-NOV-2001
INITION   Pan troglodytes DNA, clone: PTB-075I07.R, genomic survey sequence.
ESSION    AG079702
SION      AG079702.1  GI:16631504
WORDS     GSS.
RCE       Pan troglodytes (chimpanzee)
RGANISM   Pan troglodytes
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Pan.
ERENCE    1
UTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Totoki,Y., Watanabe,H. and Sakaki,Y.
ITLE      BAC end sequences of Library PTB
OURNAL    Unpublished
ERENCE    2  (bases 1 to 668)
UTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Totoki,Y., Watanabe,H. and Sakaki,Y.
ITLE      Direct Submission
OURNAL    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
          Tel:81-45-503-9111, Fax:81-45-503-9170)
MENT      Clones are derived from the chimpanzee BAC library PTB This BAC end
          was generated during the R&D process and may have higher chance of
          clone tracking errors.
           PRIMERS
              Sequencing: M13Rev
           LIBRARY
              Vector    : pKS145
              R.Site 1  : SacI
              R.Site 2  : SacI.
FEATURES          Location/Qualifiers
     source       1. .668
                  /organism="Pan troglodytes"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9598"
                  /clone="PTB-075I07.R"
                  /sex="male"
                  /cell_type="lymphoblast"
                  /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

Alignment Scores:
Pred. No.:              0.049          Length:         668
Score:                  13.00          Matches:        13
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            4.0%           Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-30 (1-329) x AG079702 (1-668)

Qy        134 LysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThr 146
              ||||||||||||||||||||||||||||||||||||||||
Db        506 AAGAATTATTCAGGACGTTTCACCTGCTGGTGGCTGACG 468

RESULT 33
AZ441303
LOCUS       AZ441303                535 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0232M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0232M24 R, genomic survey sequence.
ACCESSION   AZ441303
VERSION     AZ441303.1  GI:10565316
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 535.
FEATURES          Location/Qualifiers
     source       1. .535
                  /organism="Mus musculus"
                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="UUGC1M0232M24"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained  from the Jackson
                  Laboratory Mouse DNA Resource
```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

IGIN

ignment Scores:

ed. No.:	0.397	Length:	535
ore:	12.00	Matches:	12
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
:	11	Gaps:	0

-10-821-670A-30 (1-329) x AZ441303 (1-535)

```
         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGlu 95
            ||||||||||||||||||||||||||||||||||||
        249 GATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAG 284
```

SULT 34
879565/c
CUS AA879565 385 bp mRNA linear EST 26-MAR-1998
FINITION vx37c03.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1277380 5' similar to TR:Q24331 Q24331 TUMOROUS IMAGINAL DISCS. ;, mRNA sequence.
CESSION AA879565
RSION AA879565.1 GI:2990270
YWORDS EST.
URCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE 1 (bases 1 to 385)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
MMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:669180
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 292.
ATURES Location/Qualifiers
source 1. .385
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
/clone="IMAGE:1277380"
/sex="female"
/tissue_type="lung"
/dev_stage="6-8 month old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse lung 937302"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"

ORIGIN

Alignment Scores:

Pred. No.:	28.8	Length:	385
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.0%	Indels:	0
DB:	1	Gaps:	0

US-10-821-670A-30 (1-329) x AA879565 (1-385)

```
Qy          94 GlyGluValLeuSerHisSerPheLeuLeu 103
               |||||||||||||||||||||||||||||||
Db         346 GGAGAAGTGTTGTCACATAGTTTTCTGTTG 317
```

RESULT 35
CW885638/c
LOCUS CW885638 414 bp DNA linear GSS 08-DEC-2004
DEFINITION RPCI42_102G16.TV RPCI-42 Bos taurus genomic clone RPCI42_102G16, genomic survey sequence.
ACCESSION CW885638
VERSION CW885638.1 GI:56424578
KEYWORDS GSS.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 414)
AUTHORS Larkin,D.M., Donthu,K., LeDuc,R., Ryan,K., Liu,L., de Jong,P.J. and Lewin,H.A.
TITLE End sequencing of Holstein BAC library RPCI-42
JOURNAL Unpublished (2004)
COMMENT Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library RPCI-42 (http://bacpac.chori.org/mbovine42.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). Funding was provided in part by grant no. AG2004-34480-14417 from USDA-CSREES (Livestock Genome Sequencing Initiative) and AG58-5438-2-313 from USDA-ARS
Plate: 102 row: G column: 16
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .414
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="RPCI42_102G16"
/sex="male"
/cell_type="blood"
/clone_lib="RPCI-42"

```
                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                RPCI-42 Bovine BAC library (Male) produced by Pieter de
                Jong"
GIN

gnment Scores:
d. No.:              30.7          Length:        414
re:                  10.00         Matches:       10
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            3.0%          Indels:        0
                     13            Gaps:          0

10-821-670A-30 (1-329) x CW885638 (1-414)

       235 LysProAspProProLysAsnLeuGlnLeu 244
           ||||||||||||||||||||||||||||||
        30 AAACCAGACCCACCCAAGAACCTGCAACTG 1

ULT 36
521069/c
US       ATH521069                115 bp    DNA     linear   GSS 08-FEB-2006
INITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
         052B02, genomic survey sequence.
ESSION   AJ521069
SION     AJ521069.1  GI:26789305
WORDS    GSS; left border; T-DNA flanking sequence.
RCE      Arabidopsis thaliana (thale cress)
RGANISM  Arabidopsis thaliana
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
         rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
ERENCE   1
UTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
         Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
         Lepiniec,L., Caboche,M. and Lecharny,A.
ITLE     T-DNA integration into the Arabidopsis genome depends on sequences
         of pre-insertion sites
OURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED   12446565
ERENCE   2  (bases 1 to 115)
UTHORS   Balzergue,S.
ITLE     Direct Submission
OURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
         Gaston Cremieux, 91057 Evry cedex, FRANCE
MENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
         plants from INRA (Versailles). The DNA fragment(s) resulting from
         the PCR were directly sequenced from the left or the right border
         to determine the genomic sequence flanking the insertion. T-DNA
         derived sequences were removed. Information to order the
         corresponding mutant line and a link to a database providing a
         graphical display of the insertion site are available at
         http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
         been generated in the framework of the French plant genomics
         program 'Genoplante' (http://www.genoplante.com and
         http://genoplante-info.infobiogen.fr).
TURES                Location/Qualifiers
   source            1. .115
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="052B02"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Wassilewskija"
   misc_feature      1. .115
                     /note="T-DNA flanking sequence
                     left border"
GIN

gnment Scores:
d. No.:              96.8          Length:        115
re:                  9.00          Matches:       9
```

```
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     14            Gaps:          0

US-10-821-670A-30 (1-329) x ATH521069 (1-115)

Qy        239 ProLysAsnLeuGlnLeuLysProLeu 247
              |||||||||||||||||||||||||||
Db         59 CCCAAAAATTTACAATTAAAACCCTTA 33

RESULT 37
BQ356685
LOCUS       BQ356685                263 bp    mRNA    linear   EST 20-MAY-2002
DEFINITION  PM0-HT0335-050400-007-G05 HT0335 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ356685
VERSION     BQ356685.1  GI:21021850
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 263)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-HT0335-
            050400-007-G05&t3=2000-04-05&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 31
            High quality sequence stop: 69.
FEATURES             Location/Qualifiers
     source          1. .263
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0335"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              202           Length:        263
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     3             Gaps:          0
```

-10-821-670A-30 (1-329) x BQ356685 (1-263)

```
        101 PheLeuLeuIleHisLysLysGluAsp 109
            |||||||||||||||||||||||||||
        160 TTTTTACTGATTCACAAAAAGGAAGAC 186
```

```
SULT 38
)24612
CUS       BY024612                353 bp    mRNA    linear   EST 06-DEC-2002
FINITION  BY024612 RIKEN full-length enriched, mammary gland RCB-0527
          Jyg-MC(B) cDNA Mus musculus cDNA clone G930023O12 5', mRNA
          sequence.
CESSION   BY024612
RSION     BY024612.1  GI:26130055
YWORDS    EST.
URCE      Mus musculus (house mouse)
RGANISM   Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE   1  (bases 1 to 353)
AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
          Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
          Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
          Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
          Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
          Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
          Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
          Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
          Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
          Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
          Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
          Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
          Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
          Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
          Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
          Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
          Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
          Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
          Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
          Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
          Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
          Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
          Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
          Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
          Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
          Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
          Rogers,J., Birney,E. and Hayashizaki,Y.
ITLE      Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
  PUBMED  12466851
MENT      Contact: Yoshihide Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center(GSC), Yokohama Institute
          The Institute of Physical and Chemical Research (RIKEN)
          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel: 81-45-503-9222
          Fax: 81-45-503-9216
          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
          Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
          Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
          Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
          Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
          Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
          Hayashizaki,Y. Direct Submission
           Computational Analysis of Full-Length Mouse cDNAs Compared with
          Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
           Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new
          genes. Genome Res. 10 (10), 1617-1630 (2000)
           RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer. Genome Res.
          10 (11), 1757-1771 (2000)
           Computer-based methods for the mouse full-length cDNA
          encyclopedia: real-time sequence clustering for construction of a
          nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
           cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
           Please visit our web site (http://genome.gsc.riken.go.jp) for
          further details.
FEATURES            Location/Qualifiers
     source         1. .353
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="G930023O12"
                    /tissue_type="mammary gland"
                    /cell_line="RCB-0527 Jyg-MC(B)"
                    /clone_lib="RIKEN full-length enriched, mammary gland
                    RCB-0527 Jyg-MC(B) cDNA"
ORIGIN

Alignment Scores:
Pred. No.:                 263          Length:          353
Score:                     9.00         Matches:         9
Percent Similarity:        100.0%       Conservative:    0
Best Local Similarity:     100.0%       Mismatches:      0
Query Match:               2.7%         Indels:          0
DB:                        4            Gaps:            0

US-10-821-670A-30 (1-329) x BY024612 (1-353)

Qy        265 ThrProHisSerTyrPheSerLeuThr 273
              |||||||||||||||||||||||||||
Db         83 ACCCCTCATTCCTACTTCTCCCTCACC 109

RESULT 39
BY024263
LOCUS       BY024263                354 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  BY024263 RIKEN full-length enriched, mammary gland RCB-0527
            Jyg-MC(B) cDNA Mus musculus cDNA clone G930022C19 5', mRNA
            sequence.
ACCESSION   BY024263
VERSION     BY024263.1  GI:26129706
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
```

Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

ITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

OURNAL Nature 420, 563-573 (2002)

PUBMED 12466851

MENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

TURES Location/Qualifiers
source 1. .354
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="G930022C19"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
/clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"

GIN

gnment Scores:

d. No.:	263	Length:	354
re:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.7%	Indels:	0
	4	Gaps:	0

10-821-670A-30 (1-329) x BY024263 (1-354)

```
       265 ThrProHisSerTyrPheSerLeuThr 273
           |||||||||||||||||||||||||||
        83 ACCCCTCATTCCTACTTCTCCCTCACC 109
```

ULT 40
13557
US BY013557 355 bp mRNA linear EST 06-DEC-2002
INITION BY013557 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus musculus cDNA clone G730040C02 5', mRNA sequence.

ACCESSION BY013557
VERSION BY013557.1 GI:26073806
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 355)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers

```
   source          1. .355
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /db_xref="taxon:10090"
                   /clone="G730040C02"
                   /tissue_type="lung"
                   /cell_line="RCB-0558 LLC"
                   /clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
                   cDNA"
IGIN

ignment Scores:
ed. No.:              264          Length:        355
ore:                  9.00         Matches:       9
cent Similarity:      100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            2.7%         Indels:        0
:                     4            Gaps:          0

-10-821-670A-30 (1-329) x BY013557 (1-355)

       265 ThrProHisSerTyrPheSerLeuThr 273
           |||||||||||||||||||||||||||
        82 ACCCCTCATTCCTACTTCTCCCTCACC 108

SULT 41
)972
CUS       W00972                  361 bp    mRNA    linear   EST 18-APR-1996
FINITION  za55d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
          IMAGE:296461 5' similar to contains element L1 repetitive element
          ;, mRNA sequence.
CESSION   W00972
RSION     W00972.1  GI:1272951
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 361)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
          Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
          Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
          Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
          Wilson,R.
TITLE     The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
MMENT     Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Seq primer: mob.REGA+ET
          High quality sequence stop: 217.
ATURES              Location/Qualifiers
   source           1. .361
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="GDB:1241382"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:296461"
                    /sex="male"
                    /dev_stage="20 week-post conception fetus"
                    /lab_host="DH10B (ampicillin resistant)"
                    /clone_lib="Soares fetal liver spleen 1NFLS"
                    /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                    with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                    1st strand cDNA was primed with a Pac I - oligo(dT) primer
                    [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                    double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Pac I and cloned into the Pac I
                    and Eco RI sites of the modified pT7T3 vector.  Library
                    went through one round of normalization. Library
                    constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:              268          Length:        361
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.7%         Indels:        0
DB:                     10           Gaps:          0

US-10-821-670A-30 (1-329) x W00972 (1-361)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        118 TTTTTACTGATTCACAAAAAGGAAGAC 144

RESULT 42
BY204279
LOCUS       BY204279                382 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY204279 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730212J07 5', mRNA sequence.
ACCESSION   BY204279
VERSION     BY204279.1  GI:26384080
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 382)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
```

Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
TURES             Location/Qualifiers
  source          1. .382
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="F730212J07"
                  /cell_type="B6-derived CD11 +ve dendritic cells"
                  /clone_lib="RIKEN full-length enriched, B6-derived CD11
                  +ve dendritic cells"
GIN

gnment Scores:
d. No.:              282          Length:        382
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            2.7%         Indels:        0
                     4            Gaps:          0

10-821-670A-30 (1-329) x BY204279 (1-382)

       265 ThrProHisSerTyrPheSerLeuThr 273
           |||||||||||||||||||||||||||
        76 ACCCCTCATTCCTACTTCTCCCTCACC 102

ULT 43
83786
US       BY183786                409 bp    mRNA    linear   EST 10-DEC-2002
INITION  BY183786 RIKEN full-length enriched, NOD-derived CD11c +ve
         dendritic cells Mus musculus cDNA clone F630110G11 5', mRNA
         sequence.
ESSION   BY183786
SION     BY183786.1  GI:26320432
WORDS    EST.
RCE      Mus musculus (house mouse)
RGANISM  Mus musculus
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
         Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE   1  (bases 1 to 409)
UTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
         Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
         Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
         Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
         Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
         Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
         Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
         Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
         Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
         Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
         Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
         Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
         Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
         Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
         Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
         Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
         Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
         Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
         Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
         Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
         Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
         Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
         Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
         Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
         Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
         Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
         Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE    Analysis of the mouse transcriptome based on functional annotation
         of 60,770 full-length cDNAs
JOURNAL  Nature 420, 563-573 (2002)
PUBMED   12466851
COMMENT  Contact: Yoshihide Hayashizaki
         Laboratory for Genome Exploration Research Group, RIKEN Genomic
         Sciences Center(GSC), Yokohama Institute
         The Institute of Physical and Chemical Research (RIKEN)
         1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
         Tel: 81-45-503-9222
         Fax: 81-45-503-9216
         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
         Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
         Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
         Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
         Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
         Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
         Hayashizaki,Y. Direct Submission
         Computational Analysis of Full-Length Mouse cDNAs Compared with
         Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
         Normalization and subtraction of cap-trapper-selected cDNAs to
         prepare full-length cDNA libraries for rapid discovery of new
         genes. Genome Res. 10 (10), 1617-1630 (2000)
         RIKEN integrated sequence analysis (RISA) system--384-format
         sequencing pipeline with 384 multicapillary sequencer. Genome Res.
         10 (11), 1757-1771 (2000)
         Computer-based methods for the mouse full-length cDNA
         encyclopedia: real-time sequence clustering for construction of a
         nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
         cDNA library was prepared and sequenced in Mouse Genome
         Encyclopedia Project of Genome Exploration Research Group in Riken
         Genomic Sciences Center and Genome Science Laboratory in RIKEN.
         Division of Experimental Animal Research in Riken contributed to
         prepare mouse tissues.
         Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
         Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
         Trust/MRC building Addenbrookes Hospital Cambridge) whose
         assistance we gratefully acknowledge.
         Please visit our web site (http://genome.gsc.riken.go.jp) for
         further details.
FEATURES           Location/Qualifiers
     source        1. .409
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="NOD"
                   /db_xref="taxon:10090"
                   /clone="F630110G11"
                   /cell_type="NOD-derived CD11c +ve dendritic cells"
                   /clone_lib="RIKEN full-length enriched, NOD-derived CD11c
                   +ve dendritic cells"
```

```
IGIN

ignment Scores:
ed. No.:                300             Length:         409
ore:                    9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              2.7%            Indels:         0
:                       4               Gaps:           0

-10-821-670A-30 (1-329) x BY183786 (1-409)

       265 ThrProHisSerTyrPheSerLeuThr 273
           |||||||||||||||||||||||||||
        82 ACCCCTCATTCCTACTTCTCCCTCACC 108

SULT 44
305003/c
CUS       AQ305003                415 bp    DNA     linear   GSS 16-DEC-1998
FINITION  HS_2012_A1_E07_T7 CIT Approved Human Genomic Sperm Library D Homo
          sapiens genomic clone Plate=2012 Col=13 Row=I, genomic survey
          sequence.
CESSION   AQ305003
RSION     AQ305003.1  GI:4024789
YWORDS    GSS.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 415)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
          Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
          Hood,L.
TITLE     Sequence-tagged connectors: A sequence approach to mapping and
          scanning the human genome
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED   10449764
MMENT     Contact: Mahairas GG, Wallace JC, Hood L
          High Throughput Sequencing Center
          University of Washington
          401 Queen Anne Avenue North, Seattle, WA 98109, USA
          Tel: (206) 616-3618
          Fax: (206) 616-3887
          Email: jwallace@u.washington.edu
          Sequence Tagged Connector
          Plate: 2012  row: I  column: 13
          Class: BAC ends
          High quality sequence stop: 415.
ATURES              Location/Qualifiers
   source           1. .415
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /clone="Plate=2012 Col=13 Row=I"
                    /sex="male"
                    /clone_lib="CIT Approved Human Genomic Sperm Library D"
                    /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                    E-Coli DH10B"
IGIN

ignment Scores:
ed. No.:                303             Length:         415
ore:                    9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              2.7%            Indels:         0
:                       11              Gaps:           0

-10-821-670A-30 (1-329) x AQ305003 (1-415)

       109 AspGlyIleTrpSerThrAspIleLeu 117
           |||||||||||||||||||||||||||
```

```
Db        249 GACGGTATTTGGTCAACCGATATTCTT 223

RESULT 45
AW382621/c
LOCUS       AW382621                423 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  PM0-HT0335-171199-002-f07 HT0335 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW382621
VERSION     AW382621.1  GI:6887280
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 423)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-HT0335-
            171199-002-f07&t3=1999-11-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 151.
FEATURES              Location/Qualifiers
     source           1. .423
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /dev_stage="Adult"
                      /clone_lib="HT0335"
                      /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                      Site_2: SmaI; A mini-library was made by cloning products
                      derived from  ORESTES PCR (U.S. Letters Patent application
                      No. 196,716 -  Ludwig Institute for Cancer Research)
                      profiles into  the pUC 18 vector. Reverse transcription of
                      tissue mRNA and cDNA amplification were performed under
                      low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              309             Length:         423
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-30 (1-329) x AW382621 (1-423)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        271 TTTTTACTGATTCACAAAAAGGAAGAC 245

RESULT 46
BE153120/c
LOCUS       BE153120                435 bp    mRNA    linear   EST 21-JUN-2000
DEFINITION  PM0-HT0335-060300-006-h01 HT0335 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE153120
VERSION     BE153120.1  GI:8615841
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
ERENCE 1 (bases 1 to 435)
UTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
ITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
OURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
MENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM0-HT0335-060300-006-h01&t3=2000-03-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence stop: 435.
TURES Location/Qualifiers
source 1. .435
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0335"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
GIN

gnment Scores:

d. No.:	316	Length:	435
re:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.7%	Indels:	0
	7	Gaps:	0

10-821-670A-30 (1-329) x BE153120 (1-435)

```
101 PheLeuLeuIleHisLysLysGluAsp 109
    |||||||||||||||||||||||||||
283 TTTTTACTGATTCACAAAAAGGAAGAC 257
```

ULT 47
30861/c
US CI330861 442 bp mRNA linear EST 07-FEB-2006
INITION CI330861 Oryza sativa (japonica cultivar-group) shoot Oryza sativa (japonica cultivar-group) cDNA clone J01B3122J01M3 3', mRNA sequence.
ESSION CI330861
SION CI330861.1 GI:86865330
WORDS EST.
RCE Oryza sativa (japonica cultivar-group)
RGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
ERENCE 1 (bases 1 to 442)
AUTHORS Kikuchi,S.
TITLE Collection and mapping of over 30,000 transcription units by the rice full- length cDNA project from japonica rice
JOURNAL Unpublished (2006)
COMMENT Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA Project
URL:http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
FEATURES Location/Qualifiers
source 1. .442
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J01B3122J01M3"
/tissue_type="shoot"
/clone_lib="Oryza sativa (japonica cultivar-group) shoot"
ORIGIN

Alignment Scores:

Pred. No.:	321	Length:	442
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-30 (1-329) x CI330861 (1-442)

```
Qy        284 ArgGluLysLysAspArgLeuSerVal 292
              |||||||||||||||||||||||||||
Db        166 AGAGAAAAGAAGGATCGCCTGTCAGTG 140
```

RESULT 48
BE677126/c
LOCUS BE677126 442 bp mRNA linear EST 08-SEP-2000
DEFINITION 7d80f03.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279293 3' similar to contains Alu repetitive element;contains element MER14 repetitive element ;, mRNA sequence.
ACCESSION BE677126
VERSION BE677126.1 GI:10037667
KEYWORDS EST.

```
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 442)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
ITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
MMENT     Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. James Lupski
           cDNA Library Preparation: Lupski Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          info@image.llnl.gov
          Seq primer: -40UP from Gibco
          High quality sequence stop: 410.
ATURES              Location/Qualifiers
   source           1. .442
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:3279293"
                    /sex="male"
                    /tissue_type="dorsal root ganglia"
                    /dev_stage="adult, 36 yr"
                    /lab_host="DH10B"
                    /clone_lib="Lupski_dorsal_root_ganglion"
                    /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                    NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                    Directionally cloned using the following adaptors:
                    5'-TCGACCCACGCGTCCG-3' and
                    5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                    1 kb for average insert length 1.7 kb. This is a primary
                    library, non-amplified. Library constructed by Life
                    Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                    College of Medicine) and is available through Life
                    Technologies."
IGIN

ignment Scores:
ed. No.:                321             Length:         442
ore:                    9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              2.7%            Indels:         0
:                       7               Gaps:           0

-10-821-670A-30 (1-329) x BE677126 (1-442)

        101 PheLeuLeuIleHisLysLysGluAsp 109
            |||||||||||||||||||||||||||
        405 TTTTTACTGATTCACAAAAAGGAAGAC 379

SULT 49
143811/c
CUS       AU143811                463 bp    mRNA    linear   EST 05-AUG-2002
FINITION  AU143811 HEMBA1 Homo sapiens cDNA clone HEMBA1000076 3', mRNA
          sequence.
CESSION   AU143811
RSION     AU143811.1  GI:11005332
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 463)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE   Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
  JOURNAL Genome Res. 16 (1), 55-65 (2006)
  PUBMED  16344560
COMMENT   Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
          Research Institute; cDNA library construction: Department of
          Virology, Institute of Medical Science, University of Tokyo, and
          Helix Research Institute.
FEATURES            Location/Qualifiers
     source         1. .463
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="HEMBA1000076"
                    /tissue_type="whole embryo, mainly head"
                    /dev_stage="embryo, 10 weeks"
                    /clone_lib="HEMBA1"
                    /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              335             Length:         463
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     1               Gaps:           0

US-10-821-670A-30 (1-329) x AU143811 (1-463)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        400 TTTTTACTGATTCACAAAAAGGAAGAC 374

RESULT 50
AI754066/c
LOCUS       AI754066                477 bp    mRNA    linear   EST 20-JUN-2002
DEFINITION  cr19c06.x1 Human bone marrow stromal cells Homo sapiens cDNA clone
            HBMSC_cr19c06 3', mRNA sequence.
ACCESSION   AI754066
VERSION     AI754066.1  GI:5132330
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   Jia,L., Young,M.F., Powell,J., Yang,L., Ho,N.C., Hotchkiss,R.,
            Robey,P.G. and Francomano,C.A.
  TITLE     Gene expression profile of human bone marrow stromal cells:
            high-throughput expressed sequence tag sequencing analysis
  JOURNAL   Genomics 79 (1), 7-17 (2002)
  PUBMED    11827452
COMMENT     Contact: Libin Jia
            Medical Genetics Branch
            National Human Genome Research Institute
            10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
            Tel: 301-402-4877
            Fax: 301-496-7157
```

```
          Email: libin@helix.nih.gov
          DNA Sequencing and analyses by National Institutes of Health
          Intramural Sequencing Center (NISC).
          Plate: 19  row: c  column: 06
          Seq primer: -21M13 forward primer (ABI).
TURES               Location/Qualifiers
   source           1. .477
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="HBMSC_cr19c06"
                    /sex="mixed"
                    /tissue_type="bone marrow stroma"
                    /dev_stage="mixed"
                    /lab_host="XL1-Blue MRF'/SOLR"
                    /clone_lib="Human bone marrow stromal cells"
                    /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI;
                    mRNA made from human bone marrow stroma, cDNA made by
                    oligo-dT priming. Directionally cloned. Size-selected for
                    average insert size >0.5 kb. Library constructed by Dr.
                    Marian Young and Dr. Pamela Gehron Robey (NIDCR). Library
                    supplied by Dr. Libin Jia (NHGRI)"
IGIN

gnment Scores:
d. No.:              344            Length:        477
re:                  9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            2.7%           Indels:        0
                     1              Gaps:          0

10-821-670A-30 (1-329) x AI754066 (1-477)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       418 TTTTTACTGATTCACAAAAAGGAAGAC 392

ULT 51
83279
US       AI683279                479 bp    mRNA    linear   EST 26-MAY-1999
INITION  tw50a03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2263084 3',
         mRNA sequence.
 ESSION  AI683279
 SION    AI683279.1  GI:4893461
 WORDS   EST.
 RCE     Homo sapiens (human)
 RGANISM Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 479)
UTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
ITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
         Tumor Gene Index
OURNAL   Unpublished (1997)
MENT     Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-r@mail.nih.gov
         Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
         Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         www-bio.llnl.gov/bbrp/image/image.html
         Seq primer: -40UP from Gibco
         High quality sequence stop: 415.
TURES               Location/Qualifiers
   source           1. .479
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2263084"
                    /tissue_type="well-differentiated endometrial
                    adenocarcinoma, 7 pooled tumors"
                    /lab_host="DH10B"
                    /clone_lib="NCI_CGAP_Ut1"
                    /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                    Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                    Average insert size 1.75 kb. Life Technologies catalog #:
                    11538-014"
ORIGIN

Alignment Scores:
Pred. No.:              345            Length:        479
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            2.7%           Indels:        0
DB:                     1              Gaps:          0

US-10-821-670A-30 (1-329) x AI683279 (1-479)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        451 TTTTTACTGATTCACAAAAAGGAAGAC 477

RESULT 52
CA699592
LOCUS       CA699592                479 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  wlk8.pk0021.d7 wlk8 Triticum aestivum cDNA clone wlk8.pk0021.d7 5'
            end, mRNA sequence.
ACCESSION   CA699592
VERSION     CA699592.1  GI:25421385
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 479)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .479
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Stephens"
                     /db_xref="taxon:4565"
                     /clone="wlk8.pk0021.d7"
                     /tissue_type="leaf"
                     /clone_lib="wlk8"
                     /note="Vector: pGEM-7; Site_1: EcoRI; Site_2: XhoI; Wheat
                     (Triticum aestivum L.) seedlings 8 hr after treatment with
                     6-iodo-3-propyl-2-propyloxy-4(3H)-quinazolinone"
ORIGIN

Alignment Scores:
Pred. No.:              345            Length:        479
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            2.7%           Indels:        0
DB:                     4              Gaps:          0
```

```
-10-821-670A-30 (1-329) x CA699592 (1-479)

        239 ProLysAsnLeuGlnLeuLysProLeu 247
            |||||||||||||||||||||||||||
        394 CCCAAGAATCTTCAACTCAAGCCGTTA 420

SULT 53
325004/c
CUS       BI325004                494 bp    mRNA    linear   EST 30-JUL-2001
FINITION  ic21a08.x2 HR85 islet Homo sapiens cDNA 3', mRNA sequence.
CESSION   BI325004
RSION     BI325004.1  GI:15004190
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 494)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
          Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
          Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
          Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
          Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
          Williams,T., Jackson,Y. and Bowers,Y.
TITLE     Endocrine Pancreas Consortium
JOURNAL   Unpublished (2000)
MMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
          Endocrine Pancreas Consortium
          Harvard University, Howard Hughes Medical Institute
          Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
          MA 02138
          Tel: 617-495-1812
          Fax: 617-495-8557
          Email: dmelton@biohp.harvard.edu
          Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
          Washington University Genome Sequencing Center For information on
          obtaining a clone please contact: Dr. Hiroshi Inoue
          (hinoue@im.wustl.edu)
          Seq primer: -40UP from Gibco
          High quality sequence stop: 455.
ATURES              Location/Qualifiers
   source           1. .494
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /tissue_type="Purified pancreatic islet"
                    /lab_host="DH10B"
                    /clone_lib="HR85 islet"
                    /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                    NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                    Size-selected on agarose gel. Average insert size ~1kb. 5'
                    XhoI site was destroyed after directional cloning.
                    Amplified once. Contact information: Hiroshi Inoue, MD,
                    Metabolism Div. (Alan Permutt Lab), Washington University
                    School of Medicine, Box 8127, 660 South Euclid Ave., St.
                    Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                    314-362-1916, Fax: 314-747-2692."
IGIN

ignment Scores:
ed. No.:              354           Length:        494
ore:                  9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            2.7%          Indels:        0
:                     2             Gaps:          0

-10-821-670A-30 (1-329) x BI325004 (1-494)

        101 PheLeuLeuIleHisLysLysGluAsp 109
            |||||||||||||||||||||||||||
        400 TTTTTACTGATTCACAAAAAGGAAGAC 374
```

```
RESULT 54
AQ300559
LOCUS       AQ300559                500 bp    DNA     linear   GSS 16-DEC-1998
DEFINITION  HS_3175_B1_B09_T7 CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3175 Col=17 Row=D, genomic survey
            sequence.
ACCESSION   AQ300559
VERSION     AQ300559.1  GI:4020236
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 500)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  PUBMED    10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3175  row: D  column: 17
            Class: BAC ends
            High quality sequence stop: 500.
FEATURES              Location/Qualifiers
     source           1. .500
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /clone="Plate=3175 Col=17 Row=D"
                      /sex="male"
                      /clone_lib="CIT Approved Human Genomic Sperm Library D"
                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                      E-Coli DH10B"
ORIGIN

Alignment Scores:
Pred. No.:              358           Length:        500
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     11            Gaps:          0

US-10-821-670A-30 (1-329) x AQ300559 (1-500)

Qy          94 GlyGluValLeuSerHisSerPheLeu 102
               |||||||||||||||||||||||||||
Db         278 GGGGAGGTCCTGAGTCACTCCTTCTTA 304

RESULT 55
BM090808/c
LOCUS       BM090808                504 bp    mRNA    linear   EST 20-NOV-2001
DEFINITION  ig15e03.x1 Human Fetal Pancreas 1A Homo sapiens cDNA 3', mRNA
            sequence.
ACCESSION   BM090808
VERSION     BM090808.1  GI:17019774
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```

```
ERENCE   1  (bases 1 to 504)
UTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
         Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
         Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
         Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
         Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
         Williams,T., Jackson,Y. and Bowers,Y.
ITLE     Endocrine Pancreas Consortium
OURNAL   Unpublished (2000)
MENT     Other_ESTs: ig15e03.y1
         Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
         Endocrine Pancreas Consortium
         Harvard University, Howard Hughes Medical Institute
         Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
         MA 02138
         Tel: 617-495-1812
         Fax: 617-495-8557
         Email: dmelton@biohp.harvard.edu
         Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
         Washington University Genome Sequencing Center For information on
         obtaining a clone please contact: Dr. Hiroshi Inoue
         (hinoue@imgate.wustl.edu)
         High quality sequence stop: 447.
TURES              Location/Qualifiers
   source          1. .504
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /tissue_type="Fetal Pancreas (4 Pooled Donors, 18 - 20
                   weeks, Stratagene #738023)"
                   /dev_stage="Fetal Pancreas"
                   /clone_lib="Human Fetal Pancreas 1A"
                   /note="Vector: pBluescript SK(-); Site_1: NotI; Site_2:
                   XhoI; cDNA made by oligo-dT priming. Size-selected by
                   CHROMA SPIN-1000  (Clontech). Average insert size ~1kb. 5'
                   XhoI site was destroyed after directional cloning.
                   Amplified once.  Contact information: Hiroshi Inoue, MD,
                   Metabolism Div. (Alan Permutt Lab),  Washington University
                   School of Medicine, Box 8127, 660 South Euclid Ave., St.
                   Louis, MO 63110 E-mail: hinoue@imgate.wustl.edu Tel:
                   314-362-1916, Fax:314-747-2692."
GIN

gnment Scores:
d. No.:              361          Length:        504
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            2.7%         Indels:        0
                     2            Gaps:          0

10-821-670A-30 (1-329) x BM090808 (1-504)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       400 TTTTTACTGATTCACAAAAAGGAAGAC 374

ULT 56
67597
US       AW367597                 507 bp    mRNA    linear   EST 04-FEB-2000
INITION  MR0-HT0164-151299-012-b02 HT0164 Homo sapiens cDNA, mRNA sequence.
ESSION   AW367597
SION     AW367597.1  GI:6872247
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 507)
UTHORS   HCGP http://www.ludwig.org.br/ORESTES.
ITLE     The FAPESP/LICR Human Cancer Genome Project
OURNAL   Unpublished (1999)
COMMENT  Contact: Simpson A.J.G.
         Laboratory of Cancer Genetics
         Ludwig Institute for Cancer Research
         Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
         Brazil
         Tel: +55-11-2704922
         Fax: +55-11-2707001
         Email: asimpson@ludwig.org.br
         This sequence was derived from the FAPESP/LICR Human Cancer Genome
         Project. This entry can be seen in the following URL
         (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-HT0164-
         151299-012-b02&t3=1999-12-15&t4=1)
         Seq primer: puc 18 forward
         High quality sequence start: 13
         High quality sequence stop: 95.
FEATURES           Location/Qualifiers
     source        1. .507
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /dev_stage="Adult"
                   /clone_lib="HT0164"
                   /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                   Site_2: SmaI; A mini-library was made by cloning products
                   derived from  ORESTES PCR (U.S. Letters Patent application
                   No. 196,716 -  Ludwig Institute for Cancer Research)
                   profiles into  the pUC 18 vector. Reverse transcription of
                   tissue mRNA and cDNA amplification were performed under
                   low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              363          Length:        507
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.7%         Indels:        0
DB:                     7            Gaps:          0

US-10-821-670A-30 (1-329) x AW367597 (1-507)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        106 TTTTTACTGATTCACAAAAAGGAAGAC 132

RESULT 57
AI554405/c
LOCUS       AI554405                 510 bp    mRNA    linear   EST 13-MAY-1999
DEFINITION  tq11a12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2208478 3'
            similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION   AI554405
VERSION     AI554405.1  GI:4486768
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
```

```
        Insert Length: 2025   Std Error: 0.00
        Seq primer: -40UP from Gibco
        High quality sequence stop: 404
        POLYA=No.
ATURES              Location/Qualifiers
   source           1. .510
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2208478"
                    /tissue_type="poorly-differentiated endometrial
                    adenocarcinoma, 2 pooled tumors"
                    /lab_host="DH10B"
                    /clone_lib="NCI_CGAP_Ut3"
                    /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                    Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                    Average insert size 1.45 kb. Life Technologies catalog #:
                    11541-018"
IGIN

ignment Scores:
ed. No.:              365           Length:        510
ore:                  9.00          Matches:       9
cent Similarity:      100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            2.7%          Indels:        0
:                     1             Gaps:          0

-10-821-670A-30 (1-329) x AI554405 (1-510)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       403 TTTTTACTGATTCACAAAAAGGAAGAC 377

SULT 58
706519/c
CUS       AV706519                 516 bp    mRNA    linear   EST 09-OCT-2000
FINITION  AV706519 ADB Homo sapiens cDNA clone ADBAVE10 5', mRNA sequence.
CESSION   AV706519
RSION     AV706519.1  GI:10723798
YWORDS    EST.
URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 516)
AUTHORS   Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G.,
          Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z.,
          Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S.,
          Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
TITLE     Homo sapiens cDNA ADB clones
JOURNAL   Unpublished (2000)
MMENT     Contact: Zeguang Han
          Chinese National Human Genome Center at Shanghai
          351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
          201203, P. R. China
          Tel: 86-21-50801919(ex.45)
          Fax: 86-21-50801922
          Email: hanzg@chgc.sh.cn
          This clone is available at CHGC in Shanghai.
ATURES              Location/Qualifiers
   source           1. .516
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="ADBAVE10"
                    /tissue_type="Adrenal gland"
                    /dev_stage="Adult"
                    /lab_host="SOLR"
                    /clone_lib="ADB"
                    /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                    XhoI"
ORIGIN

Alignment Scores:
Pred. No.:              368           Length:        516
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     1             Gaps:          0

US-10-821-670A-30 (1-329) x AV706519 (1-516)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        143 TTTTTACTGATTCACAAAAAGGAAGAC 117

RESULT 59
DA098991/c
LOCUS       DA098991                 546 bp    mRNA    linear   EST 02-NOV-2005
DEFINITION  DA098991 BRACE3 Homo sapiens cDNA clone BRACE3010218 5', mRNA
            sequence.
ACCESSION   DA098991
VERSION     DA098991.1  GI:78757572
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 546)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES            Location/Qualifiers
     source         1. .546
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="BRACE3010218"
                    /tissue_type="cerebellum"
                    /clone_lib="BRACE3"
                    /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              387           Length:        546
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     9             Gaps:          0
```

-10-821-670A-30 (1-329) x DA098991 (1-546)

```
       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
        98 TTTTTACTGATTCACAAAAAGGAAGAC 72
```

```
ULT 60
43328/c
US       BE143328                548 bp    mRNA    linear   EST 21-JUN-2000
INITION  MR0-HT0162-191099-002-b03 HT0162 Homo sapiens cDNA, mRNA sequence.
ESSION   BE143328
SION     BE143328.1  GI:8606049
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 548)
UTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
         Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
         Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
         Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
         O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
         Simpson,A.J.
ITLE     Shotgun sequencing of the human transcriptome with ORF expressed
         sequence tags
OURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED  10737800
MENT     Contact: Simpson A.J.G.
         Laboratory of Cancer Genetics
         Ludwig Institute for Cancer Research
         Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
         Brazil
         Tel: +55-11-2704922
         Fax: +55-11-2707001
         Email: asimpson@ludwig.org.br
         This sequence was derived from the FAPESP/LICR Human Cancer Genome
         Project. This entry can be seen in the following URL
         (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR0-HT0162-191
         099-002-b03&t3=1999-10-19&t4=1)
         Seq primer: puc 18 forward
         High quality sequence start: 9
         High quality sequence stop: 528.
TURES              Location/Qualifiers
  source           1. .548
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /dev_stage="Adult"
                   /clone_lib="HT0162"
                   /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                   Site_2: SmaI; A mini-library was made by cloning products
                   derived from  ORESTES PCR (U.S. Letters Patent application
                   No. 196,716 -  Ludwig Institute for Cancer Research)
                   profiles into  the pUC 18 vector. Reverse transcription of
                   tissue mRNA and cDNA amplification were performed under
                   low stringency conditions."
GIN
```

```
gnment Scores:
d. No.:              389            Length:        548
re:                  9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            2.7%           Indels:        0
                     7              Gaps:          0
```

-10-821-670A-30 (1-329) x BE143328 (1-548)

```
        15 LeuLeuAlaProProLeuMetAlaIle 23
           |||||||||||||||||||||||||||
       439 CTACTTGCCCCACCCCTAATGGCCATA 413
```

```
RESULT 61
DB284546/c
LOCUS       DB284546                553 bp    mRNA    linear   EST 10-DEC-2005
DEFINITION  DB284546 UTERU3 Homo sapiens cDNA clone UTERU3012510 5', mRNA
            sequence.
ACCESSION   DB284546
VERSION     DB284546.1  GI:83439601
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 553)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES             Location/Qualifiers
     source          1. .553
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UTERU3012510"
                     /tissue_type="uterus"
                     /clone_lib="UTERU3"
                     /note="Vector: pME18SFL3"
ORIGIN
```

```
Alignment Scores:
Pred. No.:              392            Length:        553
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            2.7%           Indels:        0
DB:                     9              Gaps:          0
```

US-10-821-670A-30 (1-329) x DB284546 (1-553)

```
Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        483 TTTTTACTGATTCACAAAAAGGAAGAC 457
```

```
RESULT 62
DA102042/c
LOCUS       DA102042                561 bp    mRNA    linear   EST 01-NOV-2005
DEFINITION  DA102042 BRACE3 Homo sapiens cDNA clone BRACE3014468 5', mRNA
            sequence.
ACCESSION   DA102042
VERSION     DA102042.1  GI:78562825
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
```

```
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
FERENCE   1  (bases 1 to 561)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE     Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
JOURNAL   Genome Res. 16 (1), 55-65 (2006)
 PUBMED   16344560
MMENT     Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
ATURES              Location/Qualifiers
   source           1. .561
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="BRACE3014468"
                    /tissue_type="cerebellum"
                    /clone_lib="BRACE3"
                    /note="Vector: pME18SFL3"
IGIN

lignment Scores:
ed. No.:               397          Length:        561
ore:                   9.00         Matches:       9
cent Similarity:       100.0%       Conservative:  0
st Local Similarity:   100.0%       Mismatches:    0
ery Match:             2.7%         Indels:        0
:                      9            Gaps:          0

-10-821-670A-30 (1-329) x DA102042 (1-561)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       459 TTTTTACTGATTCACAAAAAGGAAGAC 433

SULT 63
054731
CUS       CW054731                 563 bp    DNA     linear   GSS 28-OCT-2004
FINITION  104_295_10516691_115_30176 Sorghum methylation filtered library
          (LibID: 104) Sorghum bicolor genomic clone 10516691, genomic survey
          sequence.
CESSION   CW054731
RSION     CW054731.1  GI:54731461
YWORDS    GSS.
URCE      Sorghum bicolor (sorghum)
ORGANISM  Sorghum bicolor
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Sorghum.
FERENCE   1  (bases 1 to 563)
AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
          Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
          McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
          Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
          Martienssen,R.A.
  TITLE   Sorghum genome sequencing by methylation filtration
  JOURNAL PLoS Biol. 3 (1), e13 (2005)
   PUBMED 15660154
COMMENT   Contact: Bedell JA
          Orion Genomics, LLC
          4041 Forest Park Ave, St. Louis, MO 63108, USA
          Tel: 314 615 6979
          Fax: 314 615 5975
          Email: jbedell@oriongenomics.com
          Plate: 295  row: k  column: 09
          Seq primer: M13/pUC Reverse
          Class: methylation filtered
          High quality sequence stop: 563.
FEATURES            Location/Qualifiers
     source         1. .563
                    /organism="Sorghum bicolor"
                    /mol_type="genomic DNA"
                    /cultivar="ATx623"
                    /db_xref="taxon:4558"
                    /clone="10516691"
                    /clone_lib="Sorghum methylation filtered library (LibID:
                    104)"
                    /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                    prepared from purified nuclei was randomly sheared,
                    end-repaired, size fractionated to enrich for the 0.5 to 5
                    kb fraction, ligated into HincII-digested pBCSK(-) vector
                    and electroporated into E. coli cells. This is a
                    methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:               398          Length:        563
Score:                   9.00         Matches:       9
Percent Similarity:      100.0%       Conservative:  0
Best Local Similarity:   100.0%       Mismatches:    0
Query Match:             2.7%         Indels:        0
DB:                      13           Gaps:          0

US-10-821-670A-30 (1-329) x CW054731 (1-563)

Qy        121 LysGluSerLysAsnLysIlePheLeu 129
              |||||||||||||||||||||||||||
Db        533 AAAGAATCAAAGAACAAGATCTTCTTA 559

RESULT 64
DB349096
LOCUS       DB349096                 566 bp    mRNA    linear   EST 04-DEC-2005
DEFINITION  DB349096 TRACH3 Homo sapiens cDNA clone TRACH3005200 3', mRNA
            sequence.
ACCESSION   DB349096
VERSION     DB349096.1  GI:83258035
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 566)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
```

```
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
TURES             Location/Qualifiers
   source         1. .566
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="TRACH3005200"
                  /tissue_type="trachea"
                  /clone_lib="TRACH3"
                  /note="Vector: pME18SFL3"
GIN

gnment Scores:
d. No.:              400           Length:        566
re:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            2.7%          Indels:        0
                     9             Gaps:          0

10-821-670A-30 (1-329) x DB349096 (1-566)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       393 TTTTTACTGATTCACAAAAAGGAAGAC 419

ULT 65
907722
US        BM907722                572 bp    mRNA    linear   EST 12-MAR-2002
INITION   AGENCOURT_6618905 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5736102
          5', mRNA sequence.
ESSION    BM907722
SION      BM907722.1  GI:19358101
WORDS     EST.
RCE       Homo sapiens (human)
RGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
ERENCE    1  (bases 1 to 572)
UTHORS    NIH-MGC http://mgc.nci.nih.gov/.
ITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
OURNAL    Unpublished (1999)
MENT      Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: DCTD/DTP/Gazdar
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM12744  row: b  column: 07
          High quality sequence stop: 572.
 TURES            Location/Qualifiers
   source         1. .572
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:5736102"
                  /tissue_type="large cell carcinoma"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH_MGC_68"
                  /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                  Average insert size 1.8 kb.   Library constructed by Life
                  Technologies. "
ORIGIN

Alignment Scores:
Pred. No.:              404           Length:        572
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-30 (1-329) x BM907722 (1-572)

Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        156 TTTTTACTGATTCACAAAAAGGAAGAC 182

RESULT 66
CK818181/c
LOCUS       CK818181                593 bp    mRNA    linear   EST 11-MAR-2004
DEFINITION  ic21a08.y5 HR85 islet Homo sapiens cDNA clone IMAGE: 5', mRNA
            sequence.
ACCESSION   CK818181
VERSION     CK818181.1  GI:44835106
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 593)
  AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
            Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
            Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
            McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
            Bowers,Y.
  TITLE     WashU-Harvard Pancreas EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            This read is a 5' RESEQUENCE of a previously sequenced pancreas
            clone
            Good hit to opposite strand read. . .wrong orientation BUT PASSED FOR
            MOUSE-PANCREAS VERIFICATION
            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .593
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:"
                      /tissue_type="Purified pancreatic islet"
                      /lab_host="DH10B"
                      /clone_lib="HR85 islet"
                      /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                      NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                      Size-selected on agarose gel. Average insert size ~1kb. 5'
                      XhoI site was destroyed after directional cloning.
                      Amplified once. Contact information: Hiroshi Inoue, MD,
                      Metabolism Div. (Alan Permutt Lab), Washington University
                      School of Medicine, Box 8127, 660 South Euclid Ave., St.
                      Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                      314-362-1916, Fax: 314-747-2692."
ORIGIN
```

```
lgnment Scores:
ed. No.:                417             Length:         593
ore:                    9.00            Matches:        9
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              2.7%            Indels:         0
:                       5               Gaps:           0

-10-821-670A-30 (1-329) x CK818181 (1-593)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           ||||||||||||||||||||||||||||
       408 TTTTTACTGATTCACAAAAAGGAAGAC 382

SULT 67
136151/c
CUS         CW136151                624 bp    DNA     linear   GSS 29-OCT-2004
FINITION    104_521_11118228_148_34843_048 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 11118228, genomic survey
            sequence.
CESSION     CW136151
RSION       CW136151.1  GI:54828698
YWORDS      GSS.
URCE        Sorghum bicolor (sorghum)
ORGANISM    Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
FERENCE     1  (bases 1 to 624)
AUTHORS     Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
ITLE        Sorghum genome sequencing by methylation filtration
OURNAL      PLoS Biol. 3 (1), e13 (2005)
 PUBMED     15660154
MMENT       Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 521  row: b  column: 12
            Seq primer: SWfor Forward
            Class: methylation filtered
            High quality sequence stop: 624.
ATURES                  Location/Qualifiers
   source               1. .624
                        /organism="Sorghum bicolor"
                        /mol_type="genomic DNA"
                        /cultivar="ATx623"
                        /db_xref="taxon:4558"
                        /clone="11118228"
                        /clone_lib="Sorghum methylation filtered library (LibID:
                        104)"
                        /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                        prepared from purified nuclei was randomly sheared,
                        end-repaired, size fractionated to enrich for the 0.5 to 5
                        kb fraction, ligated into HincII-digested pBCSK(-) vector
                        and electroporated into E. coli cells. This is a
                        methylation filtered library."
EGIN

lgnment Scores:
ed. No.:                436             Length:         624
ore:                    9.00            Matches:        9
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              2.7%            Indels:         0
:                       13              Gaps:           0

-10-821-670A-30 (1-329) x CW136151 (1-624)

Qy          121 LysGluSerLysAsnLysIlePheLeu 129
                ||||||||||||||||||||||||||||
Db          324 AAAGAATCAAAGAACAAGATCTTCTTA 298

RESULT 68
BU813156/c
LOCUS       BU813156                631 bp    mRNA    linear   EST 15-OCT-2002
DEFINITION  N006A02 Populus bark cDNA library Populus tremula x Populus
            tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION   BU813156
VERSION     BU813156.1  GI:23968892
KEYWORDS    EST.
SOURCE      Populus tremula x Populus tremuloides
  ORGANISM  Populus tremula x Populus tremuloides
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
  TITLE     The poplar tree transcriptome: Analysis of expressed sequence tags
            from multiple libraries
  JOURNAL   Unpublished (2002)
COMMENT     Contact: BHALERAO RUPALI R.
            Umea Plant Science Center
            Department of Plant Physiology
            University of Umea, 901 87 Umea, Sweden
            Tel: +46 90 786 5279
            Fax: +46 90 786 6676
            Email: rupali.bhalerao@plantphys.umu.se.
FEATURES              Location/Qualifiers
     source           1. .631
                      /organism="Populus tremula x Populus tremuloides"
                      /mol_type="mRNA"
                      /db_xref="taxon:47664"
                      /tissue_type="bark"
                      /clone_lib="Populus bark cDNA library"
ORIGIN

Alignment Scores:
Pred. No.:              441             Length:         631
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x BU813156 (1-631)

Qy           11 PheSerLeuValLeuLeuAlaProPro 19
                ||||||||||||||||||||||||||
Db          190 TTCTCTCTTGTCCTGCTCGCTCCCCCT 164

RESULT 69
CW136150
LOCUS       CW136150                638 bp    DNA     linear   GSS 29-OCT-2004
DEFINITION  104_521_11118228_116_34847_048 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 11118228, genomic survey
            sequence.
ACCESSION   CW136150
VERSION     CW136150.1  GI:54828697
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 638)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
```

```
ITLE     Sorghum genome sequencing by methylation filtration
OURNAL   PLoS Biol. 3 (1), e13 (2005)
 PUBMED  15660154
MENT     Contact: Bedell JA
         Orion Genomics, LLC
         4041 Forest Park Ave, St. Louis, MO 63108, USA
         Tel: 314 615 6979
         Fax: 314 615 5975
         Email: jbedell@oriongenomics.com
         Plate: 521  row: b  column: 12
         Seq primer: T3 Reverse
         Class: methylation filtered
         High quality sequence stop: 638.
TURES             Location/Qualifiers
   source         1. .638
                  /organism="Sorghum bicolor"
                  /mol_type="genomic DNA"
                  /cultivar="ATx623"
                  /db_xref="taxon:4558"
                  /clone="11118228"
                  /clone_lib="Sorghum methylation filtered library (LibID:
                  104)"
                  /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                  prepared from purified nuclei was randomly sheared,
                  end-repaired, size fractionated to enrich for the 0.5 to 5
                  kb fraction, ligated into HincII-digested pBCSK(-) vector
                  and electroporated into E. coli cells. This is a
                  methylation filtered library."
GIN

gnment Scores:
d. No.:              445          Length:        638
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            2.7%         Indels:        0
                     13           Gaps:          0

10-821-670A-30 (1-329) x CW136150 (1-638)

       121 LysGluSerLysAsnLysIlePheLeu 129
           |||||||||||||||||||||||||||
       525 AAAGAATCAAAGAACAAGATCTTCTTA 551

ULT 70
44654
US       CL344654                645 bp    DNA     linear   GSS 19-AUG-2004
INITION  RPCI44_278P18.r RPCI-44 Sus scrofa genomic clone RPCI44_278P18,
         genomic survey sequence.
ESSION   CL344654
SION     CL344654.1  GI:51396622
WORDS    GSS.
RCE      Sus scrofa (pig)
RGANISM  Sus scrofa
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
         Sus.
ERENCE   1  (bases 1 to 645)
UTHORS   Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
         Beever,J.E. and Schook,L.B.
ITLE     Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
         Through Comparative Genomics
OURNAL   Unpublished (2004)
MENT     Other_GSSs: RPCI44_278P18.f
         Contact: Lawrence B. Schook
         Department of Animal Sciences
         University of Illinois at Urbana Champaign
         1201 W. Gregory Dr., Urbana, IL 61801, USA
         Tel: 217 265 5326
         Fax: 217 244 5617
         Email: schook@uiuc.edu
         Clones are derived from the porcine BAC library RPCI-44
         (http://www.bacpac.chori.org/porcine242.htm). For BAC library
         availability, please contact Pieter de Jong (pdejong@chori.org).
         Clones may be purchased from BACPAC Resources
         (http://BACPACorders.chori.org). This work was undertaken as part
         of the International Swine Genome Sequencing Consortium by
         University of Illinois at Urbana Champaign, USA with funds provided
         by grant No. AG2002-34480-11828 from USDA-CSREES and
         AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
         Initiative)
         Plate: 278  row: P  column: 18
         Seq primer: SP6
         Class: BAC ends.
FEATURES          Location/Qualifiers
     source       1. .645
                  /organism="Sus scrofa"
                  /mol_type="genomic DNA"
                  /strain="four pigs (breed: 37.5% Yorks Landrace and 25%
                  Meishan)"
                  /db_xref="taxon:9823"
                  /clone="RPCI44_278P18"
                  /sex="male"
                  /cell_type="blood"
                  /clone_lib="RPCI-44"
                  /note="Vector: pTARBAC2; Site_1: EcoRI; Site_2: EcoRI;
                  porcine male BAC library produced by Pieter de Jong"
ORIGIN

Alignment Scores:
Pred. No.:           449          Length:        645
Score:               9.00         Matches:       9
Percent Similarity:  100.0%       Conservative:  0
Best Local Similarity: 100.0%     Mismatches:    0
Query Match:         2.7%         Indels:        0
DB:                  13           Gaps:          0

US-10-821-670A-30 (1-329) x CL344654 (1-645)

Qy        274 PheGlyValGlnValGlnGlyLysAsn 282
              |||||||||||||||||||||||||||
Db         29 TTTGGTGTTCAGGTTCAGGGCAAGAAC 55

RESULT 71
DT874689/c
LOCUS       DT874689                 648 bp    mRNA    linear   EST 18-SEP-2005
DEFINITION  AGENCOURT_58684019 NIH_ZGC_5 Danio rerio cDNA clone IMAGE:8101578
            5', mRNA sequence.
ACCESSION   DT874689
VERSION     DT874689.1  GI:75844429
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 648)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: John Postlethwait, University of Oregon
             cDNA Library Preparation: Dr. Sumio Sugano
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM17510  row: o  column: 16
            High quality sequence start: 8
            High quality sequence stop: 559.
FEATURES          Location/Qualifiers
```

```
   source          1. .648
                   /organism="Danio rerio"
                   /mol_type="mRNA"
                   /db_xref="taxon:7955"
                   /clone="IMAGE:8101578"
                   /tissue_type="contains eggs from one female, from all
                   stages of development as well as support cells"
                   /lab_host="DH10B TonA"
                   /clone_lib="NIH_ZGC_5"
                   /note="Organ: ovary; Vector: pME18S-FL3; Site_1: DraIII;
                   Site_2: DraIII; 1st strand cDNA was primed with an
                   oligo(dT) primer
                   [GCGGCTGAAGACGGCCTATGTGGCCTTTTTTTTTTTTTTTT];
                   double-stranded cDNA was ligated to a DraIII adaptor
                   [GGCCUACUGG], digested and directionally cloned into
                   distinct DraIII sites of the pME18S-FL3. Library was size
                   selected for 1.0 kb, with a average insert size of ~1.2kb.
                   Library constructed by Yutaka Suzuki (University of Tokyo
                   Institute of Medical Science). Custom primers recommended
                   for sequencing: 5' end primer 5'-GGATGTTGCCTTTACTTCTA-3'
                   and 3' end primer 5'-CGACCTGCAGCTCGAGCACA-3'. Note: This
                   is a Zebrafish Gene Collection (ZGC) library"
IGIN

ignment Scores:
ed. No.:              451             Length:         648
ore:                  9.00            Matches:        9
cent Similarity:      100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            2.7%            Indels:         0
:                     10              Gaps:           0

-10-821-670A-30 (1-329) x DT874689 (1-648)

       225 ThrSerSerPhePheIleArgAspIle 233
           |||||||||||||||||||||||||||
        29 ACGTCCTCTTTCTTCATTCGCGACATC 3

SULT 72
374083/c
CUS         CW374083                649 bp    DNA     linear   GSS 01-NOV-2004
FINITION    fsbb001f050m06k0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f050m06, genomic survey
            sequence.
CESSION     CW374083
RSION       CW374083.1  GI:55092527
YWORDS      GSS.
URCE        Sorghum bicolor (sorghum)
ORGANISM    Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
FERENCE     1  (bases 1 to 649)
AUTHORS     Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
ITLE        Sorghum genome sequencing by methylation filtration
JOURNAL     PLoS Biol. 3 (1), e13 (2005)
  PUBMED    15660154
MMENT       Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f050  row: m  column: 06
            Seq primer: k Reverse
            Class: methylation filtered
            High quality sequence stop: 649.
ATURES              Location/Qualifiers
   source           1. .649
                    /organism="Sorghum bicolor"
                    /mol_type="genomic DNA"
                    /cultivar="ATx623"
                    /db_xref="taxon:4558"
                    /clone="fsbb001f050m06"
                    /clone_lib="Sorghum methylation filtered library (LibID:
                    104)"
                    /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                    prepared from purified nuclei was randomly sheared,
                    end-repaired, size fractionated to enrich for the 0.5 to 5
                    kb fraction, ligated into HincII-digested pBCSK(-) vector
                    and electroporated into E. coli cells. This is a
                    methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              452             Length:         649
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     13              Gaps:           0

US-10-821-670A-30 (1-329) x CW374083 (1-649)

Qy          121 LysGluSerLysAsnLysIlePheLeu 129
                ||||||||||||||||||||||||||
Db          323 AAAGAATCAAAGAACAAGATCTTCTTA 297

RESULT 73
BG696339
LOCUS       BG696339                650 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602658709F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4801803 5',
            mRNA sequence.
ACCESSION   BG696339
VERSION     BG696339.1  GI:13961382
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 650)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10695  row: a  column: 04
            High quality sequence stop: 650.
FEATURES            Location/Qualifiers
     source         1. .650
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:4801803"
                    /lab_host="DH10B (T1 phage-resistant)"
                    /clone_lib="NCI_CGAP_Skn3"
                    /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                    Average insert size 1.5kb.  Library constructed by Life
                    Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

Alignment Scores:
Pred. No.:              453             Length:         650
```

```
:re:                    9.00            Matches:        9
:cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              2.7%            Indels:         0
                        2               Gaps:           0

10-821-670A-30 (1-329) x BG696339 (1-650)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           ||||||||||||||||||||||||||||
       372 TTTTTACTGATTCACAAAAAGGAAGAC 398

:ULT 74
)44592
:US       CL344592                  657 bp    DNA     linear   GSS 19-AUG-2004
:INITION  RPCI44_278D6.r RPCI-44 Sus scrofa genomic clone RPCI44_278D6,
          genomic survey sequence.
:ESSION   CL344592
:SION     CL344592.1  GI:51396560
:WORDS    GSS.
:RCE      Sus scrofa (pig)
:RGANISM  Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
          Sus.
:ERENCE   1  (bases 1 to 657)
:UTHORS   Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
          Beever,J.E. and Schook,L.B.
:ITLE     Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
          Through Comparative Genomics
)URNAL    Unpublished (2004)
'MENT     Other_GSSs: RPCI44_278D6.f
          Contact: Lawrence B. Schook
          Department of Animal Sciences
          University of Illinois at Urbana Champaign
          1201 W. Gregory Dr., Urbana, IL 61801, USA
          Tel: 217 265 5326
          Fax: 217 244 5617
          Email: schook@uiuc.edu
          Clones are derived from the porcine BAC library RPCI-44
          (http://www.bacpac.chori.org/porcine242.htm). For BAC library
          availability, please contact Pieter de Jong (pdejong@chori.org).
          Clones may be purchased from BACPAC Resources
          (http://BACPACorders.chori.org). This work was undertaken as part
          of the International Swine Genome Sequencing Consortium by
          University of Illinois at Urbana Champaign, USA with funds provided
          by grant No. AG2002-34480-11828 from USDA-CSREES and
          AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
          Initiative)
          Plate: 278  row: D  column: 6
          Seq primer: SP6
          Class: BAC ends.
\TURES              Location/Qualifiers
   source           1. .657
                    /organism="Sus scrofa"
                    /mol_type="genomic DNA"
                    /strain="four pigs (breed: 37.5% Yorks Landrace and 25%
                    Meishan)"
                    /db_xref="taxon:9823"
                    /clone="RPCI44_278D6"
                    /sex="male"
                    /cell_type="blood"
                    /clone_lib="RPCI-44"
                    /note="Vector: pTARBAC2; Site_1: EcoRI; Site_2: EcoRI;
                    porcine male BAC library produced by Pieter de Jong"
:GIN

.gnment Scores:
:d. No.:                457             Length:         657
:re:                    9.00            Matches:        9
:cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              2.7%            Indels:         0
DB:                     13              Gaps:           0

US-10-821-670A-30 (1-329) x CL344592 (1-657)

Qy        274 PheGlyValGlnValGlnGlyLysAsn 282
              |||||||||||||||||||||||||||
Db         27 TTTGGTGTTCAGGTTCAGGGCAAGAAC 53

RESULT 75
BU773963/c
LOCUS       BU773963                  661 bp    mRNA    linear   EST 23-OCT-2003
DEFINITION  SJEGBC03 SJE Schistosoma japonicum cDNA similar to
            gi|639869|dbj|BAA07127.1| (D37885) choline kinase R2 [Rattus
            norvegicus], mRNA sequence.
ACCESSION   BU773963
VERSION     BU773963.1  GI:28341279
KEYWORDS    EST.
SOURCE      Schistosoma japonicum
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 661)
  AUTHORS   Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
            Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
            Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
            McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
  TITLE     Evolutionary and biomedical implications of a Schistosoma japonicum
            complementary DNA resource
  JOURNAL   Nat. Genet. 35 (2), 139-147 (2003)
   PUBMED   12973349
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn.
FEATURES             Location/Qualifiers
     source          1. .661
                     /organism="Schistosoma japonicum"
                     /mol_type="mRNA"
                     /db_xref="taxon:6182"
                     /tissue_type="Whole egg"
                     /dev_stage="egg"
                     /lab_host="rabbits"
                     /clone_lib="SJE"
ORIGIN

Alignment Scores:
Pred. No.:              459             Length:         661
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x BU773963 (1-661)

Qy        223 AsnTyrThrSerSerPhePheIleArg 231
              |||||||||||||||||||||||||||
Db        306 AACTACACTTCTAGTTTCTTCATAAGA 280

RESULT 76
AW956339
LOCUS       AW956339                  677 bp    mRNA    linear   EST 01-JUN-2000
DEFINITION  EST368409 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW956339
VERSION     AW956339.1  GI:8146022
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

```
          Hominidae; Homo.
?ERENCE   1  (bases 1 to 677)
AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
          Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
          Quackenbush,J.
?ITLE     Assessment of gene expression patterns in a model of colon tumor
          metastasis using a 19,200 element cDNA microarray
JOURNAL   Unpublished (2000)
MMENT     Contact: John Quackenbush
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 3528
          Fax: 301 838 0208
          Email: johnq@tigr.org
          Plate: 90
          Seq primer: Reverse.
ATURES              Location/Qualifiers
   source           1. .677
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone_lib="MAGE resequences, MAGD"
                    /note="Vector: pBluescriptSKm"
IGIN

gnment Scores:
d. No.:              469            Length:        677
ore:                 9.00           Matches:       9
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ery Match:           2.7%           Indels:        0
:                    7              Gaps:          0

-10-821-670A-30 (1-329) x AW956339 (1-677)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       330 TTTTTACTGATTCACAAAAAGGAAGAC 356

SULT 77
724059
CUS       DR724059                  683 bp    mRNA    linear   EST 15-JUL-2005
?INITION  AGENCOURT_55148409 NICHD_XGC_Emb9 Xenopus laevis cDNA clone
          IMAGE:7973954 3', mRNA sequence.
CESSION   DR724059
RSION     DR724059.1  GI:70898171
?WORDS    EST.
URCE      Xenopus laevis (African clawed frog)
ORGANISM  Xenopus laevis
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
          Xenopodinae; Xenopus; Xenopus.
?ERENCE   1  (bases 1 to 683)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
?ITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
MMENT     Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Igor Dawid
           cDNA Library Preparation: Express Genomics
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM17094  row: i  column: 24
          High quality sequence start: 170
          High quality sequence stop: 404.
ATURES              Location/Qualifiers
   source           1. .683
                    /organism="Xenopus laevis"
                    /mol_type="mRNA"
                    /db_xref="taxon:8355"
                    /clone="IMAGE:7973954"
                    /tissue_type="Embryonic stage 17/19"
                    /lab_host="DH10B TonA"
                    /clone_lib="NICHD_XGC_Emb9"
                    /note="Organ: embryo; Vector: pExpress-1; Site_1: EcoRV;
                    Site_2: NotI; cDNA was primed using oligo-dT primer:
                    5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                    the EcoRV/NotI sites of pExpress-1. Size-selection 1.4kb
                    resulted in an average insert size of 2.1kb. This is a
                    non-normalized primary library (normalized library is
                    NICHD_XGC_Emb10) and was constructed by Express Genomics
                    (Frederick, MD). Note: this is a Xenopus Gene Collection
                    (http://xgc.nci.nih.gov/) library."
ORIGIN

Alignment Scores:
Pred. No.:              473            Length:        683
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            2.7%           Indels:        0
DB:                     10             Gaps:          0

US-10-821-670A-30 (1-329) x DR724059 (1-683)

Qy          96 ValLeuSerHisSerPheLeuLeuIle 104
               |||||||||||||||||||||||||||
Db         457 GTTTTAAGTCACTCTTTTCTTCTTATT 483

RESULT 78
CA413781
LOCUS       CA413781                  688 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-EZ0-bat-p-08-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens cDNA clone
            UI-H-EZ0-bat-p-08-0-UI 3', mRNA sequence.
ACCESSION   CA413781
VERSION     CA413781.1  GI:24776432
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthoapedics
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 313-608, >ALU
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .688
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-H-EZ0-bat-p-08-0-UI"
                      /tissue_type="Chondrosarcoma Grade II"
                      /dev_stage="Adult"
                      /lab_host="DH10B (Life Technologies)"
                      /clone_lib="NCI_CGAP_Ch1"
```

```
                /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                NCI_CGAP_Ch1 is a cDNA library containing the following
                tissue(s): Chondrosarcoma Grade II. The library was
                constructed according to Bonaldo, Lennon and Soares,
                Genome Research, 6:791-806, 1996. First strand cDNA
                synthesis was primed with an oligo-dT primer containing a
                Not I site. Double stranded cDNA was ligated to an EcoR I
                adaptor, digested with Not I, and cloned directionally
                into pT7T3-Pac vector. The oligonucleotide used to prime
                the synthesis of first-strand cDNA contains a library tag
                sequence that is located between the Not I site and the
                (dT)18 tail. The sequence tag for this library is
                TGATCACGCT.
                TAG_TISSUE=grade-2-chondrosarcoma
                TAG_LIB=UI-H-EZ0
                TAG_SEQ=ATCTAATATG"
GIN

gnment Scores:
d. No.:              476           Length:        688
re:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            2.7%          Indels:        0
                     4             Gaps:          0

10-821-670A-30 (1-329) x CA413781 (1-688)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       201 TTTTTACTGATTCACAAAAAGGAAGAC 227

ULT 79
170377
US       CW470377                692 bp    DNA     linear   GSS 02-NOV-2004
INITION  fsbb001f223i17k0 Sorghum methylation filtered library (LibID: 104)
         Sorghum bicolor genomic clone fsbb001f223i17, genomic survey
         sequence.
ESSION   CW470377
SION     CW470377.1  GI:55218338
WORDS    GSS.
RCE      Sorghum bicolor (sorghum)
RGANISM  Sorghum bicolor
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
         clade; Panicoideae; Andropogoneae; Sorghum.
ERENCE   1  (bases 1 to 692)
UTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
         Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
         McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
         Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
         Martienssen,R.A.
ITLE     Sorghum genome sequencing by methylation filtration
OURNAL   PLoS Biol. 3 (1), e13 (2005)
 PUBMED  15660154
MENT     Contact: Bedell JA
         Orion Genomics, LLC
         4041 Forest Park Ave, St. Louis, MO 63108, USA
         Tel: 314 615 6979
         Fax: 314 615 5975
         Email: jbedell@oriongenomics.com
         Plate: fsbb001f223  row: i  column: 17
         Seq primer: k Reverse
         Class: methylation filtered
         High quality sequence stop: 692.
TURES              Location/Qualifiers
   source          1. .692
                   /organism="Sorghum bicolor"
                   /mol_type="genomic DNA"
                   /cultivar="ATx623"
                   /db_xref="taxon:4558"
                   /clone="fsbb001f223i17"
                   /clone_lib="Sorghum methylation filtered library (LibID:
                   104)"
                   /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                   prepared from purified nuclei was randomly sheared,
                   end-repaired, size fractionated to enrich for the 0.5 to 5
                   kb fraction, ligated into HincII-digested pBCSK(-) vector
                   and electroporated into E. coli cells. This is a
                   methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              478           Length:        692
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     13            Gaps:          0

US-10-821-670A-30 (1-329) x CW470377 (1-692)

Qy        121 LysGluSerLysAsnLysIlePheLeu 129
              |||||||||||||||||||||||||||
Db         37 AAAGAATCAAAGAACAAGATCTTCTTA 63

RESULT 80
BE387304
LOCUS       BE387304                697 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  601275594F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616655 5',
            mRNA sequence.
ACCESSION   BE387304
VERSION     BE387304.1  GI:9332669
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM282  row: k  column: 24
            High quality sequence start: 82
            High quality sequence stop: 534.
FEATURES              Location/Qualifiers
     source           1. .697
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3616655"
                      /tissue_type="melanotic melanoma"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_20"
                      /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Alignment Scores:
Pred. No.:              482           Length:        697
```

```
ore:                    9.00          Matches:        9
cent Similarity:        100.0%        Conservative:   0
t Local Similarity:     100.0%        Mismatches:     0
ery Match:              2.7%          Indels:         0
:                       7             Gaps:           0

-10-821-670A-30 (1-329) x BE387304 (1-697)

        101 PheLeuLeuIleHisLysLysGluAsp 109
            |||||||||||||||||||||||||||
        117 TTTTTACTGATTCACAAAAAGGAAGAC 143

SULT 81
009739/c
CUS         BQ009739                700 bp    mRNA    linear   EST 26-MAR-2002
FINITION    UI-H-ED0-aya-h-21-0-UI.s1 NCI_CGAP_ED0 Homo sapiens cDNA clone
            IMAGE:5836100 3', mRNA sequence.
CESSION     BQ009739
RSION       BQ009739.1  GI:19734640
YWORDS      EST.
URCE        Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
FERENCE     1  (bases 1 to 700)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
MMENT       Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             The following repetitive elements were found in this cDNA
            sequence: 11-306, >ALU (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
ATURES                  Location/Qualifiers
   source               1. .700
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:5836100"
                        /tissue_type="Chondrosarcoma"
                        /dev_stage="Adult"
                        /lab_host="DH10B (Life Technologies)"
                        /clone_lib="NCI_CGAP_ED0"
                        /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                        (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                        Site_2: Not I; NCI_CGAP_ED0 is a cDNA library containing
                        the following tissue(s): Chondrosarcoma cell line CS5. The
                        library was constructed according to Bonaldo, Lennon and
                        Soares, Genome Research, 6:791-806, 1996. First strand
                        cDNA synthesis was primed with an oligo-dT primer
                        containing a Not I site. Double stranded cDNA was ligated
                        to an EcoR I adaptor, digested with Not I, and cloned
                        directionally into pT7T3-Pac vector. The oligonucleotide
                        used to prime the synthesis of first-strand cDNA contains
                        a library tag sequence that is located between the Not I
                        site and the (dT)18 tail. The sequence tag for this
                        library is GCTCAAGGCT.
                        TAG_TISSUE=chondrosarcoma
                        TAG_LIB=UI-H-ED0
                        TAG_SEQ=CGTCAAGGCT"
GIN

gnment Scores:
d. No.:                 483           Length:         700
```

```
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-30 (1-329) x BQ009739 (1-700)

Qy          101 PheLeuLeuIleHisLysLysGluAsp 109
                |||||||||||||||||||||||||||
Db          418 TTTTTACTGATTCACAAAAAGGAAGAC 392

RESULT 82
CN279085/c
LOCUS       CN279085                707 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000424715748 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN279085
VERSION     CN279085.1  GI:47295499
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 707)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 707   Std Error: 0.00.
FEATURES              Location/Qualifiers
     source           1. .707
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="embryonic stem cells, cell lines H1, H7, and
                      H9"
                      /clone_lib="GRN_ES"
                      /note="oligo dT primed, full-length enriched cDNA library
                      from undifferentiated hES cell lines H1 (p32), H7 (p29),
                      and H9 (p26) maintained in feeder-free conditions"
ORIGIN

Alignment Scores:
Pred. No.:              488           Length:         707
Score:                  9.00          Matches:        9
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.7%          Indels:         0
DB:                     8             Gaps:           0

US-10-821-670A-30 (1-329) x CN279085 (1-707)

Qy          101 PheLeuLeuIleHisLysLysGluAsp 109
                |||||||||||||||||||||||||||
Db          235 TTTTTACTGATTCACAAAAAGGAAGAC 209

RESULT 83
CN412356
LOCUS       CN412356                722 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000532543092 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN412356
VERSION     CN412356.1  GI:47399950
```

```
WORDS    EST.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 722)
UTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
         Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
         Lebkowski,J and Stanton,L.W.
ITLE     Transcriptome characterization elucidates signaling networks that
         control human ES cell growth and differentiation
OURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
 PUBMED  15146197
MENT     Contact: Brandenberger R
         Regenerative Medicine
         Geron Corporation
         230 Constitution Drive, Menlo Park, CA 94025, USA
         Tel: 650 473 8658
         Fax: 650 473 7760
         Email: rbrandenberger@geron.com
         Insert Length: 722   Std Error: 0.00.
TURES             Location/Qualifiers
   source         1. .722
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /tissue_type="embryonic stem cells, cell lines H1, H7, and
                  H9"
                  /clone_lib="GRN_ES"
                  /note="oligo dT primed, full-length enriched cDNA library
                  from undifferentiated hES cell lines H1 (p32), H7 (p29),
                  and H9 (p26) maintained in feeder-free conditions"
IGIN

gnment Scores:
d. No.:              497          Length:        722
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            2.7%         Indels:        0
                     8            Gaps:          0

10-821-670A-30 (1-329) x CN412356 (1-722)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           |||||||||||||||||||||||||||
       395 TTTTTACTGATTCACAAAAAGGAAGAC 421

ULT 84
194937/c
US       DN494937                 746 bp    mRNA    linear   EST 10-MAR-2005
INITION  N006A02.5pR Populus bark cDNA library Populus tremula x Populus
         tremuloides cDNA clone N006A02 5', mRNA sequence.
ESSION   DN494937
SION     DN494937.1  GI:60705127
WORDS    EST.
RCE      Populus tremula x Populus tremuloides
RGANISM  Populus tremula x Populus tremuloides
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
         rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
ERENCE   1  (bases 1 to 746)
UTHORS   Sterky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,
         Brunner,A.M., Charbonnel-Campaa,L., Lindvall,J.J., Tandre,K.,
         Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P.,
         Nilsson,O., Sandberg,G., Karlsson,J., Lundeberg,J. and Jansson,S.
ITLE     A Populus EST resource for plant functional genomics
OURNAL   Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
 PUBMED  15353603
MENT     Other_ESTs: N006A02
         Contact: Bo Segerman
         Umea Plant Science Center, Department of Plant Physiology
         Umea University
         901 87 Umea, Sweden
         Tel: +46 90 786 5279
         Fax: +46 90 786 6676
         Email: bo.segerman@plantphys.umu.se.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Populus tremula x Populus tremuloides"
                     /mol_type="mRNA"
                     /db_xref="taxon:47664"
                     /clone="N006A02"
                     /tissue_type="bark"
                     /clone_lib="Populus bark cDNA library"
ORIGIN

Alignment Scores:
Pred. No.:                512          Length:        746
Score:                    9.00         Matches:       9
Percent Similarity:       100.0%       Conservative:  0
Best Local Similarity:    100.0%       Mismatches:    0
Query Match:              2.7%         Indels:        0
DB:                       9            Gaps:          0

US-10-821-670A-30 (1-329) x DN494937 (1-746)

Qy          11 PheSerLeuValLeuLeuAlaProPro 19
               |||||||||||||||||||||||||||
Db         152 TTCTCTCTTGTCCTGCTCGCTCCCCCT 126

RESULT 85
BU633670/c
LOCUS       BU633670                 757 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FL1-bgv-k-06-0-UI.s1 NCI_CGAP_FL1 Homo sapiens cDNA clone
            UI-H-FL1-bgv-k-06-0-UI 3', mRNA sequence.
ACCESSION   BU633670
VERSION     BU633670.1  GI:23300919
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 21-151, >MER20#DNA/MER1_type 302-597, >ALU (matched
            compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FL1-bgv-k-06-0-UI"
                     /tissue_type="Cell lines"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FL1"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_FL1 is a normalized cDNA library
```

derived from a pool of mRNA obtained from 4 cell lines from grade III chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGGTCGGTG. The cell lines were provided by Dr. James Martin from the University of Iowa.
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_LIB=UI-H-FL1
TAG_SEQ=GAGGTCGGTG"

:GIN

:ignment Scores:

ed. No.:	518	Length:	757
ore:	9.00	Matches:	9
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.7%	Indels:	0
	3	Gaps:	0

-10-821-670A-30 (1-329) x BU633670 (1-757)

```
Qy        101 PheLeuLeuIleHisLysLysGluAsp 109
              |||||||||||||||||||||||||||
Db        709 TTTTTACTGATTCACAAAAAGGAAGAC 683
```

SULT 86
446084/c

CUS	BP446084	763 bp	mRNA	linear	EST	30-DEC-2003

FINITION BP446084 full-length enriched swine cDNA library, adult liver Sus scrofa cDNA clone LVR010002F10 5', mRNA sequence.
CESSION BP446084
RSION BP446084.1 GI:40436151
YWORDS EST.
URCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
FERENCE 1 (bases 1 to 763)
AUTHORS Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasima,N. and Awata,T.
TITLE PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED 14681463
MMENT Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA library
Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

ATURES	Location/Qualifiers
source	1. .763
	/organism="Sus scrofa"
	/mol_type="mRNA"
	/db_xref="taxon:9823"
	/clone="LVR010002F10"
	/tissue_type="liver"
	/dev_stage="adult"
	/clone_lib="full-length enriched swine cDNA library, adult liver"

ORIGIN

Alignment Scores:

Pred. No.:	522	Length:	763
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x BP446084 (1-763)

```
Qy         64 GlnSerSerGluValLeuGlySerGly 72
              |||||||||||||||||||||||||||
Db        646 CAATCCTCAGAGGTACTTGGGAGCGGA 620
```

RESULT 87
BU375548

LOCUS	BU375548	780 bp	mRNA	linear	EST	28-NOV-2002

DEFINITION 603807808F1 CSEQCHN74 Gallus gallus cDNA clone ChEST789p2 5', mRNA sequence.
ACCESSION BU375548
VERSION BU375548.1 GI:25883549
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 780)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES	Location/Qualifiers
source	1. .780
	/organism="Gallus gallus"
	/mol_type="mRNA"
	/strain="Compton Line 15I"
	/db_xref="taxon:9031"
	/clone="ChEST789p2"
	/sex="Female"
	/dev_stage="adult"
	/lab_host="DH10B"
	/clone_lib="CSEQCHN74"
	/note="Organ: kidney + adrenal; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

```
gnment Scores:
d. No.:              532           Length:        780
re:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            2.7%          Indels:        0
                     3             Gaps:          0

10-821-670A-30 (1-329) x BU375548 (1-780)

       201 ProAlaAlaGluGluSerLeuProIle 209
           |||||||||||||||||||||||||||
       682 CCTGCCGCGGAAGAGAGCTTGCCTATC 708

ULT 88
56171/c
US       BZ056171                796 bp    DNA     linear   GSS 09-OCT-2002
INITION  llb95f10.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
         sequence.
ESSION   BZ056171
SION     BZ056171.1  GI:23661434
WORDS    GSS.
RCE      Brassica oleracea
RGANISM  Brassica oleracea
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
         rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
ERENCE   1  (bases 1 to 796)
UTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
         Nash,W., Rabinowicz,P.D. and Wilson,R.K.
ITLE     Whole genome shotgun reads from Brassica oleracea
OURNAL   Unpublished (2002)
MENT     Contact: Richard K. Wilson
         Genome Sequencing Center
         Washington University School of Medicine
         Email: submissions@watson.wustl.edu
         Plate: llb95  row: f  column: 10
         Seq primer: -21UPpOT forward
         Class: shotgun
         High quality sequence start: 23
         High quality sequence stop: 551.
TURES             Location/Qualifiers
   source         1. .796
                  /organism="Brassica oleracea"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:3712"
                  /clone_lib="B.oleracea002"
                  /note="Vector: pOTw13; Whole genome shotgun library from
                  flowering buds. DNA was purified  from a crude nuclear
                  prep using Brassica oleracea TO1000DH3 buds  provided by
                  Thosmas Osborn at the University of Wisconsin. Genomic
                  DNA was provided by Pablo Rabinowicz (CSHL) and the
                  shotgun library  prepared at Washington University Genome
                  Sequencing Center."
GIN

gnment Scores:
d. No.:              542           Length:        796
re:                  9.00          Matches:       9
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            2.7%          Indels:        0
                     11            Gaps:          0

10-821-670A-30 (1-329) x BZ056171 (1-796)

        73 LysThrLeuThrIleGlnValLysGlu 81
           |||||||||||||||||||||||||||
       651 AAAACATTAACAATCCAAGTGAAAGAA 625

ULT 89
20584
```

```
LOCUS       BZ020584                798 bp    DNA     linear   GSS 08-OCT-2002
DEFINITION  oeg90c01.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BZ020584
VERSION     BZ020584.1  GI:23580317
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: oeg90  row: c  column: 01
            Seq primer: -21UPpOT forward
            Class: shotgun
            High quality sequence start: 120
            High quality sequence stop: 335.
FEATURES             Location/Qualifiers
     source          1. .798
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="B.oleracea002"
                     /note="Vector: pOTw13; Whole genome shotgun library from
                     flowering buds. DNA was purified  from a crude nuclear
                     prep using Brassica oleracea TO1000DH3 buds  provided by
                     Thosmas Osborn at the University of Wisconsin. Genomic
                     DNA was provided by Pablo Rabinowicz (CSHL) and the
                     shotgun library  prepared at Washington University Genome
                     Sequencing Center."
ORIGIN

Alignment Scores:
Pred. No.:              543           Length:        798
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     11            Gaps:          0

US-10-821-670A-30 (1-329) x BZ020584 (1-798)

Qy        217 HisLysLeuLysTyrGluAsnTyrThr 225
              |||||||||||||||||||||||||||
Db        687 CATAAGTTAAAATATGAAAATTATACT 713

RESULT 90
CT202661/c
LOCUS       CT202661                798 bp    DNA     linear   GSS 02-NOV-2005
DEFINITION  Sus scrofa genomic clone CH242-149M11, genomic survey sequence.
ACCESSION   CT202661
VERSION     CT202661.1  GI:79718123
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 149M11. 149M11
```

is part of the CHORI-242 BAC Library created by P. de Jong. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.

ATURES Location/Qualifiers
source 1. .798
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="CH242-149M11"
/tissue_type="White blood cells"
/note="vector pTARBAC1.3_BamHI
sex female"

IGIN

ignment Scores:
ed. No.: 543 Length: 798
ore: 9.00 Matches: 9
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 2.7% Indels: 0
: 14 Gaps: 0

-10-821-670A-30 (1-329) x CT202661 (1-798)

100 SerPheLeuLeuIleHisLysLysGlu 108
||||||||||||||||||||||||||||
728 TCTTTTTTACTCATCCATAAAAAAGAA 702

SULT 91
518405/c
CUS DN518405 802 bp mRNA linear EST 10-MAR-2005
FINITION 1259097 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
CESSION DN518405
RSION DN518405.1 GI:60728595
YWORDS EST.
URCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
FERENCE 1 (bases 1 to 802)
AUTHORS Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
MMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: RLK8037 row: F column: 24
Seq primer: TAGAAGGCACAGTCGAGG.
ATURES Location/Qualifiers
source 1. .802
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 7BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI; Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."

IGIN

ignment Scores:
ed. No.: 546 Length: 802
ore: 9.00 Matches: 9
rcent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 9 Gaps: 0

US-10-821-670A-30 (1-329) x DN518405 (1-802)

Qy 69 LeuGlySerGlyLysThrLeuThrIle 77
|||||||||||||||||||||||||||||
Db 312 TTGGGATCAGGGAAAACATTAACCATT 286

RESULT 92
BG332928/c
LOCUS BG332928 819 bp mRNA linear EST 27-FEB-2001
DEFINITION 602430781F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4548381 5', mRNA sequence.
ACCESSION BG332928
VERSION BG332928.1 GI:13139366
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1238 row: a column: 22
High quality sequence stop: 151.
FEATURES Location/Qualifiers
source 1. .819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4548381"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.: 556 Length: 819
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-30 (1-329) x BG332928 (1-819)

Qy 10 TrpPheSerLeuValLeuLeuAlaPro 18
|||||||||||||||||||||||||||
Db 653 TGGTTTTCTTTAGTTCTTCTTGCTCCT 627

RESULT 93
DN521145

```
:US       DN521145                819 bp    mRNA    linear   EST 11-MAR-2005
:INITION  1263973 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
:ESSION   DN521145
:SION     DN521145.1  GI:60961723
:WORDS    EST.
:RCE      Bos taurus (cattle)
:RGANISM  Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bos.
:ERENCE   1  (bases 1 to 819)
:UTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
          Wray,J.E. and Keele,J.W.
:ITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
:OURNAL   Unpublished (2003)
:MENT     Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called with phred v0.020425.c and
          trimmed with the aid of the trim_alt option. Vector identified with
          cross_match v0.990329.
          Plate: RLK8037  row: F  column: 24
          Seq primer: GTAATACGACTCACTATAGGG.
:TURES               Location/Qualifiers
   source            1. .819
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 7BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including ovary, hindbrain, uterus, and day-30 whole
                     embryos."
:GIN

.gnment Scores:
:d. No.:              556           Length:        819
:re:                  9.00          Matches:       9
:cent Similarity:     100.0%        Conservative:  0
:t Local Similarity:  100.0%        Mismatches:    0
:ry Match:            2.7%          Indels:        0
:                     9             Gaps:          0

-10-821-670A-30 (1-329) x DN521145 (1-819)

        69 LeuGlySerGlyLysThrLeuThrIle 77
           |||||||||||||||||||||||||||
       512 TTGGGATCAGGGAAAACATTAACCATT 538

:ULT 94
:16281/c
:US       BF616281                829 bp    mRNA    linear   EST 22-OCT-2001
:INITION  HVSMEc0006B06f Hordeum vulgare seedling shoot EST library
          HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare subsp.
          vulgare cDNA clone HVSMEc0006B06f, mRNA sequence.
:ESSION   BF616281
:SION     BF616281.2  GI:16312057
:WORDS    EST.
:RCE      Hordeum vulgare subsp. vulgare
:RGANISM  Hordeum vulgare subsp. vulgare
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Pooideae; Triticeae; Hordeum.
:ERENCE   1  (bases 1 to 829)
:UTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
          Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
          Fenton,R.D., Oates,R. and Main,D.
:ITLE     Development of a genetically and physically anchored EST resource
          for barley genomics: Morex unstressed seedling shoot cDNA library
  JOURNAL Unpublished (2001)
COMMENT   On Dec 18, 2000 this sequence version replaced gi:11880015.
          Contact: Wing RA
          Clemson University Genomics Institute
          Clemson University
          100 Jordan Hall, Clemson, SC 29634, USA
          Tel: 864 656 7288
          Fax: 864 656 4293
          Email: rwing@clemson.edu
          Total hq bases = 100
          Seq primer: AATTAACCCTCACTAAAGGG
          High quality sequence start: 10
          High quality sequence stop: 640.
FEATURES             Location/Qualifiers
     source          1. .829
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="Morex"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="HVSMEc0006B06f"
                     /tissue_type="Seedling shoot"
                     /lab_host="TJC121"
                     /clone_lib="Hordeum vulgare seedling shoot EST library
                     HVcDNA0003 (Etiolated and unstressed)"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedling shoots were
                     then harvested, total RNA was prepared, poly(A) RNA was
                     purified, one primary unamplified cDNA library was made,
                     and 1 million pfu were in vivo excised to give pBluescript
                     SK(-) cDNA phagemids. These steps were performed in the TJ
                     Close laboratory at the University of California,
                     Riverside (Choi, Close, Fenton). Phagemids were plated and
                     picked at the Clemson University Genomics Institute (CUGI)
                     (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
                     Oates, Rambo, Main). The sequence has been trimmed to
                     remove vector sequence and contains a minimum of 100 bases
                     of phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
ORIGIN

Alignment Scores:
Pred. No.:              562           Length:        829
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.7%          Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-30 (1-329) x BF616281 (1-829)

Qy          11 PheSerLeuValLeuLeuAlaProPro 19
               |||||||||||||||||||||||||||
Db         466 TTTTCTCTTGTCCTCCTGGCCCCCCCC 440

RESULT 95
BG582789/c
LOCUS       BG582789                841 bp    mRNA    linear   EST 11-APR-2001
DEFINITION  EST484535 GVN Medicago truncatula cDNA clone pGVN-70P19 5' end,
            mRNA sequence.
ACCESSION   BG582789
```

```
:RSION     BG582789.1  GI:13597853
:YWORDS    EST.
:URCE      Medicago truncatula (barrel medic)
 ORGANISM  Medicago truncatula
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
           Medicago.
:FERENCE   1  (bases 1 to 841)
 AUTHORS   Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S.,
           Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
 TITLE     ESTs from one month old nitrogen-fixing root nodules of Medicago
           truncatula, 2001
 JOURNAL   Unpublished (2001)
:MMENT     Contact: Carroll P. Vance
           Department of Agronomy and Plant Genetics
           University of Minnesota
           411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
           Tel: 612 625 5715
           Fax: 651-649-5058
           Email: vance004@maroon.tc.umn.edu
           University of Minnesota name: M383861e TIGR sequence name:
           MTCDY94TK More information is available at: http://www.medicago.org
           Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
:ATURES              Location/Qualifiers
    source           1. .841
                     /organism="Medicago truncatula"
                     /mol_type="mRNA"
                     /cultivar="genotype A17"
                     /db_xref="taxon:3880"
                     /clone="pGVN-70P19"
                     /tissue_type="N2-fixing root nodules"
                     /dev_stage="effective root nodules harvested one month
                     post inoculation with Sinorhizobium meliloti"
                     /lab_host="E. coli strain XLOLR"
                     /clone_lib="GVN"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; cDNA was prepared from polyA+ enriched RNA from
                     effective root nodules harvested one month post
                     inoculation with Sinorhizobium meliloti. The cDNA was
                     directionally ligated into the Uni-ZAP XR vector from
                     Stratagene and packaged using Gigapack III Gold packaging
                     extracts. Plasmids containing cDNA inserts were excised
                     from the recombinant lambda-ZAP phage using Ex-Assist
                     helper phage and propagated in XLOLR cells."
:IGIN

.ignment Scores:
:ed. No.:              569          Length:        841
:ore:                  9.00         Matches:       9
:rcent Similarity:     100.0%       Conservative:  0
:st Local Similarity:  100.0%       Mismatches:    0
:ery Match:            2.7%         Indels:        0
:                      2            Gaps:          0

:-10-821-670A-30 (1-329) x BG582789 (1-841)

        281 LysAsnAsnArgGluLysLysAspArg 289
            |||||||||||||||||||||||||||
        136 AAAAACAATAGAGAAAAAAAAGATAGA 110

:SULT 96
'551254/c
:CUS       CR551254                 864 bp    mRNA    linear   EST 24-MAR-2005
:FINITION  CR551254 Normalized and Subtracted bovine embryonic and
           extraembryonic tissues (bcaz/BE03) Bos taurus cDNA clone
           bcaz0001.m.23 5', mRNA sequence.
.CESSION   CR551254
:RSION     CR551254.2  GI:61760533
:YWORDS    EST.
:URCE      Bos taurus (cattle)
 ORGANISM  Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
           Pecora; Bovidae; Bovinae; Bos.
REFERENCE  1  (bases 1 to 864)
  AUTHORS  Renard,J.P., Lewin,H.A., Yang,J., Hernandez,A., Degrelle,S.,
           Everts,R.E. and Hue,I.
  TITLE    Embryonic ESTs (bcaz)
  JOURNAL  Unpublished (2004)
COMMENT    On Jul 12, 2004 this sequence version replaced gi:50246164.
           Contact: Renard JP
           Biologie du Developpement et Reproduction
           INRA
           Domaine de Vilvert 78350 Jouy en Josas, FRANCE
           Email: jean-paul.renard@jouy.inra.fr
           Sequence cleaned of vector, adaptator and repetitions. Contact us
           at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
           sequence. AGENAE Resource centre. Francois PIUMI,
           Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
           genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
           FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
           Plate: bcaz0001a  row: m  column: 23.
FEATURES             Location/Qualifiers
     source          1. .864
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="bcaz0001.m.23"
                     /tissue_type="embryo (day 36 and day 64), extra-embryonic
                     tissue (day 14 to 25)"
                     /lab_host="DH10B"
                     /clone_lib="Normalized and Subtracted bovine embryonic and
                     extraembryonic tissues (bcaz/BE03)"
                     /note="Vector: pGEMZf11; Funding for EST sequencing was
                     provided by funds dedicated to J.P.RENARD (BDR, Inra).
                     Funding for construction and subtraction of the cDNA
                     library was provided by USDA ARS contract No 58-1275-2-020
                     to H. A. Lewin The cDNA library was constructed,
                     normalized and subtracted by Dr. A. Hernandez (W.M. Keck
                     Center, University of Illinois Urbana-Champaign) and S.
                     Degrelle (BDR, Inra) as described in Bonaldo et al.(1996),
                     Genome Research 6, 791-806. BE03 library is a normalized
                     library of embryonic tissues subtracted with 7800 known
                     EST sequences. The double-stranded cDNA was size selected
                     (>450 bp), adaptored with EcoRI adaptors at both ends and
                     digested with NotI. The cDNA was then directionally cloned
                     into EcoRI-NotI digested pGEM11Zf(+) phagemid vector.
                     Insert size was between 450-2200 bp. Tagged oligo-dT was
                     used to identify the origin of the ESTs where possible.
                     (A18)TGCGT = extraembryonic tissue; (A18)TCGGT = 36-day
                     oldfetus; (A18)TGCGA = 64-day old fetus (organs);
                     (A18)TCGGA = 64-day old fetus (body)"
ORIGIN

Alignment Scores:
Pred. No.:              583          Length:        864
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.7%         Indels:        0
DB:                     8            Gaps:          0

US-10-821-670A-30 (1-329) x CR551254 (1-864)

Qy          99 HisSerPheLeuLeuIleHisLysLys 107
               |||||||||||||||||||||||||||
Db         791 CATTCATTTCTTTTAATTCACAAAAAG 765

RESULT 97
AQ895672/c
LOCUS       AQ895672                 876 bp    DNA     linear   GSS 10-NOV-1999
DEFINITION  HS_4861_B1_B07_T7A CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=4861 Col=13 Row=D, genomic survey
            sequence.
ACCESSION   AQ895672
```

```
SION     AQ895672.1  GI:6351862
WORDS    GSS.
RCE      Homo sapiens (human)
RGANISM  Homo sapiens
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
         Hominidae; Homo.
ERENCE   1  (bases 1 to 876)
UTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
         Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
         Hood,L.
ITLE     Sequence-tagged connectors: A sequence approach to mapping and
         scanning the human genome
OURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED  10449764
MENT     Contact: Mahairas GG, Wallace JC, Hood L
         High Throughput Sequencing Center
         University of Washington
         401 Queen Anne Avenue North, Seattle, WA 98109, USA
         Tel: (206) 616-3618
         Fax: (206) 616-3887
         Email: jwallace@u.washington.edu
         Clones may be purchased from Research Genetics (info@resgen.com).
         BAC end Web Server: http://www.htsc.washington.edu
         Plate: 4861  row: D  column: 13
         Seq primer: T7
         Class: BAC ends
         High quality sequence stop: 876.
TURES             Location/Qualifiers
   source         1. .876
                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
                  /clone="Plate=4861 Col=13 Row=D"
                  /sex="male"
                  /clone_lib="CIT Approved Human Genomic Sperm Library D"
                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                  E-Coli DH10B"
GIN

gnment Scores:
d. No.:              590          Length:        876
re:                  9.00         Matches:       9
cent Similarity:     100.0%       Conservative:  0
t Local Similarity:  100.0%       Mismatches:    0
ry Match:            2.7%         Indels:        0
                     11           Gaps:          0

10-821-670A-30 (1-329) x AQ895672 (1-876)

        14 ValLeuLeuAlaProProLeuMetAla 22
           ||||||||||||||||||||||||||||
       642 GTCCTCCTGGCTCCCCCACTCATGGCC 616

ULT 98
.15638/c
US       CX115638                 893 bp    mRNA    linear   EST 03-JUN-2005
INITION  EI100A06 A normalized whole-life-cycle cDNA library of rice Oryza
         sativa (indica cultivar-group) cDNA clone EI100A06 5', mRNA
         sequence.
ESSION   CX115638
SION     CX115638.1  GI:66928790
WORDS    EST.
RCE      Oryza sativa (indica cultivar-group)
RGANISM  Oryza sativa (indica cultivar-group)
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
         clade; Ehrhartoideae; Oryzeae; Oryza.
ERENCE   1  (bases 1 to 893)
UTHORS   Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan,D.,
         Han,B., Zhang,Q. and Wang,S.
ITLE     Features of the expressed sequences revealed by a large-scale
         analysis of ESTs from a normalized cDNA library of the elite indica
         rice cultivar Minghui 63
  JOURNAL  Plant J. 42 (5), 772-780 (2005)
   PUBMED  15918889
COMMENT    Contact: Wang S
           National Key Laboratory of Crop Genetic Improvement
           Hauzhong Agricultural University
           Wuhan 430070, China
           Tel: 86-27-87282044
           Fax: 86-27-87287092
           Email: shipingwang@hotmail.com
           Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .893
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="mRNA"
                     /strain="indica"
                     /cultivar="Minghui 63"
                     /db_xref="taxon:39946"
                     /clone="EI100A06"
                     /tissue_type="whole plant"
                     /dev_stage="whole-life-cycle"
                     /lab_host="E. coli DH10B"
                     /clone_lib="A normalized whole-life-cycle cDNA library of
                     rice"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; The
                     library is constructed based on the strategy of satuation
                     hybridization with genomic DNA using rice cultivar Minghui
                     63. This library consists of cDNA from 15 directionally
                     cloned cDNA libraries constructed with different tissues
                     from 9 developmental stages."
ORIGIN

Alignment Scores:
Pred. No.:              600          Length:        893
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.7%         Indels:        0
DB:                     8            Gaps:          0

US-10-821-670A-30 (1-329) x CX115638 (1-893)

Qy         12 SerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||
Db        680 AGCTTGGTCCTTTAGCCCCCCCCCTC 654

RESULT 99
BI258748
LOCUS       BI258748                 894 bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  602970329F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109966 5',
            mRNA sequence.
ACCESSION   BI258748
VERSION     BI258748.1  GI:14815408
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11266  row: i  column: 07
```

High quality sequence stop: 851.

FEATURES Location/Qualifiers
source 1. .894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5109966"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."

IGIN

ignment Scores:

ed. No.:	601	Length:	894
core:	9.00	Matches:	9
ercent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.7%	Indels:	0
:	2	Gaps:	0

-10-821-670A-30 (1-329) x BI258748 (1-894)

Qy 101 PheLeuLeuIleHisLysLysGluAsp 109
||||||||||||||||||||||||||
Db 699 TTTTTACTGATTCACAAAAAGGAAGAC 725

SULT 100
088766
CUS BI088766 895 bp mRNA linear EST 20-JUN-2001
FINITION 602851556F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4993380 5', mRNA sequence.
CCESSION BI088766
RSION BI088766.1 GI:14507096
YWORDS EST.
URCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
FERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
MMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11013 row: o column: 13
High quality sequence stop: 623.

EATURES Location/Qualifiers
source 1. .895
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4993380"
/cell_line="MGC36"
/lab_host="DH10B"
/clone_lib="NIH_MGC_10"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."

IGIN

Alignment Scores:

Pred. No.:	602	Length:	895
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x BI088766 (1-895)

Qy 279 GlnGlyLysAsnAsnArgGluLysLys 287
||||||||||||||||||||||||||
Db 837 CAGGGGAAAAACAATAGAGAGAAGAAA 863

Search completed: June 10, 2006, 16:34:23
Job time : 4575.64 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 01:43:45 ; Search time 187.551 Seconds
(without alignments)
4923.420 Million cell updates/sec

tle: US-10-821-670A-30
rfect score: 329
quence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 1403666 seqs, 935554401 residues

rd size: 1

tal number of hits satisfying chosen parameters: 2800955

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlp
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110458_27682/app_query.fasta_1
B=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rni
INMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
RANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
LIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
AXLEN=2000000000 -HOST=abss05p
SER=US10821670_@CGN_1_1_677_@runat_07062006_110458_27682 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	329	100.0	987	3	US-09-917-265A-29	Sequence 29, Appl
2	329	100.0	987	3	US-09-917-265A-31	Sequence 31, Appl
3	328	99.7	985	3	US-09-917-265A-55	Sequence 55, Appl
4	328	99.7	985	3	US-09-917-265A-57	Sequence 57, Appl
5	317	96.4	2193	3	US-09-011-143-5	Sequence 5, Appli
6	317	96.4	2193	3	US-09-302-495-5	Sequence 5, Appli
7	317	96.4	2193	3	US-10-079-616-5	Sequence 5, Appli
8	307	93.3	921	3	US-09-011-143-6	Sequence 6, Appli
9	307	93.3	921	3	US-09-011-143-7	Sequence 7, Appli
10	307	93.3	921	3	US-09-302-495-6	Sequence 6, Appli
11	307	93.3	921	3	US-09-302-495-7	Sequence 7, Appli
12	307	93.3	921	3	US-10-079-616-6	Sequence 6, Appli
13	307	93.3	921	3	US-10-079-616-7	Sequence 7, Appli
14	217	66.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c 15	217	66.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
16	206	62.6	921	3	US-09-917-265A-26	Sequence 26, Appl
c 17	206	62.6	921	3	US-09-917-265A-28	Sequence 28, Appl
18	206	62.6	1533	3	US-09-917-265A-43	Sequence 43, Appl
c 19	206	62.6	1533	3	US-09-917-265A-45	Sequence 45, Appl
20	37	11.2	921	3	US-09-917-265A-52	Sequence 52, Appl
c 21	37	11.2	921	3	US-09-917-265A-54	Sequence 54, Appl
22	37	11.2	987	3	US-09-917-265A-58	Sequence 58, Appl
c 23	37	11.2	987	3	US-09-917-265A-60	Sequence 60, Appl
24	37	11.2	990	3	US-09-079-984A-1	Sequence 1, Appli
25	37	11.2	990	3	US-09-079-984A-11	Sequence 11, Appl
26	37	11.2	990	3	US-09-390-729-1	Sequence 1, Appli
27	37	11.2	990	3	US-09-390-729-11	Sequence 11, Appl
28	37	11.2	1533	3	US-09-917-265A-66	Sequence 66, Appl
c 29	37	11.2	1533	3	US-09-917-265A-68	Sequence 68, Appl
30	37	11.2	1599	3	US-09-917-265A-61	Sequence 61, Appl
c 31	37	11.2	1599	3	US-09-917-265A-63	Sequence 63, Appl
32	37	11.2	2267	3	US-09-917-265A-107	Sequence 107, App
c 33	37	11.2	2267	3	US-09-917-265A-109	Sequence 109, App
34	35	10.6	987	2	US-08-186-529-1	Sequence 1, Appli
35	35	10.6	987	2	US-08-640-386A-1	Sequence 1, Appli
36	35	10.6	1018	2	US-08-184-009-194	Sequence 194, App
37	35	10.6	1018	2	US-08-458-356-194	Sequence 194, App
38	35	10.6	1018	3	US-08-460-736-194	Sequence 194, App
39	35	10.6	1018	3	US-09-535-370-194	Sequence 194, App
40	35	10.6	1018	3	US-09-663-667-194	Sequence 194, App
41	35	10.6	1389	3	US-09-634-368-4	Sequence 4, Appli
42	35	10.6	1399	2	US-08-751-767A-3	Sequence 3, Appli
43	35	10.6	1560	2	US-08-751-767A-11	Sequence 11, Appl
44	35	10.6	1623	2	US-08-751-767A-9	Sequence 9, Appli
45	35	10.6	2307	3	US-09-949-016-5452	Sequence 5452, Ap
46	35	10.6	2362	2	US-08-265-087-1	Sequence 1, Appli
47	35	10.6	2362	2	US-08-621-493-1	Sequence 1, Appli
48	35	10.6	2362	2	US-08-965-688-1	Sequence 1, Appli
49	35	10.6	2362	3	US-09-260-173-1	Sequence 1, Appli
50	35	10.6	2362	3	US-09-924-703-3	Sequence 3, Appli
51	35	10.6	6139	2	US-08-751-767A-7	Sequence 7, Appli
52	23	7.0	987	3	US-08-848-760B-24	Sequence 24, Appl
53	23	7.0	987	3	US-09-826-025-24	Sequence 24, Appl
54	23	7.0	1870	3	US-09-310-842-4	Sequence 4, Appli
55	23	7.0	2318	3	US-09-851-062-3	Sequence 3, Appli
56	23	7.0	2318	3	US-09-949-016-315	Sequence 315, App
57	22	6.7	16002	3	US-09-949-016-12057	Sequence 12057, A
58	22	6.7	16003	3	US-09-949-016-17194	Sequence 17194, A
59	17	5.2	73	3	US-09-823-549-77	Sequence 77, Appl
c 60	17	5.2	601	3	US-09-949-016-24253	Sequence 24253, A
c 61	17	5.2	601	3	US-09-949-016-190686	Sequence 190686,
62	17	5.2	1061	2	US-08-385-335A-13	Sequence 13, Appl
63	17	5.2	1409	3	US-09-634-368-3	Sequence 3, Appli
64	17	5.2	1472	3	US-09-634-368-2	Sequence 2, Appli
65	17	5.2	1569	3	US-09-634-368-12	Sequence 12, Appl
66	17	5.2	2013	3	US-09-634-368-11	Sequence 11, Appl
67	17	5.2	2709	3	US-09-634-368-13	Sequence 13, Appl
68	17	5.2	6295	2	US-08-659-206A-4	Sequence 4, Appli
69	17	5.2	7287	2	US-08-659-206A-1	Sequence 1, Appli
70	12	3.6	38	3	US-09-011-143-12	Sequence 12, Appl
71	12	3.6	38	3	US-09-302-495-12	Sequence 12, Appl
72	12	3.6	38	3	US-10-079-616-12	Sequence 12, Appl
c 73	12	3.6	601	3	US-09-949-016-24250	Sequence 24250, A
c 74	12	3.6	601	3	US-09-949-016-24251	Sequence 24251, A
c 75	12	3.6	601	3	US-09-949-016-190683	Sequence 190683,
c 76	12	3.6	601	3	US-09-949-016-190684	Sequence 190684,
77	9	2.7	28	3	US-09-917-265A-85	Sequence 85, Appl
78	9	2.7	37	3	US-09-917-265A-87	Sequence 87, Appl
79	9	2.7	532	3	US-09-513-999C-4018	Sequence 4018, Ap
80	8	2.4	25	3	US-09-887-145-37	Sequence 37, Appl

81	8	2.4	25	3	US-09-917-265A-86	Sequence 86, Appl
82	8	2.4	32	3	US-09-011-143-13	Sequence 13, Appl
83	8	2.4	32	3	US-09-302-495-13	Sequence 13, Appl
84	8	2.4	32	3	US-10-079-616-13	Sequence 13, Appl
85	8	2.4	37	3	US-09-917-265A-99	Sequence 99, Appl
86	8	2.4	39	3	US-09-079-984A-13	Sequence 13, Appl
87	8	2.4	39	3	US-09-390-729-13	Sequence 13, Appl
88	8	2.4	44	3	US-09-011-143-14	Sequence 14, Appl
89	8	2.4	44	3	US-09-302-495-14	Sequence 14, Appl
90	8	2.4	44	3	US-10-079-616-14	Sequence 14, Appl
91	8	2.4	427	3	US-09-270-767-2298	Sequence 2298, Ap
92	8	2.4	427	3	US-09-270-767-17580	Sequence 17580, A
93	8	2.4	540	3	US-09-445-724B-13	Sequence 13, Appl
94	8	2.4	549	3	US-09-533-559-4743	Sequence 4743, Ap
95	8	2.4	601	3	US-09-949-016-70299	Sequence 70299, A
96	8	2.4	601	3	US-09-949-016-87513	Sequence 87513, A
97	8	2.4	601	3	US-09-949-016-110703	Sequence 110703,
98	8	2.4	601	3	US-09-949-016-110704	Sequence 110704,
99	8	2.4	601	3	US-09-949-016-110705	Sequence 110705,
100	8	2.4	601	3	US-09-949-016-138629	Sequence 138629,
101	8	2.4	601	3	US-09-949-016-168993	Sequence 168993,
102	8	2.4	601	3	US-09-949-016-168994	Sequence 168994,
103	8	2.4	601	3	US-09-949-016-168995	Sequence 168995,
104	8	2.4	601	3	US-09-949-016-202770	Sequence 202770,
105	8	2.4	633	5	US-09-974-300-5194	Sequence 5194, Ap
106	8	2.4	830	3	US-09-621-976-1463	Sequence 1463, Ap
107	8	2.4	885	3	US-09-328-352-1423	Sequence 1423, Ap
108	8	2.4	2961	3	US-09-949-016-2226	Sequence 2226, Ap
109	8	2.4	3342	2	US-08-254-989-1	Sequence 1, Appli
110	8	2.4	5874	3	US-08-843-417-9	Sequence 9, Appli
111	8	2.4	5874	3	US-09-527-013-9	Sequence 9, Appli
112	8	2.4	6758	3	US-09-902-540-1033	Sequence 1033, Ap
113	8	2.4	7173	3	US-09-949-016-17491	Sequence 17491, A
114	8	2.4	14185	3	US-09-949-016-14809	Sequence 14809, A
115	8	2.4	17085	3	US-09-949-016-16507	Sequence 16507, A
116	8	2.4	28976	3	US-09-949-002-689	Sequence 689, App
117	8	2.4	28976	3	US-09-949-002-698	Sequence 698, App
118	8	2.4	41815	3	US-09-949-016-17447	Sequence 17447, A
119	8	2.4	68444	3	US-09-949-016-13968	Sequence 13968, A
120	8	2.4	72843	3	US-09-949-016-12574	Sequence 12574, A
121	8	2.4	81927	3	US-09-949-016-15623	Sequence 15623, A
122	8	2.4	87350	3	US-08-781-891-79	Sequence 79, Appl
123	8	2.4	87350	3	US-09-618-166-79	Sequence 79, Appl
124	8	2.4	87543	3	US-09-791-211-3	Sequence 3, Appli
125	8	2.4	104428	3	US-09-949-016-12737	Sequence 12737, A
126	8	2.4	104429	3	US-09-949-016-13814	Sequence 13814, A
127	8	2.4	145320	3	US-09-949-016-15858	Sequence 15858, A
128	8	2.4	168575	3	US-09-426-290-1	Sequence 1, Appli
129	8	2.4	194889	3	US-09-949-016-15654	Sequence 15654, A
130	8	2.4	393753	3	US-09-949-016-14573	Sequence 14573, A
131	8	2.4	393753	3	US-09-949-016-14574	Sequence 14574, A
132	8	2.4	670689	3	US-09-949-016-12505	Sequence 12505, A
133	8	2.4	670690	3	US-09-949-016-14207	Sequence 14207, A
134	8	2.4	784019	3	US-09-949-016-14033	Sequence 14033, A
135	8	2.4	818128	3	US-09-949-016-14546	Sequence 14546, A
136	8	2.4	818128	3	US-09-949-016-14547	Sequence 14547, A
137	8	2.4	818128	3	US-09-949-016-14548	Sequence 14548, A
138	8	2.4	818128	3	US-09-949-016-14549	Sequence 14549, A
139	8	2.4	818128	3	US-09-949-016-14550	Sequence 14550, A
140	8	2.4	818128	3	US-09-949-016-14551	Sequence 14551, A
141	8	2.4	818128	3	US-09-949-016-14552	Sequence 14552, A
142	8	2.4	818128	3	US-09-949-016-14553	Sequence 14553, A
143	8	2.4	818128	3	US-09-949-016-14554	Sequence 14554, A
144	8	2.4	818128	3	US-09-949-016-14555	Sequence 14555, A
145	8	2.4	818128	3	US-09-949-016-14556	Sequence 14556, A
146	8	2.4	818128	3	US-09-949-016-14557	Sequence 14557, A
147	8	2.4	818128	3	US-09-949-016-14558	Sequence 14558, A
148	8	2.4	818128	3	US-09-949-016-14559	Sequence 14559, A
149	8	2.4	818128	3	US-09-949-016-14560	Sequence 14560, A
150	8	2.4	818128	3	US-09-949-016-14561	Sequence 14561, A
151	8	2.4	818128	3	US-09-949-016-14562	Sequence 14562, A
152	8	2.4	818128	3	US-09-949-016-14564	Sequence 14564, A
153	8	2.4	818128	3	US-09-949-016-14565	Sequence 14565, A
c 154	8	2.4	818128	3	US-09-949-016-14566	Sequence 14566, A
c 155	8	2.4	818128	3	US-09-949-016-14567	Sequence 14567, A
c 156	8	2.4	828152	3	US-09-949-016-12777	Sequence 12777, A
157	8	2.4	1830121	3	US-09-557-884-1	Sequence 1, Appli
158	8	2.4	1830121	3	US-09-643-990A-1	Sequence 1, Appli
159	8	2.4	1830121	3	US-10-158-865-1	Sequence 1, Appli
160	7	2.1	24	3	US-09-823-549-48	Sequence 48, Appl
c 161	7	2.1	25	3	US-09-917-265A-88	Sequence 88, Appl
162	7	2.1	25	3	US-09-396-196G-42419	Sequence 42419, A
163	7	2.1	25	3	US-09-396-196G-42420	Sequence 42420, A
c 164	7	2.1	37	4	US-09-701-271A-7	Sequence 7, Appli
c 165	7	2.1	39	3	US-09-079-984A-14	Sequence 14, Appl
c 166	7	2.1	39	3	US-09-390-729-14	Sequence 14, Appl
167	7	2.1	44	2	US-08-823-516-115	Sequence 115, App
168	7	2.1	44	3	US-08-759-038-123	Sequence 123, App
169	7	2.1	44	3	US-08-758-314-123	Sequence 123, App
170	7	2.1	44	3	US-09-684-938-123	Sequence 123, App
171	7	2.1	44	3	US-09-308-825A-123	Sequence 123, App
172	7	2.1	44	3	US-09-940-244-115	Sequence 115, App
173	7	2.1	44	3	US-09-381-212-115	Sequence 115, App
174	7	2.1	44	3	US-09-713-601A-115	Sequence 115, App
175	7	2.1	45	3	US-09-777-430C-60	Sequence 60, Appl
176	7	2.1	50	2	US-08-823-516-118	Sequence 118, App
177	7	2.1	50	3	US-08-759-038-126	Sequence 126, App
178	7	2.1	50	3	US-08-758-314-126	Sequence 126, App
179	7	2.1	50	3	US-09-940-244-118	Sequence 118, App
180	7	2.1	50	3	US-09-381-212-118	Sequence 118, App
181	7	2.1	50	3	US-09-713-601A-118	Sequence 118, App
182	7	2.1	51	3	US-09-684-938-126	Sequence 126, App
183	7	2.1	51	3	US-09-308-825A-126	Sequence 126, App
184	7	2.1	178	3	US-09-513-999C-35523	Sequence 35523, A
185	7	2.1	186	3	US-09-489-039A-260	Sequence 260, App
186	7	2.1	241	3	US-09-270-767-8558	Sequence 8558, Ap
187	7	2.1	241	3	US-09-270-767-23840	Sequence 23840, A
c 188	7	2.1	259	3	US-09-513-999C-29666	Sequence 29666, A
189	7	2.1	287	3	US-09-313-294A-2940	Sequence 2940, Ap
c 190	7	2.1	295	3	US-09-082-092-2	Sequence 2, Appli
c 191	7	2.1	295	3	US-09-885-722A-2	Sequence 2, Appli
192	7	2.1	300	4	US-09-297-648-247	Sequence 247, App
193	7	2.1	326	3	US-08-916-576B-16	Sequence 16, Appl
194	7	2.1	326	3	US-10-078-337-16	Sequence 16, Appl
c 195	7	2.1	327	3	US-09-513-999C-320	Sequence 320, App
c 196	7	2.1	331	3	US-09-513-999C-33699	Sequence 33699, A
c 197	7	2.1	338	3	US-09-513-999C-30716	Sequence 30716, A
c 198	7	2.1	378	3	US-09-513-999C-21946	Sequence 21946, A
c 199	7	2.1	383	3	US-09-621-976-15609	Sequence 15609, A
200	7	2.1	405	3	US-09-270-767-8945	Sequence 8945, Ap

ALIGNMENTS

```
RESULT 1
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
```

```
  LOCATION: (1)..(987)
-09-917-265A-29

ignment Scores:
ed. No.:                0              Length:         987
ore:                    329.00         Matches:        329
rcent Similarity:       100.0%         Conservative:   0
st Local Similarity:    100.0%         Mismatches:     0
ery Match:              100.0%         Indels:         0
:                       3              Gaps:           0

-10-821-670A-30 (1-329) x US-09-917-265A-29 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 2
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

Alignment Scores:
Pred. No.:              0              Length:         987
Score:                  329.00         Matches:        329
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-31 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
```

```
          ||||||
```

```
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
SEQ ID NO 57
   LENGTH: 985
   TYPE: DNA
   ORGANISM: Felis catus
S-09-917-265A-57

lignment Scores:
:ed. No.:              0              Length:         985
:ore:                  328.00         Matches:        328
ercent Similarity:     100.0%         Conservative:   0
st Local Similarity:   100.0%         Mismatches:     0
.ery Match:            99.7%          Indels:         0
3:                     3              Gaps:           0

S-10-821-670A-30 (1-329) x US-09-917-265A-57 (1-985)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy      321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||
Db       25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 5
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

Alignment Scores:
Pred. No.:             0              Length:         2193
Score:                 317.00         Matches:        317
Percent Similarity:    100.0%         Conservative:   0
```

```
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            96.4%           Indels:         0
:                     3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-011-143-5 (1-2193)

          13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

          33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

          53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

          73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

          93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

         113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

         133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

         153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

         173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

         193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

         213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

         233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

         253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

         273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

         293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

         313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
             |||||||||||||||||||||||||||||||||||||||||||||||||||
        1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050

SULT 6
-09-302-495-5
Sequence 5, Application US/09302495
```

```
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

Alignment Scores:
Pred. No.:              0               Length:         2193
Score:                  317.00          Matches:        317
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            96.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-302-495-5 (1-2193)

Qy          13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

Qy          33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy          53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy          73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
        280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

         93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

        113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

        133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

        153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

        173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

        193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

        233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

        273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

        293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

        313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050
```

```
ESULT 7
-10-079-616-5
 Sequence 5, Application US/10079616
 Patent No. 6566097
   GENERAL INFORMATION:
        APPLICANT: IMAMURA, Takayuki
                   MAEDA, Hiroaki
                   FUJIYASU, Takeshi
                   IMAGAWA, Yoshitaka
                   TOKIYOSHI, Sachio
        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
        NUMBER OF SEQUENCES: 26
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: BROWDY AND NEIMARK
             STREET: 419 Seventh Street, N.W., Suite 300
             CITY: Washington
             STATE: D.C.
             COUNTRY: USA
             ZIP: 20004
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2193 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.:                0              Length:          2193
Score:                    317.00         Matches:         317
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              96.4%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-30 (1-329) x US-10-079-616-5 (1-2193)

Qy          13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

Qy          33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

Qy          53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

Qy          73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

Qy          93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

Qy         113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

Qy         133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

Qy         153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

Qy         173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

       193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

       213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

       233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

       253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

       273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

       293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

       313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
           |||||||||||||||||||||||||||||||||||||||||||||||||||
      1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050

SULT 8
-09-011-143-6
Sequence 6, Application US/09011143
Patent No. 6472509
 GENERAL INFORMATION:
   APPLICANT:  IMAMURA, Takayuki
   APPLICANT:  MAEDA, Hiroaki
   APPLICANT:  FUJIYASU, Takeshi
   APPLICANT:  IMAGAWA, Yoshitaka
   APPLICANT:  TOKIYOSHI, Sachio
   TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
   NUMBER OF SEQUENCES:  26
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  BROWDY AND NEIMARK
     STREET:  419 Seventh Street, N.W., Suite 300
     CITY:  Washington
     STATE:  D.C.
     COUNTRY:  USA
     ZIP:  20004
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/011,143
     FILING DATE:  04-FEB-1998
     CLASSIFICATION:  536
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  PCT/JP97/01824
     FILING DATE:  29-MAY-1997
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  JP 165249/1996
     FILING DATE:  04-JUN-1996
   ATTORNEY/AGENT INFORMATION:
     NAME:  BROWDY, Roger L.
     REGISTRATION NUMBER:  25,618
     REFERENCE/DOCKET NUMBER:  IMAMURA=1
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  202-628-5197
     TELEFAX:  202-737-3528
 INFORMATION FOR SEQ ID NO:  6:
   SEQUENCE CHARACTERISTICS:

;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6

Alignment Scores:
Pred. No.:                0              Length:          921
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              93.3%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-30 (1-329) x US-09-011-143-6 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
```

```
Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

SULT 9
-09-011-143-7
Sequence 7, Application US/09011143
Patent No. 6472509
 GENERAL INFORMATION:
   APPLICANT:  IMAMURA, Takayuki
   APPLICANT:  MAEDA, Hiroaki
   APPLICANT:  FUJIYASU, Takeshi
   APPLICANT:  IMAGAWA, Yoshitaka
   APPLICANT:  TOKIYOSHI, Sachio
   TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
   NUMBER OF SEQUENCES:  26
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  BROWDY AND NEIMARK
     STREET:  419 Seventh Street, N.W., Suite 300
     CITY:  Washington
     STATE:  D.C.
     COUNTRY:  USA
     ZIP:  20004
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/011,143
     FILING DATE:  04-FEB-1998
     CLASSIFICATION:  536
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  PCT/JP97/01824
     FILING DATE:  29-MAY-1997
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  JP 165249/1996
     FILING DATE:  04-JUN-1996
   ATTORNEY/AGENT INFORMATION:
     NAME:  BROWDY, Roger L.
     REGISTRATION NUMBER:  25,618
     REFERENCE/DOCKET NUMBER:  IMAMURA=1
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  202-628-5197
     TELEFAX:  202-737-3528
  INFORMATION FOR SEQ ID NO:  7:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  921 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-09-011-143-7

ignment Scores:
ed. No.:              0            Length:        921
core:                 307.00       Matches:       307
rcent Similarity:     100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            93.3%        Indels:        0
:                     3            Gaps:          0

-10-821-670A-30 (1-329) x US-09-011-143-7 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 10
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
```

```
          STREET: 419 Seventh Street, N.W., Suite 300
          CITY: Washington
          STATE: D.C.
          COUNTRY: USA
          ZIP: 20004
       COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/302,495
          FILING DATE: 30-Apr-1999
          CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
          APPLICATION NUMBER: US/09/011,143
          FILING DATE: 04-FEB-1998
          APPLICATION NUMBER: PCT/JP97/01824
          FILING DATE: 29-MAY-1997
          APPLICATION NUMBER: JP 165249/1996
          FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
          NAME: BROWDY, Roger L.
          REGISTRATION NUMBER: 25,618
          REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
    INFORMATION FOR SEQ ID NO: 6:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 921 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
-09-302-495-6

ignment Scores:
ed. No.:              0              Length:        921
ore:                  307.00         Matches:       307
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            93.3%          Indels:        0
:                     3              Gaps:          0

-10-821-670A-30 (1-329) x US-09-302-495-6 (1-921)

         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy      163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy      183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy      243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy      323 TrpAlaSerValSerCysSer 329
            |||||||||||||||||||||
Db      901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 11
US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
```

```
          FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
          NAME: BROWDY, Roger L.
          REGISTRATION NUMBER: 25,618
          REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
   INFORMATION FOR SEQ ID NO: 7:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 921 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
:-09-302-495-7

.ignment Scores:
.ed. No.:              0            Length:        921
'ore:                  307.00       Matches:       307
rcent Similarity:      100.0%       Conservative:  0
.st Local Similarity:  100.0%       Mismatches:    0
.ery Match:            93.3%        Indels:        0
::                     3            Gaps:          0

:-10-821-670A-30 (1-329) x US-09-302-495-7 (1-921)

;        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

;        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

;        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

;        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

;       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

;       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

;       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

;       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)       421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

;       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

;       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

;       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

;       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy      263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy      283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy      303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy      323 TrpAlaSerValSerCysSer 329
            |||||||||||||||||||||
Db      901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 12
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

Alignment Scores:
Pred. No.:             0            Length:        921
```

```
ɔre:                    307.00          Matches:        307
rcent Similarity:       100.0%          Conservative:   0
ɜt Local Similarity:    100.0%          Mismatches:     0
ɔry Match:              93.3%           Indels:         0
:                       3               Gaps:           0

·10-821-670A-30 (1-329) x US-10-079-616-6 (1-921)

        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

       323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
       901 TGGGCATCCGTGTCCTGCAGT 921

3ULT 13
```

```
US-10-079-616-7
; Sequence 7, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

Alignment Scores:
Pred. No.:              0               Length:         921
Score:                  307.00          Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            93.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-079-616-7 (1-921)

Qy          23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy          43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy          63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
```

```
        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

       323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
       901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 14
S-09-917-265A-38
 Sequence 38, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 38
   LENGTH: 1599
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:
Pred. No.:              3e-224          Length:         1599
Score:                  217.00          Matches:        317
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            66.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-38 (1-1599)

Qy          12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy          32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy          52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy          72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy          92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy         112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy         132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy         152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy         172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy         192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy         212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy         232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy         252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy         272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy         292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933
```

```
       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
       934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987

SULT 15
-09-917-265A-40/c
Sequence 40, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Felis catus
-09-917-265A-40

gnment Scores:
d. No.:                3e-224          Length:         1599
re:                    217.00          Matches:        317
cent Similarity:       99.7%           Conservative:   0
t Local Similarity:    99.7%           Mismatches:     1
ry Match:              66.0%           Indels:         0
:                      3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-917-265A-40 (1-1599)

        12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

        32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

        52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

        72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

        92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

       112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

       132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

       152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

       172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy       192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy       212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy       232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy       252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy       272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy       292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

Qy       312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613

RESULT 16
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-26

Alignment Scores:
Pred. No.:             1.31e-212       Length:         921
Score:                 206.00          Matches:        306
Percent Similarity:    99.7%           Conservative:   0
Best Local Similarity: 99.7%           Mismatches:     1
Query Match:           62.6%           Indels:         0
DB:                    3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-26 (1-921)

Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

       323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
       901 TGGGCATCCGTGTCCTGCAGT 921

SULT 17
-09-917-265A-28/c
Sequence 28, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
  LENGTH: 921
  TYPE: DNA

;   ORGANISM: Felis catus
US-09-917-265A-28

Alignment Scores:
Pred. No.:              1.31e-212       Length:         921
Score:                  206.00          Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            62.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-28 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22
```

```
       323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
        21 TGGGCATCCGTGTCCTGCAGT 1

;ULT 18
-09-917-265A-43
;equence 43, Application US/09917265A
>atent No. 6818444
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
3EQ ID NO 43
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1533)
-09-917-265A-43

;gnment Scores:
;d. No.:              2.16e-212      Length:         1533
>re:                  206.00         Matches:        306
rcent Similarity:     99.7%          Conservative:   0
;t Local Similarity:  99.7%          Mismatches:     1
;ry Match:            62.6%          Indels:         0
:                     3              Gaps:           0

-10-821-670A-30 (1-329) x US-09-917-265A-43 (1-1533)

        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         323 TrpAlaSerValSerCysSer 329
               |||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 19
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.:              2.16e-212      Length:         1533
Score:                  206.00         Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            62.6%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-45 (1-1533)

Qy          23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy          43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy          63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354
```

```
        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

       323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
       633 TGGGCATCCGTGTCCTGCAGT 613

SULT 20
-09-917-265A-52
Sequence 52, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 52
  LENGTH: 921
  TYPE: DNA
  ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-52

Alignment Scores:
Pred. No.:                3.71e-30        Length:         921
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.2%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-52 (1-921)

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy         223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 21
US-09-917-265A-54/c
; Sequence 54, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-54

Alignment Scores:
Pred. No.:                3.71e-30        Length:         921
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.2%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-54 (1-921)

Qy         203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy         223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 22
US-09-917-265A-58
; Sequence 58, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
```

```
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
EQ ID NO 58
  LENGTH: 987
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(987)
09-917-265A-58

gnment Scores:
d. No.:              3.97e-30       Length:        987
re:                  37.00          Matches:       37
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            11.2%          Indels:        0
:                    3              Gaps:          0

10-821-670A-30 (1-329) x US-09-917-265A-58 (1-987)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 23
-09-917-265A-60/c
equence 60, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
EQ ID NO 60
  LENGTH: 987
  TYPE: DNA
  ORGANISM: Canis familiaris
09-917-265A-60

gnment Scores:
d. No.:              3.97e-30       Length:        987
re:                  37.00          Matches:       37
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            11.2%          Indels:        0
:                    3              Gaps:          0

10-821-670A-30 (1-329) x US-09-917-265A-60 (1-987)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 24
US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

Alignment Scores:
Pred. No.:              3.98e-30       Length:        990
Score:                  37.00          Matches:       37
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.2%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-30 (1-329) x US-09-079-984A-1 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 25
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
```

```
   APPLICANT:  Yamada, Katsushige
   TITLE OF INVENTION:  Canine interleukin 12, a production method
   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
   TITLE OF INVENTION:  method using it
   NUMBER OF SEQUENCES:  16
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Miller & Christenbury Intellectual Property
     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
     STREET:  1600 Market Street, 39th Floor
     CITY:  Philadelphia
     STATE:  PA
     COUNTRY:  USA
     ZIP:  19103
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy Disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  WordPerfect 5.1
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/079,984A
     FILING DATE:  15-MAY-1998
   ATTORNEY/AGENT INFORMATION:
     NAME:  Austin R. Miller
     REGISTRATION NUMBER:  16,602
     REFERENCE/DOCKET NUMBER:  1051-98
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (215) 563-1810
     TELEFAX:  (215) 568-6946
 INFORMATION FOR SEQ ID NO:  11:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  990 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA to mRNA
   ORIGINAL SOURCE:
     ORGANISM:  Canis familiaris
   FEATURE:
     NAME/KEY:  Canine IL12
     LOCATION:  1 to 987
     IDENTIFICATION METHOD:  Similarity
-09-079-984A-11

ignment Scores:
ed. No.:              3.98e-30      Length:        990
ore:                  37.00         Matches:       37
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            11.2%         Indels:        0
:                     3             Gaps:          0

-10-821-670A-30 (1-329) x US-09-079-984A-11 (1-990)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

SULT 26
-09-390-729-1
Sequence 1, Application US/09390729
Patent No. 6562334
 GENERAL INFORMATION:
   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
   APPLICANT:  Yamada, Katsushige
   TITLE OF INVENTION:  Canine interleukin 12, a production method
   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
   TITLE OF INVENTION:  method using it
   NUMBER OF SEQUENCES:  16
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Miller & Christenbury Intellectual Property
     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
     STREET:  1600 Market Street, 39th Floor
     CITY:  Philadelphia
     STATE:  PA
     COUNTRY:  USA
     ZIP:  19103
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy Disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  WordPerfect 5.1
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/390,729
     FILING DATE:
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  09/079,984
     FILING DATE:  15-MAY-1998
   ATTORNEY/AGENT INFORMATION:
     NAME:  Austin R. Miller
     REGISTRATION NUMBER:  16,602
     REFERENCE/DOCKET NUMBER:  1051-98
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (215) 563-1810
     TELEFAX:  (215) 568-6946
 INFORMATION FOR SEQ ID NO:  1:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  990 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA to mRNA
   ORIGINAL SOURCE:
     ORGANISM:  Canis familiaris
   FEATURE:
     NAME/KEY:  Canine IL12
     LOCATION:  1 to 987
     IDENTIFICATION METHOD:  Similarity
US-09-390-729-1

Alignment Scores:
Pred. No.:              3.98e-30      Length:        990
Score:                  37.00         Matches:       37
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            11.2%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-30 (1-329) x US-09-390-729-1 (1-990)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 27
US-09-390-729-11
; Sequence 11, Application US/09390729
; Patent No. 6562334
; GENERAL INFORMATION:
;   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;   APPLICANT:  Yamada, Katsushige
;   TITLE OF INVENTION:  Canine interleukin 12, a production method
;   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;   TITLE OF INVENTION:  method using it
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Miller & Christenbury Intellectual Property
;     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;     STREET:  1600 Market Street, 39th Floor
```

```
    CITY:  Philadelphia
    STATE:  PA
    COUNTRY:  USA
    ZIP:  19103
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy Disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  WordPerfect 5.1
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/09/390,729
    FILING DATE:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  09/079,984
    FILING DATE:  15-MAY-1998
  ATTORNEY/AGENT INFORMATION:
    NAME:  Austin R. Miller
    REGISTRATION NUMBER:  16,602
    REFERENCE/DOCKET NUMBER:  1051-98
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (215) 563-1810
    TELEFAX:  (215) 568-6946
INFORMATION FOR SEQ ID NO:  11:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  990 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  double
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA to mRNA
  ORIGINAL SOURCE:
    ORGANISM:  Canis familiaris
  FEATURE:
    NAME/KEY:  Canine IL12
    LOCATION:  1 to 987
    IDENTIFICATION METHOD:  Similarity
-09-390-729-11

gnment Scores:
d. No.:                3.98e-30        Length:         990
re:                    37.00           Matches:        37
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              11.2%           Indels:         0
                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-390-729-11 (1-990)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 28
-09-917-265A-66
equence 66, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE:  2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 66
 LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-66

Alignment Scores:
Pred. No.:                6.11e-30        Length:         1533
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.2%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-66 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 29
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

Alignment Scores:
Pred. No.:                6.11e-30        Length:         1533
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.2%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-68 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 30
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
```

TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 61
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
-09-917-265A-61

ignment Scores:

ed. No.:	6.37e-30	Length:	1599
ore:	37.00	Matches:	37
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	11.2%	Indels:	0
:	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-917-265A-61 (1-1599)

```
        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

SULT 31
-09-917-265A-63/c
Sequence 63, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
-09-917-265A-63

ignment Scores:

ed. No.:	6.37e-30	Length:	1599
ore:	37.00	Matches:	37
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	11.2%	Indels:	0
:	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-917-265A-63 (1-1599)

```
        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db 933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 32
US-09-917-265A-107
; Sequence 107, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)..(1140)
US-09-917-265A-107

Alignment Scores:

Pred. No.:	8.96e-30	Length:	2267
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-917-265A-107 (1-2267)

```
Qy      203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy      223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870
```

RESULT 33
US-09-917-265A-109/c
; Sequence 109, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265A-109

Alignment Scores:

Pred. No.:	8.96e-30	Length:	2267
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0

```
:                    3              Gaps:          0

-10-821-670A-30 (1-329) x US-09-917-265A-109 (1-2267)

        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            ||||||||||||||||||||||||||||||||||||||||||||||||||
       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

SULT 34
-08-186-529-1
Sequence 1, Application US/08186529
Patent No. 5573764
 GENERAL INFORMATION:
   APPLICANT:  Sykes, Megan
   APPLICANT:  Wolf, Stanley F.
   TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
   TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
     STREET:  87 CambridgePark Drive
     CITY:  Cambridge
     STATE:  MA
     COUNTRY:  USA
     ZIP:  02140
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/186,529
     FILING DATE:
     CLASSIFICATION:  424
   ATTORNEY/AGENT INFORMATION:
     NAME:  McDaniels, Patricia A.
     REGISTRATION NUMBER:  33,194
     REFERENCE/DOCKET NUMBER:  GI 5225
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  617-498-8401
     TELEFAX:  617-876-5851
 INFORMATION FOR SEQ ID NO:  1:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  987 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   ORIGINAL SOURCE:
     ORGANISM:  Homo sapiens
     CELL TYPE:  Lymphoblast
     CELL LINE:  RPMI 8866
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  1..987
-08-186-529-1

gnment Scores:
d. No.:              5.72e-28       Length:        987
re:                  35.00          Matches:       35
rcent Similarity:    100.0%         Conservative:  0
st Local Similarity: 100.0%         Mismatches:    0
ery Match:           10.6%          Indels:        0
:                    2              Gaps:          0

-10-821-670A-30 (1-329) x US-08-186-529-1 (1-987)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 35
US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1

Alignment Scores:
Pred. No.:              5.72e-28       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x US-08-640-386A-1 (1-987)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

```
SULT 36
-08-184-009-194
Sequence 194, Application US/08184009
Patent No. 5833975
 GENERAL INFORMATION:
   APPLICANT:  Paoletti, Enzo
   APPLICANT:  Tartaglia, James
   APPLICANT:  Cox, William I.
   TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
   NUMBER OF SEQUENCES:  217
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Curtis, Morris & Safford
     STREET:  530 Fifth Avenue
     CITY:  New York
     STATE:  NY
     COUNTRY:  USA
     ZIP:  10036
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/184,009
     FILING DATE:  19-JAN-1994
     CLASSIFICATION:  435
   ATTORNEY/AGENT INFORMATION:
     NAME:  Frommer, William S.
     REGISTRATION NUMBER:  25,506
     REFERENCE/DOCKET NUMBER:  454310-2530
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (212) 840-3333
     TELEFAX:  (212) 840-0712
     TELEX:  425066CURTMS
 INFORMATION FOR SEQ ID NO:  194:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1018 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-08-184-009-194

ignment Scores:
ed. No.:                5.9e-28         Length:         1018
ore:                    35.00           Matches:        35
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              10.6%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-30 (1-329) x US-08-184-009-194 (1-1018)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

SULT 37
-08-458-356-194
Sequence 194, Application US/08458356
Patent No. 5942235
 GENERAL INFORMATION:
   APPLICANT:  Paoletti, Enzo
   APPLICANT:  Tartaglia, James
   APPLICANT:  Cox, William I.
   TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
   NUMBER OF SEQUENCES:  217
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Curtis, Morris & Safford
     STREET:  530 Fifth Avenue
     CITY:  New York
     STATE:  NY
     COUNTRY:  USA
     ZIP:  10036
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/458,356
     FILING DATE:  02-JUN-1995
     CLASSIFICATION:  424
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  US 08/184,009
     FILING DATE:  19-JAN-1994
   ATTORNEY/AGENT INFORMATION:
     NAME:  Frommer, William S.
     REGISTRATION NUMBER:  25,506
     REFERENCE/DOCKET NUMBER:  454310-2530
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (212) 840-3333
     TELEFAX:  (212) 840-0712
     TELEX:  425066CURTMS
 INFORMATION FOR SEQ ID NO:  194:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1018 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
US-08-458-356-194

Alignment Scores:
Pred. No.:              5.9e-28         Length:         1018
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x US-08-458-356-194 (1-1018)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 38
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/460,736
    FILING DATE:  02-JUN-1995
    CLASSIFICATION:  514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/184,009
    FILING DATE:  19-JAN-1994
  ATTORNEY/AGENT INFORMATION:
    NAME:  Frommer, William S.
    REGISTRATION NUMBER:  25,506
    REFERENCE/DOCKET NUMBER:  454310-2530
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (212) 840-3333
    TELEFAX:  (212) 840-0712
    TELEX:  425066CURTMS
INFORMATION FOR SEQ ID NO:  194:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  1018 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
-08-460-736-194

ignment Scores:
ed. No.:              5.9e-28        Length:        1018
ore:                  35.00          Matches:       35
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            10.6%          Indels:        0
                      3              Gaps:          0

-10-821-670A-30 (1-329) x US-08-460-736-194 (1-1018)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

SULT 39
-09-535-370-194
equence 194, Application US/09535370
Patent No. 6537594
  GENERAL INFORMATION:
      APPLICANT: Paoletti, Enzo
                 Tartaglia, James
                 Cox, William I.
      TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
      NUMBER OF SEQUENCES: 217
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Curtis, Morris & Safford
           STREET: 530 Fifth Avenue
           CITY: New York
           STATE: NY
           COUNTRY: USA
           ZIP: 10036
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/535,370
           FILING DATE: 24-Mar-2000
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/460,736
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Frommer, William S.
           REGISTRATION NUMBER: 25,506
           REFERENCE/DOCKET NUMBER: 454310-2530
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (212) 840-3333
           TELEFAX: (212) 840-0712
           TELEX: 425066CURTMS
  INFORMATION FOR SEQ ID NO: 194:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 1018 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-535-370-194

Alignment Scores:
Pred. No.:              5.9e-28        Length:        1018
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            10.6%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-30 (1-329) x US-09-535-370-194 (1-1018)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 40
US-09-663-667-194
; Sequence 194, Application US/09663667
; Patent No. 6780407
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,667
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/184,009
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 194:
```

```
       SEQUENCE CHARACTERISTICS:
            LENGTH: 1018 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 194:
-09-663-667-194

ignment Scores:
ed. No.:                5.9e-28         Length:         1018
ore:                    35.00           Matches:        35
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              10.6%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-663-667-194 (1-1018)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

SULT 41
-09-634-368-4
Sequence 4, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
 APPLICANT:  Gillies, Stephen
 APPLICANT:  Lo, Kin Ming
 TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
 FILE REFERENCE:  LEX-010
 CURRENT APPLICATION NUMBER: US/09/634,368
 CURRENT FILING DATE:  2000-08-09
 PRIOR APPLICATION NUMBER:  60/147,924
 PRIOR FILING DATE:  1999-08-09
 NUMBER OF SEQ ID NOS:  32
 SOFTWARE:  PatentIn Ver. 2.0
SEQ ID NO 4
  LENGTH: 1389
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: human
  OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
-09-634-368-4

ignment Scores:
ed. No.:                8e-28           Length:         1389
ore:                    35.00           Matches:        35
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              10.6%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-634-368-4 (1-1389)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

SULT 42
-08-751-767A-3
Sequence 3, Application US/08751767A
Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..1026
US-08-751-767A-3

Alignment Scores:
Pred. No.:              8.06e-28        Length:         1399
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x US-08-751-767A-3 (1-1399)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 43
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
```

```
     STATE:  VA
     COUNTRY:  USA
     ZIP:  22201
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/751,767A
     FILING DATE:  08-NOV-1996
     CLASSIFICATION:  536
   ATTORNEY/AGENT INFORMATION:
     NAME:  SADOFF, B.J.
     REGISTRATION NUMBER:  36,663
     REFERENCE/DOCKET NUMBER:  117-221
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  7038164091
     TELEFAX:  7038164100
 INFORMATION FOR SEQ ID NO:  11:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1560 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  1..1557
-08-751-767A-11

:gnment Scores:
:d. No.:                8.96e-28        Length:         1560
)re:                    35.00           Matches:        35
rcent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
ery Match:              10.6%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-30 (1-329) x US-08-751-767A-11 (1-1560)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        583 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 642

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        643 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 687

;ULT 44
-08-751-767A-9
;equence 9, Application US/08751767A
'atent No. 5994104
 GENERAL INFORMATION:
   APPLICANT:  ANDERSON, ROBERT J.
   APPLICANT:  GRANT, HUGH
   APPLICANT:  MACDONALD, IAN D.
   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
   NUMBER OF SEQUENCES:  80
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  NIXON & VANDERHYE P.C.
     STREET:  1100 NORTH GLEBE ROAD
     CITY:  ARLINGTON
     STATE:  VA
     COUNTRY:  USA
     ZIP:  22201
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/751,767A
     FILING DATE:  08-NOV-1996
     CLASSIFICATION:  536
   ATTORNEY/AGENT INFORMATION:
     NAME:  SADOFF, B.J.
     REGISTRATION NUMBER:  36,663
     REFERENCE/DOCKET NUMBER:  117-221
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  7038164091
     TELEFAX:  7038164100
 INFORMATION FOR SEQ ID NO:  9:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1623 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  1..1620
US-08-751-767A-9

Alignment Scores:
Pred. No.:              9.32e-28        Length:         1623
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x US-08-751-767A-9 (1-1623)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 45
US-09-949-016-5452
; Sequence 5452, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5452
;   LENGTH: 2307
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5452

Alignment Scores:
Pred. No.:              1.32e-27        Length:         2307
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-949-016-5452 (1-2307)
```

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        648 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 707

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        708 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 752

:SULT 46
-08-265-087-1
Sequence 1, Application US/08265087
Patent No. 5571515
 GENERAL INFORMATION:
   APPLICANT:  Scott, Phillip
   APPLICANT:  Trinchieri, Giorgio
   TITLE OF INVENTION:  Compositions and Methods for Use of
   TITLE OF INVENTION:  IL-12 as an Adjuvant
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Howson and Howson
     STREET:  Spring House Corporate Center, PO Box 457
     CITY:  Spring House
     STATE:  Pennsylvania
     COUNTRY:  USA
     ZIP:  19477
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/265,087
     FILING DATE:
     CLASSIFICATION:  424
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  US 08/229,282
     FILING DATE:  18-APR-1994
   ATTORNEY/AGENT INFORMATION:
     NAME:  Bak, Mary E.
     REGISTRATION NUMBER:  31,215
     REFERENCE/DOCKET NUMBER:  WST51AUSA
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  215-540-9206
     TELEFAX:  215-540-5818
 INFORMATION FOR SEQ ID NO:  1:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  2362 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  unknown
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  33..1016
-08-265-087-1

ignment Scores:
ed. No.:                1.35e-27        Length:         2362
ore:                    35.00           Matches:        35
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              10.6%           Indels:         0
:                       2               Gaps:           0

-10-821-670A-30 (1-329) x US-08-265-087-1 (1-2362)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 47
US-08-621-493-1
; Sequence 1, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-621-493-1

Alignment Scores:
Pred. No.:              1.35e-27        Length:         2362
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x US-08-621-493-1 (1-2362)

Qy      217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy      237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
Db      738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 48
US-08-965-688-1
; Sequence 1, Application US/08965688
```

```
Patent No. 5976539
 GENERAL INFORMATION:
   APPLICANT:  Scott, Phillip
   APPLICANT:  Trinchieri, Giorgio
   TITLE OF INVENTION:  Compositions and Methods for Use of
   TITLE OF INVENTION:  IL-12 as an Adjuvant
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Howson and Howson
     STREET:  Spring House Corporate Center, PO Box 457
     CITY:  Spring House
     STATE:  Pennsylvania
     COUNTRY:  USA
     ZIP:  19477
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/965,688
     FILING DATE:
     CLASSIFICATION:
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  08/621,493
     FILING DATE:  25-MAR-1996
     APPLICATION NUMBER:  08/265,087
     FILING DATE:  17-JUN-1994
     APPLICATION NUMBER:  US 08/229,282
     FILING DATE:  18-APR-1994
   ATTORNEY/AGENT INFORMATION:
     NAME:  Bak, Mary E.
     REGISTRATION NUMBER:  31,215
     REFERENCE/DOCKET NUMBER:  WST51AUSA
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  215-540-9206
     TELEFAX:  215-540-5818
 INFORMATION FOR SEQ ID NO:  1:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  2362 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  unknown
   MOLECULE TYPE:  cDNA
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  33..1016
-08-965-688-1

ignment Scores:
ed. No.:              1.35e-27      Length:        2362
ore:                  35.00         Matches:       35
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            10.6%         Indels:        0
                      2             Gaps:          0

-10-821-670A-30 (1-329) x US-08-965-688-1 (1-2362)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

SULT 49
-09-260-173-1
Sequence 1, Application US/09260173
Patent No. 6168923
  GENERAL INFORMATION:
       APPLICANT: Scott, Phillip
;                 Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2362 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  33..1016
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

Alignment Scores:
Pred. No.:              1.35e-27      Length:        2362
Score:                  35.00         Matches:       35
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            10.6%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-30 (1-329) x US-09-260-173-1 (1-2362)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 50
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
```

```
 APPLICANT:  PERUSSIA, BICE
 APPLICANT:  CLARK, STEVEN C.
 APPLICANT:  WONG, GORDON G.
 APPLICANT:  HEWICK, RODNEY
 APPLICANT:  KOBAYASHI, MICHIKO
 TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
 FILE REFERENCE: 01142.0142.0100
 CURRENT APPLICATION NUMBER: US/09/924,703
 CURRENT FILING DATE:  2001-08-09
 PRIOR APPLICATION NUMBER: 09/325,958
 PRIOR FILING DATE: 1999-06-04
 PRIOR APPLICATION NUMBER: 08/858,000
 PRIOR FILING DATE: 1997-05-16
 PRIOR APPLICATION NUMBER: 08/403,013
 PRIOR FILING DATE: 1995-03-13
 PRIOR APPLICATION NUMBER: 07/584,941
 PRIOR FILING DATE: 1990-09-18
 PRIOR APPLICATION NUMBER: 07/307,817
 PRIOR FILING DATE: 1989-02-07
 PRIOR APPLICATION NUMBER: 07/269,945
 PRIOR FILING DATE: 1988-11-10
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
   LENGTH: 2362
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
   NAME/KEY: CDS
   LOCATION: (33)..(1016)
-09-924-703-3

ignment Scores:
ed. No.:                1.35e-27        Length:         2362
ore:                    35.00           Matches:        35
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              10.6%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-924-703-3 (1-2362)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

SULT 51
-08-751-767A-7
Sequence 7, Application US/08751767A
Patent No. 5994104
 GENERAL INFORMATION:
   APPLICANT:  ANDERSON, ROBERT J.
   APPLICANT:  GRANT, HUGH
   APPLICANT:  MACDONALD, IAN D.
   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
   NUMBER OF SEQUENCES:  80
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  NIXON & VANDERHYE P.C.
     STREET:  1100 NORTH GLEBE ROAD
     CITY:  ARLINGTON
     STATE:  VA
     COUNTRY:  USA
     ZIP:  22201
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

Alignment Scores:
Pred. No.:              3.43e-27        Length:         6139
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x US-08-751-767A-7 (1-6139)

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3867 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3926

Qy       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
             |||||||||||||||||||||||||||||||||||||||||||||
Db      3927 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3971

RESULT 52
US-08-848-760B-24
; Sequence 24, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
```

```
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (352) 375-8100
           TELEFAX: (352) 372-5800
  INFORMATION FOR SEQ ID NO: 24:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
           DESCRIPTION: /desc = "DNA"
      SEQUENCE DESCRIPTION: SEQ ID NO: 24:
-08-848-760B-24

:gnment Scores:
ed. No.:                5.16e-15        Length:         987
>re:                    23.00           Matches:        23
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              7.0%            Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-08-848-760B-24 (1-987)

        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        466 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 525

        176 SerAlaGlu 178
            |||||||||
        526 TCTGCAGAG 534

SULT 53
-09-826-025-24
Sequence 24, Application US/09826025
Patent No. 6730512
  GENERAL INFORMATION:
      APPLICANT: Chang, Lung-Ji
      TITLE OF INVENTION: Combination Immunogene Therapy
      NUMBER OF SEQUENCES: 25
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Medlen & Carroll, LLP
           STREET: 220 Montgomery Street, Suite 2200
           CITY: San Francisco
           STATE: California
           COUNTRY: United States of America
           ZIP: 94104
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/826,025
           FILING DATE: 04-Apr-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/838,702
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Ingolia, Diane E.
           REGISTRATION NUMBER: 40,027
           REFERENCE/DOCKET NUMBER: CHANG-02687
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (415) 705-8410
           TELEFAX: (415) 397-8338
  INFORMATION FOR SEQ ID NO: 24:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: double
           TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
;           DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

Alignment Scores:
Pred. No.:              5.16e-15        Length:         987
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-826-025-24 (1-987)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 525

Qy        176 SerAlaGlu 178
              |||||||||
Db        526 TCTGCAGAG 534

RESULT 54
US-09-310-842-4
; Sequence 4, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

Alignment Scores:
Pred. No.:              9.66e-15        Length:         1870
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-310-842-4 (1-1870)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
      1098 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1157

       176 SerAlaGlu 178
           |||||||||
      1158 TCTGCAGAG 1166

SULT 55
-09-851-062-3
Sequence 3, Application US/09851062
Patent No. 6448081
GENERAL INFORMATION:
 APPLICANT: Brenda F. Baker
 APPLICANT:  Susan M. Freier
 TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
 FILE REFERENCE: RTS-0247
 CURRENT APPLICATION NUMBER: US/09/851,062
 CURRENT FILING DATE:  2001-05-07
 NUMBER OF SEQ ID NOS: 87
SEQ ID NO 3
  LENGTH: 2318
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (14)...(1000)
-09-851-062-3

ignment Scores:
ed. No.:              1.19e-14       Length:         2318
ore:                  23.00          Matches:        23
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            7.0%           Indels:         0
:                     3              Gaps:           0

-10-821-670A-30 (1-329) x US-09-851-062-3 (1-2318)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       479 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 538

       176 SerAlaGlu 178
           |||||||||
       539 TCTGCAGAG 547

SULT 56
-09-949-016-315
Sequence 315, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 315
  LENGTH: 2318
  TYPE: DNA
  ORGANISM: Human
-09-949-016-315

ignment Scores:
ed. No.:              1.19e-14       Length:         2318
ore:                  23.00          Matches:        23
Percent Similarity:   100.0%         Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:          7.0%           Indels:         0
DB:                   3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-949-016-315 (1-2318)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 538

Qy        176 SerAlaGlu 178
              |||||||||
Db        539 TCTGCAGAG 547

RESULT 57
US-09-949-016-12057
; Sequence 12057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12057
;   LENGTH: 16002
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12057

Alignment Scores:
Pred. No.:            9.5e-13        Length:         16002
Score:                22.00          Matches:        22
Percent Similarity:   100.0%         Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:          6.7%           Indels:         0
DB:                   3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-949-016-12057 (1-16002)

Qy        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9948 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 10007

Qy        273 ThrPhe 274
              ||||||
Db      10008 ACATTC 10013

RESULT 58
US-09-949-016-17194
; Sequence 17194, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
```

```
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
;EQ ID NO 17194
  LENGTH: 16003
  TYPE: DNA
  ORGANISM: Human
·09-949-016-17194

.gnment Scores:
:d. No.:                9.5e-13        Length:         16003
)re:                    22.00          Matches:        22
:cent Similarity:       100.0%         Conservative:   0
:t Local Similarity:    100.0%         Mismatches:     0
:ry Match:              6.7%           Indels:         0
                        3              Gaps:           0

·10-821-670A-30 (1-329) x US-09-949-016-17194 (1-16003)

        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       9948 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 10007

        273 ThrPhe 274
            ||||||
      10008 ACATTC 10013

;ULT 59
·09-823-549-77
;equence 77, Application US/09823549
?atent No. 6664442
;ENERAL INFORMATION:
 APPLICANT: McConlogue, Lisa  C
 APPLICANT:  Games, Kate D.
 APPLICANT:  Yednock, Theodore A.
 APPLICANT:  Hua, Tan
 APPLICANT:  Messersmith, Elizabeth
 APPLICANT:  Bard, Frederique
 TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
 FILE REFERENCE: 015270-009110US
 CURRENT APPLICATION NUMBER: US/09/823,549
 CURRENT FILING DATE:  2001-03-30
 PRIOR APPLICATION NUMBER: US 60/193,847
 PRIOR FILING DATE: 2000-03-30
 NUMBER OF SEQ ID NOS: 85
 SOFTWARE: PatentIn version 3.1
;EQ ID NO 77
  LENGTH: 73
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: IL-12 p40, #1 marker
·09-823-549-77

.gnment Scores:
:d. No.:                1.21e-09       Length:         73
)re:                    17.00          Matches:        17
:cent Similarity:       100.0%         Conservative:   0
:t Local Similarity:    100.0%         Mismatches:     0
:ry Match:              5.2%           Indels:         0
                        3              Gaps:           0

·10-821-670A-30 (1-329) x US-09-823-549-77 (1-73)

        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            |||||||||||||||||||||||||||||||||||||||||||||||||||
          9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59

;ULT 60
·09-949-016-24253/c
;equence 24253, Application US/09949016
?atent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24253
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24253

Alignment Scores:
Pred. No.:              9.54e-09       Length:         601
Score:                  17.00          Matches:        17
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            5.2%           Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-949-016-24253 (1-601)

Qy          162 SerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGlu 178
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          264 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAG 214

RESULT 61
US-09-949-016-190686/c
; Sequence 190686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190686
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190686

Alignment Scores:
Pred. No.:              9.54e-09       Length:         601
Score:                  17.00          Matches:        17
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            5.2%           Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-949-016-190686 (1-601)

Qy          162 SerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGlu 178
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          264 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAG 214
```

```
SULT 62
-08-385-335A-13
Sequence 13, Application US/08385335A
Patent No. 5891680
 GENERAL INFORMATION:
   APPLICANT:  Lieschke, Graham J.
   APPLICANT:  Mulligan, Richard C.
   TITLE OF INVENTION:  Bioactive Fusion Proteins
   NUMBER OF SEQUENCES:  34
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
     STREET:  Two Militia Drive
     CITY:  Lexington
     STATE:  Massachusetts
     COUNTRY:  USA
     ZIP:  02173
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/385,335A
     FILING DATE:  08-FEB-1995
     CLASSIFICATION:  530
   ATTORNEY/AGENT INFORMATION:
     NAME:  Granahan, Patricia
     REGISTRATION NUMBER:  32,227
     REFERENCE/DOCKET NUMBER:  WHI95-01
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  617-861-6240
     TELEFAX:  617-861-9540
 INFORMATION FOR SEQ ID NO:  13:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  1061 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  unknown
     TOPOLOGY:  unknown
   MOLECULE TYPE:  DNA (genomic)
-08-385-335A-13

ignment Scores:
ed. No.:                1.66e-08        Length:         1061
ore:                    17.00           Matches:        17
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              5.2%            Indels:         0
:                       2               Gaps:           0

-10-821-670A-30 (1-329) x US-08-385-335A-13 (1-1061)

        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
        716 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 766

SULT 63
-09-634-368-3
Sequence 3, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
 APPLICANT:  Gillies, Stephen
 APPLICANT:  Lo, Kin Ming
 TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
 FILE REFERENCE:  LEX-010
 CURRENT APPLICATION NUMBER: US/09/634,368
 CURRENT FILING DATE:  2000-08-09
 PRIOR APPLICATION NUMBER:  60/147,924
 PRIOR FILING DATE:  1999-08-09
 NUMBER OF SEQ ID NOS:  32
 SOFTWARE:  PatentIn Ver. 2.0
SEQ ID NO 3
  LENGTH: 1409
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: murine
  OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-09-634-368-3

Alignment Scores:
Pred. No.:              2.2e-08         Length:         1409
Score:                  17.00           Matches:        17
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.2%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-634-368-3 (1-1409)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740

RESULT 64
US-09-634-368-2
; Sequence 2, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-2

Alignment Scores:
Pred. No.:              2.29e-08        Length:         1472
Score:                  17.00           Matches:        17
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.2%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-634-368-2 (1-1472)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740

RESULT 65
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
```

```
 SOFTWARE:  PatentIn Ver. 2.0
;EQ ID NO 12
  LENGTH: 1569
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: murine
  OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
-09-634-368-12

:gnment Scores:
ed. No.:              2.44e-08       Length:        1569
ore:                  17.00          Matches:       17
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            5.2%           Indels:        0
:                     3              Gaps:          0

-10-821-670A-30 (1-329) x US-09-634-368-12 (1-1569)

        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
       1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

;ULT 66
-09-634-368-11
;equence 11, Application US/09634368
?atent No. 6617135
;ENERAL INFORMATION:
 APPLICANT:  Gillies, Stephen
 APPLICANT:  Lo, Kin Ming
 TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
 FILE REFERENCE:  LEX-010
 CURRENT APPLICATION NUMBER: US/09/634,368
 CURRENT FILING DATE:  2000-08-09
 PRIOR APPLICATION NUMBER:  60/147,924
 PRIOR FILING DATE:  1999-08-09
 NUMBER OF SEQ ID NOS:  32
 SOFTWARE:  PatentIn Ver. 2.0
;EQ ID NO 11
  LENGTH: 2013
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: murine
  OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
-09-634-368-11

:gnment Scores:
ed. No.:              3.12e-08       Length:        2013
ore:                  17.00          Matches:       17
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            5.2%           Indels:        0
:                     3              Gaps:          0

-10-821-670A-30 (1-329) x US-09-634-368-11 (1-2013)

        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
       1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

;ULT 67
-09-634-368-13
;equence 13, Application US/09634368
?atent No. 6617135
;ENERAL INFORMATION:
 APPLICANT:  Gillies, Stephen
 APPLICANT:  Lo, Kin Ming
 TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
 FILE REFERENCE:  LEX-010
 CURRENT APPLICATION NUMBER: US/09/634,368
 CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

Alignment Scores:
Pred. No.:            4.17e-08       Length:        2709
Score:                17.00          Matches:       17
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          5.2%           Indels:        0
DB:                   3              Gaps:          0

US-10-821-670A-30 (1-329) x US-09-634-368-13 (1-2709)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1977

RESULT 68
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
```

```
     LOCATION:  2377..3384
     OTHER INFORMATION:  /product= "p40 gene product"
-08-659-206A-4

ignment Scores:
ed. No.:              9.52e-08       Length:        6295
ore:                  17.00          Matches:       17
rcent Similarity:     100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            5.2%           Indels:        0
:                     2              Gaps:          0

-10-821-670A-30 (1-329) x US-08-659-206A-4 (1-6295)

        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
       3046 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 3096

SULT 69
-08-659-206A-1
Sequence 1, Application US/08659206A
Patent No. 5922685
 GENERAL INFORMATION:
   APPLICANT:  Rakhmilevich, Alexander
   TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
   NUMBER OF SEQUENCES:  6
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Quarles & Brady
     STREET:  1 South Pinckney Street
     CITY:  Madison
     STATE:  WI
     COUNTRY:  US
     ZIP:  53703
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/659,206A
     FILING DATE:
     CLASSIFICATION:  435
   ATTORNEY/AGENT INFORMATION:
     NAME:  Seay, Nicholas J
     REGISTRATION NUMBER:  27386
     REFERENCE/DOCKET NUMBER:  110229.91144
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  608-251-5000
     TELEFAX:  608-251-9166
 INFORMATION FOR SEQ ID NO:  1:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  7287 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  double
     TOPOLOGY:  circular
   MOLECULE TYPE:  other nucleic acid
     DESCRIPTION:  /desc = "Plasmid DNA"
   IMMEDIATE SOURCE:
     CLONE:  pWRG3169
   FEATURE:
     NAME/KEY:  promoter
     LOCATION:  1..628
   FEATURE:
     NAME/KEY:  iDNA
     LOCATION:  629..810
   FEATURE:
     NAME/KEY:  CDS
     LOCATION:  join(953..1258, 1332..1673)
     OTHER INFORMATION:  /product= "p35 gene product"
   FEATURE:
     NAME/KEY:  polyA_site
     LOCATION:  1797..2024
   FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1

Alignment Scores:
Pred. No.:              1.1e-07        Length:        7287
Score:                  17.00          Matches:       17
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            5.2%           Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-30 (1-329) x US-08-659-206A-1 (1-7287)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3652 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 3702

RESULT 70
US-09-011-143-12
; Sequence 12, Application US/09011143
; Patent No. 6472509
; GENERAL INFORMATION:
;   APPLICANT:  IMAMURA, Takayuki
;   APPLICANT:  MAEDA, Hiroaki
;   APPLICANT:  FUJIYASU, Takeshi
;   APPLICANT:  IMAGAWA, Yoshitaka
;   APPLICANT:  TOKIYOSHI, Sachio
;   TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;   NUMBER OF SEQUENCES:  26
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BROWDY AND NEIMARK
;     STREET:  419 Seventh Street, N.W., Suite 300
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  USA
;     ZIP:  20004
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/011,143
;     FILING DATE:  04-FEB-1998
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/JP97/01824
;     FILING DATE:  29-MAY-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 165249/1996
;     FILING DATE:  04-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  BROWDY, Roger L.
;     REGISTRATION NUMBER:  25,618
;     REFERENCE/DOCKET NUMBER:  IMAMURA=1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  202-628-5197
;     TELEFAX:  202-737-3528
; INFORMATION FOR SEQ ID NO:  12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  38 base pairs
;     TYPE:  nucleic acid
```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
·09-011-143-12

:gnment Scores:
:d. No.: 0.000159 Length: 38
>re: 12.00 Matches: 12
:rcent Similarity: 100.0% Conservative: 0
:t Local Similarity: 100.0% Mismatches: 0
:ry Match: 3.6% Indels: 0
3 Gaps: 0

·10-821-670A-30 (1-329) x US-09-011-143-12 (1-38)

```
        23 IleTrpGluLeuGluLysAsnValTyrValValGlu 34
           ||||||||||||||||||||||||||||||||||||
         1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36
```

:ULT 71
·09-302-495-12
;equence 12, Application US/09302495
?atent No. 6518045
GENERAL INFORMATION:
APPLICANT: IMAMURA, Takayuki
MAEDA, Hiroaki
FUJIYASU, Takeshi
IMAGAWA, Yoshitaka
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/302,495
FILING DATE: 30-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/011,143
FILING DATE: 04-FEB-1998
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
-09-302-495-12

:gnment Scores:
:d. No.: 0.000159 Length: 38
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 3.6% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-30 (1-329) x US-09-302-495-12 (1-38)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGlu 34
              ||||||||||||||||||||||||||||||||||||
Db          1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36
```

RESULT 72
US-10-079-616-12
; Sequence 12, Application US/10079616
; Patent No. 6566097
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,616
; FILING DATE: 22-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/011,143
; FILING DATE: 04-FEB-1998
; APPLICATION NUMBER: PCT/JP97/01824
; FILING DATE: 29-MAY-1997
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: IMAMURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-079-616-12

Alignment Scores:
Pred. No.: 0.000159 Length: 38
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 3.6% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-30 (1-329) x US-10-079-616-12 (1-38)

```
        23 IleTrpGluLeuGluLysAsnValTyrValValGlu 34
           ||||||||||||||||||||||||||||||||||||
         1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36
```

SULT 73
-09-949-016-24250/c
Sequence 24250, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24250
LENGTH: 601
TYPE: DNA
ORGANISM: Human
-09-949-016-24250

ignment Scores:

ed. No.:	0.00238	Length:	601
ore:	12.00	Matches:	12
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	3.6%	Indels:	0
:	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-949-016-24250 (1-601)

```
        39 ProAspAlaProGlyGluMetValValLeuThrCys 50
           ||||||||||||||||||||||||||||||||||||
        81 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 46
```

SULT 74
-09-949-016-24251/c
Sequence 24251, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24251
LENGTH: 601
TYPE: DNA
ORGANISM: Human
-09-949-016-24251

ignment Scores:

ed. No.:	0.00238	Length:	601
ore:	12.00	Matches:	12
rcent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-949-016-24251 (1-601)

```
Qy         39 ProAspAlaProGlyGluMetValValLeuThrCys 50
              ||||||||||||||||||||||||||||||||||||
Db        100 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 65
```

RESULT 75
US-09-949-016-190683/c
; Sequence 190683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190683
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-190683

Alignment Scores:

Pred. No.:	0.00238	Length:	601
Score:	12.00	Matches:	12
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	3.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-949-016-190683 (1-601)

```
Qy         39 ProAspAlaProGlyGluMetValValLeuThrCys 50
              ||||||||||||||||||||||||||||||||||||
Db         81 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 46
```

RESULT 76
US-09-949-016-190684/c
; Sequence 190684, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190684
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-190684

```
gnment Scores:
ed. No.:                0.00238         Length:         601
re:                     12.00           Matches:        12
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               3.6%            Indels:         0
                        3               Gaps:           0

10-821-670A-30 (1-329) x US-09-949-016-190684 (1-601)

        39 ProAspAlaProGlyGluMetValValLeuThrCys 50
           ||||||||||||||||||||||||||||||||||
       100 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 65

ULT 77
09-917-265A-85
equence 85, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
EQ ID NO 85
  LENGTH: 28
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
09-917-265A-85

gnment Scores:
ed. No.:                0.205           Length:         28
re:                     9.00            Matches:        9
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               2.7%            Indels:         0
                        3               Gaps:           0

10-821-670A-30 (1-329) x US-09-917-265A-85 (1-28)

         1 MetHisProGlnGlnLeuValIleAla 9
           ||||||||||||||||||||||||||||
         1 ATGCATCCTCAGCAGTTGGTCATCGCC 27

ULT 78
09-917-265A-87
equence 87, Application US/09917265A
atent No. 6818444
ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
EQ ID NO 87
  LENGTH: 37
  TYPE: DNA
  ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-87

Alignment Scores:
Pred. No.:              0.269           Length:         37
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-87 (1-37)

Qy          1 MetHisProGlnGlnLeuValIleAla 9
              |||||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATCGCC 36

RESULT 79
US-09-513-999C-4018
; Sequence 4018, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 4018
;   LENGTH: 532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 144..503
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 29
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 30
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 289
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 460
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 461
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 503
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 513
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 518
```

OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: UNSURE
LOCATION: 49
OTHER INFORMATION: Xaa=Leu or Arg
FEATURE:
NAME/KEY: UNSURE
LOCATION: 106
OTHER INFORMATION: Xaa=Ile or Lys or Met or Asn or Arg or Ser or Thr
-09-513-999C-4018

ignment Scores:

ed. No.:	3.67	Length:	532
ore:	9.00	Matches:	9
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.7%	Indels:	0
:	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-513-999C-4018 (1-532)

```
       101 PheLeuLeuIleHisLysLysGluAsp 109
           ||||||||||||||||||||||||||
       462 TTTTTACTGATTCACAAAAAGGAAGAC 488
```

SULT 80
-09-887-145-37
Sequence 37, Application US/09887145
Patent No. 6780641
GENERAL INFORMATION:
APPLICANT: Kim, Seung U
TITLE OF INVENTION: Immortalized human microglia
cell and continuous cell line
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Microsoft Word version 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,145
FILING DATE: 22-Jun-2001
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: UBC-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
-09-887-145-37

ignment Scores:

ed. No.:	2.2	Length:	25
ore:	8.00	Matches:	8
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.4%	Indels:	0
:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-887-145-37 (1-25)

```
Qy         91 HisLysGlyGlyGluValLeuSer 98
              |||||||||||||||||||||||||
Db          2 CACAAAGGAGGCGAGGTTCTAAGC 25
```

RESULT 81
US-09-917-265A-86/c
; Sequence 86, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-917-265A-86

Alignment Scores:

Pred. No.:	2.2	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-917-265A-86 (1-25)

```
Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 82
US-09-011-143-13/c
; Sequence 13, Application US/09011143
; Patent No. 6472509
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: FUJIYASU, Takeshi
; APPLICANT: IMAGAWA, Yoshitaka
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,143
; FILING DATE: 04-FEB-1998
; CLASSIFICATION: 536

```
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  PCT/JP97/01824
     FILING DATE:  29-MAY-1997
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  JP 165249/1996
     FILING DATE:  04-JUN-1996
   ATTORNEY/AGENT INFORMATION:
     NAME:  BROWDY, Roger L.
     REGISTRATION NUMBER:  25,618
     REFERENCE/DOCKET NUMBER:  IMAMURA=1
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  202-628-5197
     TELEFAX:  202-737-3528
 INFORMATION FOR SEQ ID NO:  13:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  32 base pairs
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  cDNA
-09-011-143-13

:gnment Scores:
:d. No.:                2.81          Length:        32
:re:                    8.00          Matches:       8
:cent Similarity:       100.0%        Conservative:  0
:t Local Similarity:    100.0%        Mismatches:    0
:ry Match:              2.4%          Indels:        0
                        3             Gaps:          0

-10-821-670A-30 (1-329) x US-09-011-143-13 (1-32)

        176 SerAlaGluLysValArgValAsp 183
            |||||||||||||||||||||||
         32 TCAGCAGAGAAGGTCAGAGTCGAC 9

SULT 83
-09-302-495-13/c
Sequence 13, Application US/09302495
Patent No. 6518045
  GENERAL INFORMATION:
       APPLICANT: IMAMURA, Takayuki
                  MAEDA, Hiroaki
                  FUJIYASU, Takeshi
                  IMAGAWA, Yoshitaka
                  TOKIYOSHI, Sachio
       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
       NUMBER OF SEQUENCES: 26
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: BROWDY AND NEIMARK
            STREET: 419 Seventh Street, N.W., Suite 300
            CITY: Washington
            STATE: D.C.
            COUNTRY: USA
            ZIP: 20004
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/302,495
            FILING DATE: 30-Apr-1999
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: US/09/011,143
            FILING DATE: 04-FEB-1998
            APPLICATION NUMBER: PCT/JP97/01824
            FILING DATE: 29-MAY-1997
            APPLICATION NUMBER: JP 165249/1996
            FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
            NAME: BROWDY, Roger L.
            REGISTRATION NUMBER: 25,618
            REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 202-628-5197
            TELEFAX: 202-737-3528
     INFORMATION FOR SEQ ID NO: 13:
          SEQUENCE CHARACTERISTICS:
               LENGTH: 32 base pairs
               TYPE: nucleic acid
               STRANDEDNESS: single
               TOPOLOGY: linear
          MOLECULE TYPE: cDNA
          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-302-495-13

Alignment Scores:
Pred. No.:                2.81          Length:        32
Score:                    8.00          Matches:       8
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.4%          Indels:        0
DB:                       3             Gaps:          0

US-10-821-670A-30 (1-329) x US-09-302-495-13 (1-32)

Qy        176 SerAlaGluLysValArgValAsp 183
              |||||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGTCGAC 9

RESULT 84
US-10-079-616-13/c
; Sequence 13, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
```

```
           LENGTH: 32 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 13:
-10-079-616-13

ignment Scores:
ed. No.:                2.81          Length:         32
ore:                    8.00          Matches:        8
rcent Similarity:       100.0%        Conservative:   0
st Local Similarity:    100.0%        Mismatches:     0
ery Match:              2.4%          Indels:         0
:                       3             Gaps:           0

-10-821-670A-30 (1-329) x US-10-079-616-13 (1-32)

       176 SerAlaGluLysValArgValAsp 183
           ||||||||||||||||||||||||
        32 TCAGCAGAGAAGGTCAGAGTCGAC 9

SULT 85
-09-917-265A-99
Sequence 99, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265A
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 99
  LENGTH: 37
  TYPE: DNA
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Primer
-09-917-265A-99

ignment Scores:
ed. No.:                3.23          Length:         37
ore:                    8.00          Matches:        8
rcent Similarity:       100.0%        Conservative:   0
st Local Similarity:    100.0%        Mismatches:     0
ery Match:              2.4%          Indels:         0
:                       3             Gaps:           0

-10-821-670A-30 (1-329) x US-09-917-265A-99 (1-37)

         1 MetHisProGlnGlnLeuValIle 8
           ||||||||||||||||||||||||
        11 ATGCACCCTCAGCAGTTGGTCATC 34

SULT 86
-09-079-984A-13
Sequence 13, Application US/09079984A
Patent No. 6231850
 GENERAL INFORMATION:
   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
   APPLICANT:  Yamada, Katsushige
   TITLE OF INVENTION:  Canine interleukin 12, a production method
   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
   TITLE OF INVENTION:  method using it
   NUMBER OF SEQUENCES:  16
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Miller & Christenbury Intellectual Property
     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
     STREET:  1600 Market Street, 39th Floor
     CITY:  Philadelphia
     STATE:  PA
     COUNTRY:  USA
     ZIP:  19103
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy Disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  WordPerfect 5.1
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/079,984A
     FILING DATE:  15-MAY-1998
   ATTORNEY/AGENT INFORMATION:
     NAME:  Austin R. Miller
     REGISTRATION NUMBER:  16,602
     REFERENCE/DOCKET NUMBER:  1051-98
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (215) 563-1810
     TELEFAX:  (215) 568-6946
 INFORMATION FOR SEQ ID NO:  13:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  39 bases
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  other DNA; synthetic DNA
US-09-079-984A-13

Alignment Scores:
Pred. No.:              3.4           Length:         39
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.4%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-30 (1-329) x US-09-079-984A-13 (1-39)

Qy          1 MetHisProGlnGlnLeuValIle 8
              ||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATC 33

RESULT 87
US-09-390-729-13
; Sequence 13, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
```

```
     FILING DATE:  15-MAY-1998
   ATTORNEY/AGENT INFORMATION:
     NAME:  Austin R. Miller
     REGISTRATION NUMBER:  16,602
     REFERENCE/DOCKET NUMBER:  1051-98
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (215) 563-1810
     TELEFAX:  (215) 568-6946
 INFORMATION FOR SEQ ID NO:  13:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  39 bases
     TYPE:  nucleic acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
   MOLECULE TYPE:  other DNA; synthetic DNA
·09-390-729-13

.gnment Scores:
:d. No.:                3.4             Length:         39
>re:                    8.00            Matches:        8
:rcent Similarity:      100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              2.4%            Indels:         0
                        3               Gaps:           0

·10-821-670A-30 (1-329) x US-09-390-729-13 (1-39)

          1 MetHisProGlnGlnLeuValIle 8
            ||||||||||||||||||||||||
         10 ATGCATCCTCAGCAGTTGGTCATC 33

;ULT 88
·09-011-143-14
;equence 14, Application US/09011143
>atent No. 6472509
 GENERAL INFORMATION:
   APPLICANT:  IMAMURA, Takayuki
   APPLICANT:  MAEDA, Hiroaki
   APPLICANT:  FUJIYASU, Takeshi
   APPLICANT:  IMAGAWA, Yoshitaka
   APPLICANT:  TOKIYOSHI, Sachio
   TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
   NUMBER OF SEQUENCES:  26
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  BROWDY AND NEIMARK
     STREET:  419 Seventh Street, N.W., Suite 300
     CITY:  Washington
     STATE:  D.C.
     COUNTRY:  USA
     ZIP:  20004
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/09/011,143
     FILING DATE:  04-FEB-1998
     CLASSIFICATION:  536
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  PCT/JP97/01824
     FILING DATE:  29-MAY-1997
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  JP 165249/1996
     FILING DATE:  04-JUN-1996
   ATTORNEY/AGENT INFORMATION:
     NAME:  BROWDY, Roger L.
     REGISTRATION NUMBER:  25,618
     REFERENCE/DOCKET NUMBER:  IMAMURA=1
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  202-628-5197
     TELEFAX:  202-737-3528
 INFORMATION FOR SEQ ID NO:  14:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-14

Alignment Scores:
Pred. No.:              3.83            Length:         44
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.4%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-011-143-14 (1-44)

Qy        182 ValAspAsnArgAspTyrLysLys 189
              ||||||||||||||||||||||
Db         21 GTCGACAACAGGGATTATAAGAAG 44

RESULT 89
US-09-302-495-14
; Sequence 14, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 44 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-302-495-14
```

ignment Scores:
ed. No.: 3.83 Length: 44
ore: 8.00 Matches: 8
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 2.4% Indels: 0
: 3 Gaps: 0

-10-821-670A-30 (1-329) x US-09-302-495-14 (1-44)

182 ValAspAsnArgAspTyrLysLys 189
||||||||||||||||||||||
21 GTCGACAACAGGGATTATAAGAAG 44

SULT 90
-10-079-616-14
Sequence 14, Application US/10079616
Patent No. 6566097
GENERAL INFORMATION:
APPLICANT: IMAMURA, Takayuki
MAEDA, Hiroaki
FUJIYASU, Takeshi
IMAGAWA, Yoshitaka
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/079,616
FILING DATE: 22-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/011,143
FILING DATE: 04-FEB-1998
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
-10-079-616-14

ignment Scores:
ed. No.: 3.83 Length: 44
ore: 8.00 Matches: 8
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-30 (1-329) x US-10-079-616-14 (1-44)

Qy 182 ValAspAsnArgAspTyrLysLys 189
||||||||||||||||||||||
Db 21 GTCGACAACAGGGATTATAAGAAG 44

RESULT 91
US-09-270-767-2298/c
; Sequence 2298, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2298
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-2298

Alignment Scores:
Pred. No.: 35.5 Length: 427
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-30 (1-329) x US-09-270-767-2298 (1-427)

Qy 13 LeuValLeuLeuAlaProProLeu 20
||||||||||||||||||||||
Db 223 TTAGTTCTGCTAGCCCCGCCTCTG 200

RESULT 92
US-09-270-767-17580/c
; Sequence 17580, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17580
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-17580

Alignment Scores:
Pred. No.: 35.5 Length: 427
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-30 (1-329) x US-09-270-767-17580 (1-427)

Qy 13 LeuValLeuLeuAlaProProLeu 20
||||||||||||||||||||||
Db 223 TTAGTTCTGCTAGCCCCGCCTCTG 200

RESULT 93

-09-445-724B-13
Sequence 13, Application US/09445724B
Patent No. 6600020
GENERAL INFORMATION:
APPLICANT: OKANO, FUMIYOSHI
TITLE OF INVENTION: CANINE INTERLEUKIN 18, CANINE INTERLEUKIN 1 CONVERTING
TITLE OF INVENTION: ENZYME, DNA SEQUENCES ENCODING THESE, INTERLEUKIN 18
TITLE OF INVENTION: PRODUCTION METHOD AND CANINE IMMUNE DISEASE REMEDY
FILE REFERENCE: 2109-15
CURRENT APPLICATION NUMBER: US/09/445,724B
CURRENT FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 540
TYPE: DNA
ORGANISM: Caninus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(537)
-09-445-724B-13

Alignment Scores:

Pred. No.:	44.7	Length:	540
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.4%	Indels:	0
	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-445-724B-13 (1-540)

```
          1 MetHisProGlnGlnLeuValIle 8
            ||||||||||||||||||||||||
          1 ATGCATCCTCAGCAGTTGGTCATC 24
```

SULT 94
-09-533-559-4743
Sequence 4743, Application US/09533559
Patent No. 6902887
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4743
LENGTH: 549
TYPE: DNA
ORGANISM: Aspergillus oryzae
-09-533-559-4743

Alignment Scores:

Pred. No.:	45.4	Length:	549
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.4%	Indels:	0
	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-533-559-4743 (1-549)

```
         13 LeuValLeuLeuAlaProProLeu 20
```

```
                ||||||||||||||||||||||||
Db        321 CTGGTCTTGTTGGCGCCCCCGCTT 344
```

RESULT 95
US-09-949-016-70299
; Sequence 70299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70299
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-70299

Alignment Scores:

Pred. No.:	49.6	Length:	601
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-949-016-70299 (1-601)

```
Qy         97 LeuSerHisSerPheLeuLeuIle 104
              ||||||||||||||||||||||||
Db        506 CTCAGTCATTCTTTTTTACTAATT 529
```

RESULT 96
US-09-949-016-87513
; Sequence 87513, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87513
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-87513

Alignment Scores:

Pred. No.:	49.6	Length:	601
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.4%	Indels:	0

```
:                    3              Gaps:          0

-10-821-670A-30 (1-329) x US-09-949-016-87513 (1-601)

         97 LeuSerHisSerPheLeuLeuIle 104
            ||||||||||||||||||||||||
        440 CTATCACATTCCTTTCTCTTAATC 463

SULT 97
-09-949-016-110703
Sequence 110703, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 110703
  LENGTH: 601
  TYPE: DNA
  ORGANISM: Human
-09-949-016-110703

ignment Scores:
ed. No.:              49.6          Length:        601
ore:                  8.00          Matches:       8
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            2.4%          Indels:        0
:                     3             Gaps:          0

-10-821-670A-30 (1-329) x US-09-949-016-110703 (1-601)

         11 PheSerLeuValLeuLeuAlaPro 18
            ||||||||||||||||||||||||
        345 TTTTCATTAGTTCTCCTGGCTCCT 368

SULT 98
-09-949-016-110704
Sequence 110704, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE:  2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 110704
  LENGTH: 601
  TYPE: DNA
  ORGANISM: Human
-09-949-016-110704

ignment Scores:
Pred. No.:            49.6          Length:        601
Score:                8.00          Matches:       8
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          2.4%          Indels:        0
DB:                   3             Gaps:          0

US-10-821-670A-30 (1-329) x US-09-949-016-110704 (1-601)

Qy         11 PheSerLeuValLeuLeuAlaPro 18
              ||||||||||||||||||||||||
Db        271 TTTTCATTAGTTCTCCTGGCTCCT 294

RESULT 99
US-09-949-016-110705
; Sequence 110705, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110705
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-110705

Alignment Scores:
Pred. No.:            49.6          Length:        601
Score:                8.00          Matches:       8
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          2.4%          Indels:        0
DB:                   3             Gaps:          0

US-10-821-670A-30 (1-329) x US-09-949-016-110705 (1-601)

Qy         11 PheSerLeuValLeuLeuAlaPro 18
              ||||||||||||||||||||||||
Db         71 TTTTCATTAGTTCTCCTGGCTCCT 94

RESULT 100
US-09-949-016-138629
; Sequence 138629, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138629
;   LENGTH: 601
```

TYPE: DNA
ORGANISM: Human
-09-949-016-138629

:gnment Scores:

ed. No.:	49.6	Length:	601
ore:	8.00	Matches:	8
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.4%	Indels:	0
	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-949-016-138629 (1-601)

```
        12 SerLeuValLeuLeuAlaProPro 19
           ||||||||||||||||||||||
       367 TCCCTAGTACTTCTAGCGCCCCCC 390
```

rch completed: June 10, 2006, 04:51:19
time : 238.551 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 11, 2006, 22:10:55 ; Search time 1588.84 Seconds
(without alignments)
3816.589 Million cell updates/sec

tle: US-10-821-670A-30
rfect score: 329
quence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 18892170 seqs, 6143817638 residues

:d size: 1

:al number of hits satisfying chosen parameters: 37767826

nimum DB seq length: 0
:imum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110503_27781/app_query.fasta_1
B=Published_Applications_NA_Main -QFMT=fastap
UFFIX=oligo.p2n.200scores.rnpbm -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
NITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
OCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
ORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
SER=US10821670_@CGN_1_1_4932_@runat_07062006_110503_27781 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	329	100.0	987	3	US-09-917-265-29	Sequence 29, Appl
c 2	329	100.0	987	3	US-09-917-265-31	Sequence 31, Appl
3	329	100.0	987	9	US-10-821-670-29	Sequence 29, Appl
c 4	329	100.0	987	9	US-10-821-670-31	Sequence 31, Appl
5	329	100.0	990	7	US-10-041-672C-1	Sequence 1, Appli
6	329	100.0	4522	7	US-10-041-672C-10	Sequence 10, Appl
7	328	99.7	985	3	US-09-917-265-55	Sequence 55, Appl
c 8	328	99.7	985	3	US-09-917-265-57	Sequence 57, Appl
9	328	99.7	985	9	US-10-821-670-55	Sequence 55, Appl
c 10	328	99.7	985	9	US-10-821-670-57	Sequence 57, Appl
11	317	96.4	2193	6	US-10-079-616-5	Sequence 5, Appli
12	307	93.3	921	6	US-10-079-616-6	Sequence 6, Appli
13	307	93.3	921	6	US-10-079-616-7	Sequence 7, Appli
14	217	66.0	1599	3	US-09-917-265-38	Sequence 38, Appl
c 15	217	66.0	1599	3	US-09-917-265-40	Sequence 40, Appl
16	217	66.0	1599	9	US-10-821-670-38	Sequence 38, Appl
c 17	217	66.0	1599	9	US-10-821-670-40	Sequence 40, Appl
18	206	62.6	921	3	US-09-917-265-26	Sequence 26, Appl
c 19	206	62.6	921	3	US-09-917-265-28	Sequence 28, Appl
20	206	62.6	921	9	US-10-821-670-26	Sequence 26, Appl
c 21	206	62.6	921	9	US-10-821-670-28	Sequence 28, Appl
22	206	62.6	1533	3	US-09-917-265-43	Sequence 43, Appl
c 23	206	62.6	1533	3	US-09-917-265-45	Sequence 45, Appl
24	206	62.6	1533	9	US-10-821-670-43	Sequence 43, Appl
c 25	206	62.6	1533	9	US-10-821-670-45	Sequence 45, Appl
26	37	11.2	921	3	US-09-917-265-52	Sequence 52, Appl
c 27	37	11.2	921	3	US-09-917-265-54	Sequence 54, Appl
28	37	11.2	921	9	US-10-821-670-52	Sequence 52, Appl
c 29	37	11.2	921	9	US-10-821-670-54	Sequence 54, Appl
30	37	11.2	987	3	US-09-917-265-58	Sequence 58, Appl
c 31	37	11.2	987	3	US-09-917-265-60	Sequence 60, Appl
32	37	11.2	987	9	US-10-821-670-58	Sequence 58, Appl
c 33	37	11.2	987	9	US-10-821-670-60	Sequence 60, Appl
34	37	11.2	1533	3	US-09-917-265-66	Sequence 66, Appl
c 35	37	11.2	1533	3	US-09-917-265-68	Sequence 68, Appl
36	37	11.2	1533	9	US-10-821-670-66	Sequence 66, Appl
c 37	37	11.2	1533	9	US-10-821-670-68	Sequence 68, Appl
38	37	11.2	1599	3	US-09-917-265-61	Sequence 61, Appl
c 39	37	11.2	1599	3	US-09-917-265-63	Sequence 63, Appl
40	37	11.2	1599	9	US-10-821-670-61	Sequence 61, Appl
c 41	37	11.2	1599	9	US-10-821-670-63	Sequence 63, Appl
42	37	11.2	2267	3	US-09-917-265-107	Sequence 107, App
c 43	37	11.2	2267	3	US-09-917-265-109	Sequence 109, App
44	37	11.2	2267	9	US-10-821-670-107	Sequence 107, App
c 45	37	11.2	2267	9	US-10-821-670-109	Sequence 109, App
46	35	10.6	987	3	US-09-754-014-2	Sequence 2, Appli
47	35	10.6	987	3	US-09-754-014-3	Sequence 3, Appli
48	35	10.6	987	3	US-09-754-014-4	Sequence 4, Appli
49	35	10.6	987	3	US-09-836-866-2	Sequence 2, Appli
50	35	10.6	1007	8	US-10-221-975A-1	Sequence 1, Appli
51	35	10.6	1018	7	US-10-267-384-194	Sequence 194, App
52	35	10.6	1389	8	US-10-603-064-4	Sequence 4, Appli
53	35	10.6	1397	7	US-10-349-507-2	Sequence 2, Appli
54	35	10.6	1397	7	US-10-267-565-2	Sequence 2, Appli
55	35	10.6	1399	10	US-10-929-182-22	Sequence 22, Appl
56	35	10.6	2347	7	US-10-429-802-44	Sequence 44, Appl
57	35	10.6	2347	7	US-10-430-503-35	Sequence 35, Appl
58	35	10.6	2362	3	US-09-924-703-3	Sequence 3, Appli
59	35	10.6	2362	8	US-10-358-395-3	Sequence 3, Appli
60	35	10.6	5686	7	US-10-136-837-1	Sequence 1, Appli
61	35	10.6	11569	10	US-10-511-237-1	Sequence 1, Appli
62	28	8.5	2390	10	US-10-528-644A-53	Sequence 53, Appl
63	23	7.0	987	3	US-09-826-025-24	Sequence 24, Appl
64	23	7.0	987	9	US-10-785-577-24	Sequence 24, Appl
65	23	7.0	1005	7	US-10-373-456-18	Sequence 18, Appl
66	23	7.0	1017	7	US-10-373-456-20	Sequence 20, Appl
67	23	7.0	1580	9	US-10-742-405-7	Sequence 7, Appli
68	23	7.0	1828	7	US-10-373-456-2	Sequence 2, Appli
69	23	7.0	1870	6	US-10-228-811-4	Sequence 4, Appli
70	23	7.0	2318	6	US-10-172-399-7	Sequence 7, Appli
71	23	7.0	2318	9	US-10-476-961-3	Sequence 3, Appli
72	23	7.0	2466	7	US-10-373-456-1	Sequence 1, Appli
73	23	7.0	8578	3	US-09-828-825-1	Sequence 1, Appli
74	23	7.0	8578	3	US-09-828-825-3	Sequence 3, Appli

75	23	7.0	8608	3	US-09-828-825-7	Sequence 7, Appli
76	23	7.0	8623	3	US-09-828-825-5	Sequence 5, Appli
77	23	7.0	8629	3	US-09-828-825-15	Sequence 15, Appl
78	23	7.0	8638	3	US-09-828-825-9	Sequence 9, Appli
79	23	7.0	8644	3	US-09-828-825-13	Sequence 13, Appl
80	23	7.0	8659	3	US-09-828-825-11	Sequence 11, Appl
81	23	7.0	11453	10	US-10-511-237-3	Sequence 3, Appli
82	22	6.7	18340	8	US-10-240-376A-130	Sequence 130, App
83	20	6.1	270	7	US-10-029-386-16833	Sequence 16833, A
84	20	6.1	399	16	US-11-128-061-661	Sequence 661, App
85	20	6.1	399	16	US-11-128-061-4303	Sequence 4303, Ap
86	20	6.1	399	16	US-11-128-049-661	Sequence 661, App
87	20	6.1	399	16	US-11-128-049-4303	Sequence 4303, Ap
88	20	6.1	556	7	US-10-029-386-3133	Sequence 3133, Ap
89	17	5.2	73	3	US-09-823-549-77	Sequence 77, Appl
90	17	5.2	73	9	US-10-685-992-77	Sequence 77, Appl
91	17	5.2	600	16	US-11-136-527-4408	Sequence 4408, Ap
92	17	5.2	1024	16	US-11-136-527-312	Sequence 312, App
93	17	5.2	1409	8	US-10-603-064-3	Sequence 3, Appli
94	17	5.2	1472	8	US-10-603-064-2	Sequence 2, Appli
95	17	5.2	1569	8	US-10-603-064-12	Sequence 12, Appl
96	17	5.2	1610	9	US-10-742-405-5	Sequence 5, Appli
97	17	5.2	1840	6	US-10-172-399-3	Sequence 3, Appli
98	17	5.2	2013	8	US-10-603-064-11	Sequence 11, Appl
99	17	5.2	2709	8	US-10-603-064-13	Sequence 13, Appl
100	17	5.2	5966	7	US-10-136-837-3	Sequence 3, Appli
101	17	5.2	11458	10	US-10-511-237-2	Sequence 2, Appli
102	12	3.6	38	6	US-10-079-616-12	Sequence 12, Appl
103	10	3.0	21925	7	US-10-017-161-2415	Sequence 2415, Ap
104	10	3.0	21925	7	US-10-292-798-2055	Sequence 2055, Ap
105	10	3.0	26184	7	US-10-017-161-2043	Sequence 2043, Ap
106	10	3.0	26184	7	US-10-292-798-1689	Sequence 1689, Ap
107	9	2.7	28	3	US-09-917-265-85	Sequence 85, Appl
108	9	2.7	28	9	US-10-821-670-85	Sequence 85, Appl
109	9	2.7	30	8	US-10-240-376A-9	Sequence 9, Appli
110	9	2.7	37	3	US-09-917-265-87	Sequence 87, Appl
111	9	2.7	37	9	US-10-821-670-87	Sequence 87, Appl
112	9	2.7	353	9	US-10-357-930-7460	Sequence 7460, Ap
113	9	2.7	381	3	US-09-796-692-7886	Sequence 7886, Ap
114	9	2.7	381	6	US-10-040-862-7886	Sequence 7886, Ap
115	9	2.7	381	7	US-10-057-475B-7886	Sequence 7886, Ap
116	9	2.7	381	7	US-10-154-884B-7886	Sequence 7886, Ap
117	9	2.7	381	9	US-10-764-324-7886	Sequence 7886, Ap
118	9	2.7	400	8	US-10-242-535A-51196	Sequence 51196, A
119	9	2.7	400	8	US-10-085-783A-51196	Sequence 51196, A
120	9	2.7	419	8	US-10-240-376A-1	Sequence 1, Appli
121	9	2.7	419	8	US-10-240-376A-2	Sequence 2, Appli
122	9	2.7	426	9	US-10-357-930-37422	Sequence 37422, A
123	9	2.7	540	4	US-09-925-065A-564824	Sequence 564824,
124	9	2.7	540	5	US-09-925-065A-564824	Sequence 564824,
125	9	2.7	600	10	US-10-972-079-50704	Sequence 50704, A
126	9	2.7	858	6	US-10-198-846-9631	Sequence 9631, Ap
127	9	2.7	2256	9	US-10-357-930-22505	Sequence 22505, A
128	9	2.7	2256	9	US-10-357-930-24790	Sequence 24790, A
129	9	2.7	2256	9	US-10-357-930-28340	Sequence 28340, A
130	9	2.7	2433	7	US-10-369-493-24162	Sequence 24162, A
131	9	2.7	2659	6	US-10-198-846-13710	Sequence 13710, A
132	9	2.7	2709	10	US-10-750-185-41680	Sequence 41680, A
133	9	2.7	2709	10	US-10-750-623-41680	Sequence 41680, A
134	9	2.7	3284	7	US-10-108-260A-630	Sequence 630, App
135	9	2.7	179687	10	US-10-981-277-29	Sequence 29, Appl
136	9	2.7	1503841	3	US-09-795-668-1	Sequence 1, Appli
137	9	2.7	1503841	3	US-09-795-686-1	Sequence 1, Appli
138	9	2.7	1503841	3	US-09-946-807-1	Sequence 1, Appli
139	9	2.7	1503841	10	US-10-995-011-1	Sequence 1, Appli
140	8	2.4	25	3	US-09-917-265-86	Sequence 86, Appl
141	8	2.4	25	3	US-09-887-145-37	Sequence 37, Appl
142	8	2.4	25	8	US-10-719-956-231796	Sequence 231796,
143	8	2.4	25	9	US-10-821-670-86	Sequence 86, Appl
144	8	2.4	25	13	US-11-036-317-431048	Sequence 431048,
145	8	2.4	25	16	US-11-136-527-18285	Sequence 18285, A
146	8	2.4	25	16	US-11-136-527-18288	Sequence 18288, A
147	8	2.4	30	7	US-10-349-507-39	Sequence 39, Appl
148	8	2.4	30	7	US-10-267-565-34	Sequence 34, Appl
c 149	8	2.4	32	6	US-10-079-616-13	Sequence 13, Appl
150	8	2.4	37	3	US-09-917-265-99	Sequence 99, Appl
151	8	2.4	37	9	US-10-821-670-99	Sequence 99, Appl
152	8	2.4	44	6	US-10-079-616-14	Sequence 14, Appl
c 153	8	2.4	50	16	US-11-175-859-25436	Sequence 25436, A
154	8	2.4	182	9	US-10-425-115-66404	Sequence 66404, A
c 155	8	2.4	201	9	US-10-741-600-54203	Sequence 54203, A
c 156	8	2.4	201	10	US-10-995-561-40384	Sequence 40384, A
157	8	2.4	201	10	US-10-995-561-56659	Sequence 56659, A
158	8	2.4	201	10	US-10-995-561-56702	Sequence 56702, A
c 159	8	2.4	201	10	US-10-995-561-56721	Sequence 56721, A
c 160	8	2.4	201	10	US-10-995-561-56753	Sequence 56753, A
c 161	8	2.4	201	16	US-11-124-367A-32612	Sequence 32612, A
c 162	8	2.4	229	8	US-10-437-963-26379	Sequence 26379, A
c 163	8	2.4	252	3	US-09-864-761-32006	Sequence 32006, A
164	8	2.4	280	3	US-09-560-863-932	Sequence 932, App
c 165	8	2.4	296	8	US-10-424-599-57914	Sequence 57914, A
c 166	8	2.4	366	8	US-10-424-599-104364	Sequence 104364,
c 167	8	2.4	369	8	US-10-424-599-118136	Sequence 118136,
c 168	8	2.4	374	3	US-09-770-791-289	Sequence 289, App
169	8	2.4	381	8	US-10-437-963-45090	Sequence 45090, A
c 170	8	2.4	397	3	US-09-864-761-15492	Sequence 15492, A
c 171	8	2.4	416	3	US-09-783-590-7899	Sequence 7899, Ap
c 172	8	2.4	436	7	US-10-062-674-978	Sequence 978, App
c 173	8	2.4	441	4	US-09-925-065A-458395	Sequence 458395,
c 174	8	2.4	441	5	US-09-925-065A-458395	Sequence 458395,
175	8	2.4	443	12	US-10-301-480-516016	Sequence 516016,
176	8	2.4	443	12	US-10-301-480-1129425	Sequence 1129425,
c 177	8	2.4	462	7	US-10-341-961A-368	Sequence 368, App
178	8	2.4	467	12	US-10-301-480-28499	Sequence 28499, A
179	8	2.4	467	12	US-10-301-480-641908	Sequence 641908,
c 180	8	2.4	474	6	US-10-027-632-48724	Sequence 48724, A
c 181	8	2.4	474	7	US-10-027-632-48724	Sequence 48724, A
c 182	8	2.4	474	12	US-10-301-480-3946	Sequence 3946, Ap
c 183	8	2.4	474	12	US-10-301-480-3947	Sequence 3947, Ap
c 184	8	2.4	474	12	US-10-301-480-617355	Sequence 617355,
c 185	8	2.4	474	12	US-10-301-480-617356	Sequence 617356,
186	8	2.4	476	3	US-09-918-995-25870	Sequence 25870, A
187	8	2.4	491	4	US-09-925-065A-538665	Sequence 538665,
188	8	2.4	491	5	US-09-925-065A-538665	Sequence 538665,
c 189	8	2.4	494	6	US-10-027-632-198942	Sequence 198942,
c 190	8	2.4	494	7	US-10-027-632-198942	Sequence 198942,
c 191	8	2.4	500	4	US-09-925-065A-376272	Sequence 376272,
c 192	8	2.4	500	4	US-09-925-065A-376273	Sequence 376273,
c 193	8	2.4	500	4	US-09-925-065A-376274	Sequence 376274,
c 194	8	2.4	500	5	US-09-925-065A-376272	Sequence 376272,
c 195	8	2.4	500	5	US-09-925-065A-376273	Sequence 376273,
c 196	8	2.4	500	5	US-09-925-065A-376274	Sequence 376274,
197	8	2.4	507	4	US-09-925-065A-511562	Sequence 511562,
198	8	2.4	507	4	US-09-925-065A-511564	Sequence 511564,
199	8	2.4	507	5	US-09-925-065A-511562	Sequence 511562,
200	8	2.4	507	5	US-09-925-065A-511564	Sequence 511564,

ALIGNMENTS

RESULT 1
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29

LENGTH: 987
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(987)
OTHER INFORMATION:
-09-917-265-29

ignment Scores:

ed. No.:	0	Length:	987
ore:	329.00	Matches:	329
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	100.0%	Indels:	0
:	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-917-265-29 (1-987)

```
          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 2
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-31

Alignment Scores:

Pred. No.:	0	Length:	987
Score:	329.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-917-265-31 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568
```

```
       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

       161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

       321 SerAsnTrpAlaSerValSerCysSer 329
           |||||||||||||||||||||||||||
        27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

```
ULT 3
-10-821-670-29
equence 29, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
EQ ID NO 29
  LENGTH: 987
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(987)
-10-821-670-29

gnment Scores:
d. No.:              0              Length:        987
re:                  329.00         Matches:       329
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            100.0%         Indels:        0
                     9              Gaps:          0
```

```
US-10-821-670A-30 (1-329) x US-10-821-670-29 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 4
US-10-821-670-31/c
; Sequence 31, Application US/10821670
```

```
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 31
  LENGTH: 987
  TYPE: DNA
  ORGANISM: Felis catus
-10-821-670-31

ignment Scores:
ed. No.:              0            Length:        987
ore:                  329.00       Matches:       329
rcent Similarity:     100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            100.0%       Indels:        0
:                     9            Gaps:          0

-10-821-670A-30 (1-329) x US-10-821-670-31 (1-987)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy      321 SerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||||
Db       27 AGCAACTGGGCATCCGTGTCCTGCAGT 1

RESULT 5
US-10-041-672C-1
; Sequence 1, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

Alignment Scores:
Pred. No.:            0            Length:        990
Score:                329.00       Matches:       329
Percent Similarity:   100.0%       Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:          100.0%       Indels:        0
DB:                   7            Gaps:          0

US-10-821-670A-30 (1-329) x US-10-041-672C-1 (1-990)

Qy        1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy       21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy       41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy       61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy       81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

       161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

       321 SerAsnTrpAlaSerValSerCysSer 329
           |||||||||||||||||||||||||||
       961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

;ULT 6
·10-041-672C-10
;equence 10, Application US/10041672C
;ublication No. US20030157059A1
;ENERAL INFORMATION:
 APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
 APPLICANT:  Universitat Zurich
 TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
 FILE REFERENCE: NHL-NP-36
 CURRENT APPLICATION NUMBER: US/10/041,672C
 CURRENT FILING DATE:  2002-01-08
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn version 3.1
;EQ ID NO 10
  LENGTH: 4522
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: pMol-fil12p40
·10-041-672C-10

.gnment Scores:
;d. No.:              0              Length:        4522
```

```
Score:                  329.00        Matches:       329
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            100.0%        Indels:        0
DB:                     7             Gaps:          0

US-10-821-670A-30 (1-329) x US-10-041-672C-10 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
```

```
              ||||||||||||||||||||||||||
       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033

SULT 7
-09-917-265-55
Sequence 55, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
  LENGTH: 985
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(984)
  OTHER INFORMATION:
-09-917-265-55

ignment Scores:
ed. No.:              0             Length:         985
ore:                  328.00        Matches:        328
rcent Similarity:     100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            99.7%         Indels:         0
:                     3             Gaps:           0

-10-821-670A-30 (1-329) x US-09-917-265-55 (1-985)

          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 8
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-57

Alignment Scores:
Pred. No.:              0             Length:         985
Score:                  328.00        Matches:        328
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            99.7%         Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-57 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
```

```
      865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

       61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

      805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

       81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100

      745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

      101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

      685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

      121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

      625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

      141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160

      565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

      161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

      505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

      181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

      445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

      201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

      385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

      221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

      325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

      241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

      265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

      261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

      205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

      281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

      145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

      301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

       85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

      321 SerAsnTrpAlaSerValSerCys 328

       25 AGCAACTGGGCATCCGTGTCCTGC 2
```

```
ULT 9
10-821-670-55
equence 55, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
```

```
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-10-821-670-55

Alignment Scores:
Pred. No.:              0              Length:          985
Score:                  328.00         Matches:         328
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            99.7%          Indels:          0
DB:                     9              Gaps:            0

US-10-821-670A-30 (1-329) x US-10-821-670-55 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20

Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40

Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60

Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100

Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160

Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
```

```
       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

       321 SerAsnTrpAlaSerValSerCys 328
           |||||||||||||||||||||||||
       961 AGCAACTGGGCATCCGTGTCCTGC 984

SULT 10
-10-821-670-57/c
Sequence 57, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 57
  LENGTH: 985
  TYPE: DNA
  ORGANISM: Felis catus
-10-821-670-57

ignment Scores:
ed. No.:              0              Length:         985
ore:                  328.00         Matches:        328
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            99.7%          Indels:         0
:                     9              Gaps:           0

-10-821-670A-30 (1-329) x US-10-821-670-57 (1-985)

         1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

        21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy     141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy     161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy     181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy     201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy     221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy     241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy     261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy     281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy     301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy     321 SerAsnTrpAlaSerValSerCys 328
           |||||||||||||||||||||||||
Db      25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 11
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
```

```
          FILING DATE: 04-FEB-1998
          APPLICATION NUMBER: PCT/JP97/01824
          FILING DATE: 29-MAY-1997
          APPLICATION NUMBER: JP 165249/1996
          FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
          NAME: BROWDY, Roger L.
          REGISTRATION NUMBER: 25,618
          REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
   INFORMATION FOR SEQ ID NO: 5:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 2193 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
-10-079-616-5

gnment Scores:
:d. No.:              0            Length:        2193
)re:                  317.00       Matches:       317
rcent Similarity:     100.0%       Conservative:  0
:t Local Similarity:  100.0%       Mismatches:    0
:ry Match:            96.4%        Indels:        0
                      6            Gaps:          0

-10-821-670A-30 (1-329) x US-10-079-616-5 (1-2193)

         13 LeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrVal 32
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        100 CTGGTTTTGCTGGCACCTCCTCTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTT 159

         33 ValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsnThr 52
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        160 GTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACT 219

         53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        220 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 279

         73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        280 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 339

         93 GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrp 112
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        340 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 399

        113 SerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGlu 132
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        400 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 459

        133 AlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        460 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 519

        153 LysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAla 172
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        520 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 579

        173 AlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrVal 192
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        580 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 639

        193 GluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValVal 212
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        640 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 699

        213 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 232
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      700 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 759

Qy      233 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHis 252
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      760 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 819

Qy      253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      820 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 879

Qy      273 ThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerVal 292
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      880 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 939

Qy      293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      940 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 999

Qy      313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1000 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 12
US-10-079-616-6
; Sequence 6, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
```

```
-10-079-616-6

ignment Scores:
ed. No.:              2.78e-309      Length:          921
ore:                  307.00         Matches:         307
rcent Similarity:     100.0%         Conservative:    0
st Local Similarity:  100.0%         Mismatches:      0
ery Match:            93.3%          Indels:          0
:                     6              Gaps:            0

-10-821-670A-30 (1-329) x US-10-079-616-6 (1-921)

        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

       323 TrpAlaSerValSerCysSer 329
```

```
           ||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 13
US-10-079-616-7
; Sequence 7, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

Alignment Scores:
Pred. No.:              2.78e-309      Length:          921
Score:                  307.00         Matches:         307
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            93.3%          Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-30 (1-329) x US-10-079-616-7 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
```

```
 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCysSer 329
    |||||||||||||||||||||
901 TGGGCATCCGTGTCCTGCAGT 921
```

```
:ULT 14
·09-917-265-38
:equence 38, Application US/09917265
>atent No. US20020052030A1
3ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
3EQ ID NO 38
  LENGTH: 1599
```

```
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.:              3.05e-215       Length:         1599
Score:                  217.00          Matches:        317
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            66.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-38 (1-1599)

Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873
```

```
        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

        312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
        934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987

SULT 15
-09-917-265-40/c
Sequence 40, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 40
  LENGTH: 1599
  TYPE: DNA
  ORGANISM: Felis catus
-09-917-265-40

ignment Scores:
ed. No.:              3.05e-215      Length:          1599
ore:                  217.00         Matches:         317
rcent Similarity:     99.7%          Conservative:    0
st Local Similarity:  99.7%          Mismatches:      1
ery Match:            66.0%          Indels:          0
:                     3              Gaps:            0

-10-821-670A-30 (1-329) x US-09-917-265-40 (1-1599)

         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy      192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy      212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy      232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy      252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy      272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy      292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

Qy      312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613

RESULT 16
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:
Pred. No.:              3.05e-215      Length:          1599
Score:                  217.00         Matches:         317
Percent Similarity:     99.7%          Conservative:    0
Best Local Similarity:  99.7%          Mismatches:      1
Query Match:            66.0%          Indels:          0
DB:                     9              Gaps:            0

US-10-821-670A-30 (1-329) x US-10-821-670-38 (1-1599)

Qy       12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       34 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 93

Qy       32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       94 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 153
```

```
 52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
154 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

 72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

 92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 513

172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
```

```
;ULT 17
·10-821-670-40/c
;equence 40, Application US/10821670
;ublication No. US20040248261A1
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:
Pred. No.:              3.05e-215      Length:          1599
Score:                  217.00         Matches:         317
Percent Similarity:     99.7%          Conservative:    0
Best Local Similarity:  99.7%          Mismatches:      1
Query Match:            66.0%          Indels:          0
DB:                     9              Gaps:            0

US-10-821-670A-30 (1-329) x US-10-821-670-40 (1-1599)

Qy         12 SerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1566 TCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTTAT 1507

Qy         32 ValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCysAsn 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 GTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAAT 1447

Qy         52 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 ACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 1387

Qy         72 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 1327

Qy         92 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 1267

Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 1207

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 1147

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGA 1087

Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 1027

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 967

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 907

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 847

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 787

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 727

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
```

```
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      726 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 667

      312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      666 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613

SULT 18
-09-917-265-26
Sequence 26, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
  LENGTH: 921
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(921)
  OTHER INFORMATION:
-09-917-265-26

ignment Scores:
ed. No.:                5.4e-204        Length:         921
ore:                    206.00          Matches:        306
rcent Similarity:       99.7%           Conservative:   0
st Local Similarity:    99.7%           Mismatches:     1
ery Match:              62.6%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-917-265-26 (1-921)

       23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

       43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

       63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

       83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

      103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

      123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

      143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

      163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
          ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
      421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSer 329
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 19
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-28

Alignment Scores:
Pred. No.:              5.4e-204        Length:         921
Score:                  206.00          Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            62.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-28 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
```

```
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

     83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

    103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

    123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

    143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

    163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
        ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
    501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

    183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

    203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

    223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

    243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

    263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

    283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

    303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

    323 TrpAlaSerValSerCysSer 329
        |||||||||||||||||||||
     21 TGGGCATCCGTGTCCTGCAGT 1

;ULT 20
-10-821-670-26
;equence 26, Application US/10821670
?ublication No. US20040248261A1
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
;EQ ID NO 26
  LENGTH: 921
```

```
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-26

Alignment Scores:
Pred. No.:              5.4e-204        Length:         921
Score:                  206.00          Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            62.6%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-26 (1-921)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
```

```
       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

       323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
       901 TGGGCATCCGTGTCCTGCAGT 921

SULT 21
-10-821-670-28/c
Sequence 28, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
  LENGTH: 921
  TYPE: DNA
  ORGANISM: Felis catus
-10-821-670-28

ignment Scores:
ed. No.:                5.4e-204        Length:         921
ore:                    206.00          Matches:        306
rcent Similarity:       99.7%           Conservative:   0
st Local Similarity:    99.7%           Mismatches:     1
ery Match:              62.6%           Indels:         0
:                       9               Gaps:           0

-10-821-670A-30 (1-329) x US-10-821-670-28 (1-921)

        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
       501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy     203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy     223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy     243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy     263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy     283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy     303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy     323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
Db      21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 22
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:
Pred. No.:              8.6e-204        Length:         1533
Score:                  206.00          Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            62.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-43 (1-1533)

Qy      23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy      43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
```

```
 63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

 83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
    |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

323 TrpAlaSerValSerCysSer 329
    |||||||||||||||||||||
901 TGGGCATCCGTGTCCTGCAGT 921
```

```
;ULT 23
-09-917-265-45/c
;equence 45, Application US/09917265
?atent No. US20020052030A1
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
;EQ ID NO 45
```

```
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

Alignment Scores:
Pred. No.:              8.6e-204        Length:         1533
Score:                  206.00          Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            62.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-45 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

       323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
       633 TGGGCATCCGTGTCCTGCAGT 613

SULT 24
-10-821-670-43
Sequence 43, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREOF
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/10/821,670
 CURRENT FILING DATE:  2004-04-09
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 43
  LENGTH: 1533
  TYPE: DNA
  ORGANISM: Felis catus
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)..(1533)
-10-821-670-43

ignment Scores:
ed. No.:                8.6e-204        Length:         1533
ore:                    206.00          Matches:        306
rcent Similarity:       99.7%           Conservative:   0
st Local Similarity:    99.7%           Mismatches:     1
ery Match:              62.6%           Indels:         0
:                       9               Gaps:           0

-10-821-670A-30 (1-329) x US-10-821-670-43 (1-1533)

        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

       163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
           |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy     183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy     203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy     223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy     243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy     263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy     283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy     303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy     323 TrpAlaSerValSerCysSer 329
           |||||||||||||||||||||
Db     901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 25
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:
Pred. No.:              8.6e-204        Length:         1533
Score:                  206.00          Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            62.6%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-45 (1-1533)

Qy      23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy      43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy      63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
```

```
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

  83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

 103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

 123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

 143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

 163 SerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
     ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

 183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

 203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

 223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

 243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

 263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

 283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

 303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

 323 TrpAlaSerValSerCysSer 329
     |||||||||||||||||||||
 633 TGGGCATCCGTGTCCTGCAGT 613

;ULT 26
·09-917-265-52
;equence 52, Application US/09917265
>atent No. US20020052030A1
;ENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
:EQ ID NO 52
  LENGTH: 921
  TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-52

Alignment Scores:
Pred. No.:              8.07e-28        Length:         921
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-52 (1-921)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 27
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-54

Alignment Scores:
Pred. No.:              8.07e-28        Length:         921
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-54 (1-921)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 28
US-10-821-670-52
; Sequence 52, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
```

FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 52
LENGTH: 921
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(921)
-10-821-670-52

ignment Scores:

ed. No.:	8.07e-28	Length:	921
ore:	37.00	Matches:	37
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	11.2%	Indels:	0
:	9	Gaps:	0

-10-821-670A-30 (1-329) x US-10-821-670-52 (1-921)

```
        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651
```

SULT 29
-10-821-670-54/c
Sequence 54, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 54
LENGTH: 921
TYPE: DNA
ORGANISM: Canis familiaris
-10-821-670-54

ignment Scores:

ed. No.:	8.07e-28	Length:	921
ore:	37.00	Matches:	37
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	11.2%	Indels:	0
:	9	Gaps:	0

-10-821-670A-30 (1-329) x US-10-821-670-54 (1-921)

```
        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271
```

RESULT 30
US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
; OTHER INFORMATION:
US-09-917-265-58

Alignment Scores:

Pred. No.:	8.59e-28	Length:	987
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-917-265-58 (1-987)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

RESULT 31
US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-60

Alignment Scores:

Pred. No.:	8.59e-28	Length:	987
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0
DB:	3	Gaps:	0

```
10-821-670A-30 (1-329) x US-09-917-265-60 (1-987)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

ULT 32
10-821-670-58
equence 58, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 58
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(987)
10-821-670-58

gnment Scores:
d. No.:                8.59e-28        Length:         987
re:                    37.00           Matches:        37
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              11.2%           Indels:         0
                       9               Gaps:           0

10-821-670A-30 (1-329) x US-10-821-670-58 (1-987)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 33
10-821-670-60/c
equence 60, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 60
 LENGTH: 987
 TYPE: DNA
 ORGANISM: Canis familiaris

US-10-821-670-60

Alignment Scores:
Pred. No.:                8.59e-28        Length:         987
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.2%           Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-60 (1-987)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 34
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:
Pred. No.:                1.29e-27        Length:         1533
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.2%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-66 (1-1533)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 35
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
```

CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 1533
TYPE: DNA
ORGANISM: Canis familiaris
-09-917-265-68

ignment Scores:

ed. No.:	1.29e-27	Length:	1533
ore:	37.00	Matches:	37
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	11.2%	Indels:	0
:	3	Gaps:	0

-10-821-670A-30 (1-329) x US-09-917-265-68 (1-1533)

```
        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883
```

SULT 36
-10-821-670-66
Sequence 66, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66
LENGTH: 1533
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
-10-821-670-66

ignment Scores:

ed. No.:	1.29e-27	Length:	1533
ore:	37.00	Matches:	37
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	11.2%	Indels:	0
:	9	Gaps:	0

-10-821-670A-30 (1-329) x US-10-821-670-66 (1-1533)

```
        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651
```

SULT 37

US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-821-670-68

Alignment Scores:

Pred. No.:	1.29e-27	Length:	1533
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-821-670-68 (1-1533)

```
Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883
```

RESULT 38
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:

Pred. No.:	1.34e-27	Length:	1599
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.2%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-917-265-61 (1-1599)

```
       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ULT 39
09-917-265-63/c
equence 63, Application US/09917265
atent No. US20020052030A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE:  2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
EQ ID NO 63
 LENGTH: 1599
 TYPE: DNA
 ORGANISM: Canis familiaris
09-917-265-63

gnment Scores:
d. No.:              1.34e-27       Length:         1599
re:                  37.00          Matches:        37
cent Similarity:     100.0%         Conservative:   0
t Local Similarity:  100.0%         Mismatches:     0
ry Match:            11.2%          Indels:         0
                     3              Gaps:           0

10-821-670A-30 (1-329) x US-09-917-265-63 (1-1599)

       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||
       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

ULT 40
10-821-670-61
equence 61, Application US/10821670
ublication No. US20040248261A1
ENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT:  Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE:  2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
EQ ID NO 61
 LENGTH: 1599
 TYPE: DNA
 ORGANISM: Canis familiaris
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1599)
10-821-670-61

Alignment Scores:
Pred. No.:              1.34e-27       Length:         1599
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            11.2%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-61 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 41
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-63

Alignment Scores:
Pred. No.:              1.34e-27       Length:         1599
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            11.2%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-63 (1-1599)

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 42
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
```

```
SEQ ID NO 107
  LENGTH: 2267
  TYPE: DNA
  ORGANISM: Canis familiaris
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (154)..(1140)
  OTHER INFORMATION:
-09-917-265-107

ignment Scores:
ed. No.:                1.84e-27        Length:         2267
ore:                    37.00           Matches:        37
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              11.2%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-917-265-107 (1-2267)

        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

SULT 43
-09-917-265-109/c
Sequence 109, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
 APPLICANT:  Boroughs, Karen L.
 TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 FILE REFERENCE: IM-5
 CURRENT APPLICATION NUMBER: US/09/917,265
 CURRENT FILING DATE:  2001-07-27
 PRIOR APPLICATION NUMBER: 60/223,016
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
  LENGTH: 2267
  TYPE: DNA
  ORGANISM: Canis familiaris
-09-917-265-109

ignment Scores:
ed. No.:                1.84e-27        Length:         2267
ore:                    37.00           Matches:        37
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              11.2%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-917-265-109 (1-2267)

        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
            |||||||||||||||||||||||||||||||||||||||||||||||||||
       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

SULT 44
-10-821-670-107
Sequence 107, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
 APPLICANT: Wonderling, Ramani S.
; APPLICANT:  Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION:  THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE:  2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
US-10-821-670-107

Alignment Scores:
Pred. No.:              1.84e-27        Length:         2267
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-107 (1-2267)

Qy          203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy          223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 45
US-10-821-670-109/c
; Sequence 109, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-109

Alignment Scores:
Pred. No.:              1.84e-27        Length:         2267
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.2%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-109 (1-2267)

Qy          203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449
```

```
       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

:ULT 46
 09-754-014-2
:equence 2, Application US/09754014
 atent No. US20020119940A1
  GENERAL INFORMATION:
       APPLICANT: Jeff No. US20020119940A1dstrom
                  Bruce Freimark
                  Deepa Deshpande
       TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                           AND USES
       NUMBER OF SEQUENCES: 12
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: Lyon & Lyon
            STREET: 633 West Fifth Street
                    Suite 4700
            CITY: Los Angeles
            STATE: California
            COUNTRY: U.S.A.
            ZIP: 90071-2066
       COMPUTER READABLE FORM:
            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                         storage
            COMPUTER: IBM Compatible
            OPERATING SYSTEM: IBM P.C. DOS 5.0
            SOFTWARE: FastSEQ for Windows 2.0
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/754,014
            FILING DATE: 03-Jan-2001
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/948,958
            FILING DATE: <Unknown>
       ATTORNEY/AGENT INFORMATION:
            NAME: Berkman, Charles S.
            REGISTRATION NUMBER: 38,077
            REFERENCE/DOCKET NUMBER: 226/284
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: (213) 489-1600
            TELEFAX: (213) 955-0440
            TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 2:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 987 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 09-754-014-2

:gnment Scores:
:d. No.:                1.04e-25        Length:         987
:re:                    35.00           Matches:        35
 cent Similarity:       100.0%          Conservative:   0
:t Local Similarity:    100.0%          Mismatches:     0
:ry Match:              10.6%           Indels:         0
                        3               Gaps:           0

:10-821-670A-30 (1-329) x US-09-754-014-2 (1-987)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||
       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

:ULT 47
 09-754-014-3

; Sequence 3, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-754-014-3

Alignment Scores:
Pred. No.:              1.04e-25        Length:         987
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-754-014-3 (1-987)

Qy         217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy         237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
               |||||||||||||||||||||||||||||||||||||||||||||
Db         706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 48
US-09-754-014-4
; Sequence 4, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
```

```
      TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                          AND USES
      NUMBER OF SEQUENCES: 12
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Lyon & Lyon
           STREET: 633 West Fifth Street
                   Suite 4700
           CITY: Los Angeles
           STATE: California
           COUNTRY: U.S.A.
           ZIP: 90071-2066
      COMPUTER READABLE FORM:
           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                        storage
           COMPUTER: IBM Compatible
           OPERATING SYSTEM: IBM P.C. DOS 5.0
           SOFTWARE: FastSEQ for Windows 2.0
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/754,014
           FILING DATE: 03-Jan-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/948,958
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Berkman, Charles S.
           REGISTRATION NUMBER: 38,077
           REFERENCE/DOCKET NUMBER: 226/284
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 4:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
-09-754-014-4

ignment Scores:
ed. No.:                1.04e-25        Length:         987
ore:                    35.00           Matches:        35
ccent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              10.6%           Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-754-014-4 (1-987)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

SULT 49
-09-836-866-2
Sequence 2, Application US/09836866
Patent No. US20020123473A1
  GENERAL INFORMATION:
      APPLICANT: No. US20020123473A1dstrom, Jeff
                 Freimark, Bruce
                 Deshpande, Deepa
      TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
                          DELIVERY SYTEMS AND USES
      NUMBER OF SEQUENCES: 8
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Lyon & Lyon
           STREET: 633 West Fifth Street
                   Suite 4700
           CITY: Los Angeles
           STATE: California
           COUNTRY: U.S.A.
           ZIP: 90071-2066
      COMPUTER READABLE FORM:
           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                        storage
           COMPUTER: IBM Compatible
           OPERATING SYSTEM: IBM P.C. DOS 5.0
           SOFTWARE: FastSEQ for Windows 2.0
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/836,866
           FILING DATE: 16-Apr-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/949,160
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Warburg, Richard J.
           REGISTRATION NUMBER: 32,327
           REFERENCE/DOCKET NUMBER: 226/285
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 2:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-836-866-2

Alignment Scores:
Pred. No.:              1.04e-25        Length:         987
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            10.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-836-866-2 (1-987)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 50
US-10-221-975A-1
; Sequence 1, Application US/10221975A
; Publication No. US20040023332A1
; GENERAL INFORMATION:
;  APPLICANT: Pohang University of Science and Technology
;  APPLICANT:  Progen Co., Ltd.
;  APPLICANT:  Sung, Young Chul
;  APPLICANT:  Lee, Sung Hee
;  APPLICANT:  Ha, Sang Jun
;  APPLICANT:  Song, Man Ki
;  APPLICANT:  Chang, Jun
;  TITLE OF INVENTION: Genes of IL-12p40 Subunit Mutated for Improving the Activity of
;  TITLE OF INVENTION:  IL-12 and Use Thereof for DNA Vaccine Adjuvant
;  FILE REFERENCE: 59520-00005
;  CURRENT APPLICATION NUMBER: US/10/221,975A
;  CURRENT FILING DATE:  2003-04-02
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
```

LENGTH: 1007
TYPE: DNA
ORGANISM: Homo sapiens
10-221-975A-1

gnment Scores:
d. No.: 1.06e-25 Length: 1007
re: 35.00 Matches: 35
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 10.6% Indels: 0
8 Gaps: 0

10-821-670A-30 (1-329) x US-10-221-975A-1 (1-1007)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756
```

ULT 51
10-267-384-194
equence 194, Application US/10267384
ublication No. US20030198623A1
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
Tartaglia, James
Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,384
FILING DATE: 09-Oct-2002
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
10-267-384-194

gnment Scores:
d. No.: 1.07e-25 Length: 1018
re: 35.00 Matches: 35
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 10.6% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-30 (1-329) x US-10-267-384-194 (1-1018)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781
```

RESULT 52
US-10-603-064-4
; Sequence 4, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-4

Alignment Scores:
Pred. No.: 1.43e-25 Length: 1389
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.6% Indels: 0
DB: 8 Gaps: 0

US-10-821-670A-30 (1-329) x US-10-603-064-4 (1-1389)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 53
US-10-349-507-2
; Sequence 2, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
; APPLICANT: Hekimi , Siegfried
; APPLICANT: Jiang , Ning
; APPLICANT: Benard, Claire
; APPLICANT: Kebir , Hania
; APPLICANT: McCright, Brenton
; APPLICANT: Lakowski , Bernard
; TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: 11202-006-999
; CURRENT APPLICATION NUMBER: US/10/349,507
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 10/312,187
; PRIOR FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: PCT/CA01/00913
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/213,174
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/254,932
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 1397
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (41)...(1024)
-10-349-507-2

ignment Scores:

ed. No.:	1.44e-25	Length:	1397
ore:	35.00	Matches:	35
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	10.6%	Indels:	0
:	7	Gaps:	0

-10-821-670A-30 (1-329) x US-10-349-507-2 (1-1397)

```
        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

SULT 54
-10-267-565-2
Sequence 2, Application US/10267565
Publication No. US20030204059A1
GENERAL INFORMATION:
APPLICANT: Gately, Maurice
APPLICANT: Gubler, Ulrich
APPLICANT: Hulmes, Jeffery
APPLICANT: Podlaski, Frank
APPLICANT: Stern, Alvin
TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
TITLE OF INVENTION: ANTIBODIES THERETO
FILE REFERENCE: 11126-005
CURRENT APPLICATION NUMBER: US/10/267,565
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: 09/401,839
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/459,151
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 08/205,011
PRIOR FILING DATE: 1994-03-02
PRIOR APPLICATION NUMBER: 07/857,023
PRIOR FILING DATE: 1992-03-24
PRIOR APPLICATION NUMBER: 07/572,284
PRIOR FILING DATE: 1990-08-27
PRIOR APPLICATION NUMBER: 07/520,935
PRIOR FILING DATE: 1990-05-09
PRIOR APPLICATION NUMBER: 07/455,708
PRIOR FILING DATE: 1989-12-22
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1397
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
; LOCATION: (41)...(1024)
US-10-267-565-2

Alignment Scores:

Pred. No.:	1.44e-25	Length:	1397
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-267-565-2 (1-1397)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

RESULT 55
US-10-929-182-22
; Sequence 22, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
; APPLICANT: Zang, Jingwu
; APPLICANT: Hong, Jian
; TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
; TITLE OF INVENTION: Multiple Sclerosis
; FILE REFERENCE: HO-P02859US1
; CURRENT APPLICATION NUMBER: US/10/929,182
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,731
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: HUMAN
US-10-929-182-22

Alignment Scores:

Pred. No.:	1.44e-25	Length:	1399
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.6%	Indels:	0
DB:	10	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-929-182-22 (1-1399)

```
Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

RESULT 56
US-10-429-802-44
; Sequence 44, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: WONG, KA YIN
; APPLICANT: ZOU, YIYU
; TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
; FILE REFERENCE: UTSC:752US
; CURRENT APPLICATION NUMBER: US/10/429,802
; CURRENT FILING DATE: 2003-05-05

```
PRIOR APPLICATION NUMBER: 60/377,672
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 44
 LENGTH: 2347
 TYPE: DNA
 ORGANISM: Homo sapiens
10-429-802-44

gnment Scores:
d. No.:              2.31e-25       Length:        2347
re:                  35.00          Matches:       35
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            10.6%          Indels:        0
                     7              Gaps:          0

10-821-670A-30 (1-329) x US-10-429-802-44 (1-2347)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

ULT 57
10-430-503-35
equence 35, Application US/10430503
ublication No. US20040005684A1
ENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT:  LAN, KENG-LI
APPLICANT:  OU-YANG, FU
APPLICANT:  LIU, JAW-CHING
APPLICANT:  LAN, KENG-HSIN
TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
TITLE OF INVENTION:  REAGENTS
FILE REFERENCE: UTSC:797US
CURRENT APPLICATION NUMBER: US/10/430,503
CURRENT FILING DATE:  2003-05-06
PRIOR APPLICATION NUMBER: 60/383,063
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 35
 LENGTH: 2347
 TYPE: DNA
 ORGANISM: Homo sapiens
10-430-503-35

gnment Scores:
d. No.:              2.31e-25       Length:        2347
re:                  35.00          Matches:       35
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            10.6%          Indels:        0
                     7              Gaps:          0

10-821-670A-30 (1-329) x US-10-430-503-35 (1-2347)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
       748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

ULT 58
09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;    LENGTH: 2362
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;    OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;    NAME/KEY: CDS
;    LOCATION: (33)..(1016)
US-09-924-703-3

Alignment Scores:
Pred. No.:           2.32e-25       Length:        2362
Score:               35.00          Matches:       35
Percent Similarity:  100.0%         Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:         10.6%          Indels:        0
DB:                  3              Gaps:          0

US-10-821-670A-30 (1-329) x US-09-924-703-3 (1-2362)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 59
US-10-358-395-3
; Sequence 3, Application US/10358395
; Publication No. US20040044186A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/10/358,395
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US/09/924,703
;  PRIOR FILING DATE: 2001-08-09
```

```
PRIOR APPLICATION NUMBER: 09/325,958
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 08/858,000
PRIOR FILING DATE: 1997-05-16
PRIOR APPLICATION NUMBER: 08/403,013
PRIOR FILING DATE: 1995-03-13
PRIOR APPLICATION NUMBER: 07/584,941
PRIOR FILING DATE: 1990-09-18
PRIOR APPLICATION NUMBER: 07/307,817
PRIOR FILING DATE: 1989-02-07
PRIOR APPLICATION NUMBER: 07/269,945
PRIOR FILING DATE: 1988-11-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
  LENGTH: 2362
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
  OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (33)..(1016)
-10-358-395-3

ignment Scores:
ed. No.:              2.32e-25      Length:        2362
ore:                  35.00         Matches:       35
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            10.6%         Indels:        0
:                     8             Gaps:          0

-10-821-670A-30 (1-329) x US-10-358-395-3 (1-2362)

        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
            |||||||||||||||||||||||||||||||||||||||||||||
        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

SULT 60
-10-136-837-1
Sequence 1, Application US/10136837
Publication No. US20030181405A1
GENERAL INFORMATION:
 APPLICANT: NORDSTROM, Jeffrey L
 APPLICANT:  PERICLE, Federica
 APPLICANT:  ROLLAND, Alain
 APPLICANT:  RALSTON, Robert
 TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
 TITLE OF INVENTION:  Using the Same
 FILE REFERENCE: 273/082 (GM15-1USC1)
 CURRENT APPLICATION NUMBER: US/10/136,837
 CURRENT FILING DATE:  2002-04-29
 PRIOR APPLICATION NUMBER: US 09/268,135
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
  LENGTH: 5686
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Human IL-12 Plasmid pIN1143
-10-136-837-1

ignment Scores:
ed. No.:              5.18e-25      Length:        5686
ore:                  35.00         Matches:       35
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            10.6%       Indels:        0
DB:                     7           Gaps:          0

US-10-821-670A-30 (1-329) x US-10-136-837-1 (1-5686)

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3864 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3923

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              |||||||||||||||||||||||||||||||||||||||||||||
Db       3924 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3968

RESULT 61
US-10-511-237-1
; Sequence 1, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 11569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.hscIL-12 for regulated expre
;   OTHER INFORMATION: human IL-12
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2709)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2710)..(4308)
;   OTHER INFORMATION: Human single-chain IL-12
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (4020)..(4023)
;   OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-1
```

```
gnment Scores:
d. No.:               9.93e-25        Length:         11569
re:                   35.00           Matches:        35
cent Similarity:      100.0%          Conservative:   0
t Local Similarity:   100.0%          Mismatches:     0
ry Match:             10.6%           Indels:         0
                      10              Gaps:           0

10-821-670A-30 (1-329) x US-10-511-237-1 (1-11569)

       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3355 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3414

       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||||||||||||||||||||||||||
      3415 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3459

ULT 62
10-528-644A-53
equence 53, Application US/10528644A
ublication No. US20050287117A1
ENERAL INFORMATION:
APPLICANT: SUNG, Young Chul
APPLICANT:  YOUN, Jin-Won
APPLICANT:  YANG, Se-Hwan
APPLICANT:  PARK, Su-Hwan
APPLICANT:  LEE, Chang Geun
TITLE OF INVENTION: A VACCINE ENHANCING THE PROTECTIVE IMMUNITY TO
TITLE OF INVENTION:  HEPATITIS C VIRUS USING PLASMID DNA AND RECOMBINANT ADENOVIRUS
FILE REFERENCE: 428.1049
CURRENT APPLICATION NUMBER: US/10/528,644A
CURRENT FILING DATE:  2005-03-18
PRIOR APPLICATION NUMBER: PCT/KR03/01951
PRIOR FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: KR 2002-0058712
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: KR 2002-68496
PRIOR FILING DATE: 2002-11-06
NUMBER OF SEQ ID NOS: 54
SOFTWARE: KopatentIn 1.71
EQ ID NO 53
 LENGTH: 2390
 TYPE: DNA
 ORGANISM: Homo sapiens (hIL-12m)
10-528-644A-53

gnment Scores:
d. No.:               4.65e-18        Length:         2390
re:                   28.00           Matches:        28
cent Similarity:      100.0%          Conservative:   0
t Local Similarity:   100.0%          Mismatches:     0
ry Match:             8.5%            Indels:         0
                      10              Gaps:           0

10-821-670A-30 (1-329) x US-10-528-644A-53 (1-2390)

       224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      2070 TACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAG 2129

       244 LeuLysProLeuLysAsnSerArg 251
           |||||||||||||||||||||||
      2130 CTGAAGCCATTAAAGAATTCTCGG 2153

ULT 63
09-826-025-24
equence 24, Application US/09826025
atent No. US20020162123A1
 GENERAL INFORMATION:
      APPLICANT: Chang, Lung-Ji
      TITLE OF INVENTION: Combination Immunogene Therapy
      NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/826,025
;            FILING DATE: 04-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 987 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

Alignment Scores:
Pred. No.:            3.38e-13        Length:         987
Score:                23.00           Matches:        23
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          7.0%            Indels:         0
DB:                   3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-826-025-24 (1-987)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 525

Qy        176 SerAlaGlu 178
              |||||||||
Db        526 TCTGCAGAG 534

RESULT 64
US-10-785-577-24
; Sequence 24, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
```

```
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/10/785,577
          FILING DATE: 23-Feb-2004
          CLASSIFICATION: 424
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: US/08/838,702
          FILING DATE: 9-Apr-1997
     ATTORNEY/AGENT INFORMATION:
          NAME: Ingolia, Diane E.
          REGISTRATION NUMBER: 40,027
          REFERENCE/DOCKET NUMBER: CHANG-02687
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (415) 705-8410
          TELEFAX: (415) 397-8338
  INFORMATION FOR SEQ ID NO: 24:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 987 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
     MOLECULE TYPE: other nucleic acid
          DESCRIPTION: /desc = "DNA"
     SEQUENCE DESCRIPTION: SEQ ID NO: 24:
-10-785-577-24

ignment Scores:
ed. No.:                3.38e-13        Length:         987
ore:                    23.00           Matches:        23
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              7.0%            Indels:         0
:                       9               Gaps:           0

-10-821-670A-30 (1-329) x US-10-785-577-24 (1-987)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       466 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 525

       176 SerAlaGlu 178
           |||||||||
       526 TCTGCAGAG 534

SULT 65
-10-373-456-18
Sequence 18, Application US/10373456
Publication No. US20040009146A1
GENERAL INFORMATION:
 APPLICANT: Podhajcer, Osvaldo
 TITLE OF INVENTION: Anti-Tumor Vaccine and Method
 FILE REFERENCE: 1423P-US/101141-14
 CURRENT APPLICATION NUMBER: US/10/373,456
 CURRENT FILING DATE:  2003-02-25
 PRIOR APPLICATION NUMBER: US 60/359,836
 PRIOR FILING DATE: 2002-02-26
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
  LENGTH: 1005
  TYPE: DNA
  ORGANISM: Homo sapiens
-10-373-456-18

ignment Scores:
ed. No.:                3.43e-13        Length:         1005
ore:                    23.00           Matches:        23
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              7.0%            Indels:         0
:                       7               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-373-456-18 (1-1005)

Qy      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      474 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 533

Qy      176 SerAlaGlu 178
            |||||||||
Db      534 TCTGCAGAG 542

RESULT 66
US-10-373-456-20
; Sequence 20, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 1017
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-20

Alignment Scores:
Pred. No.:              3.47e-13        Length:         1017
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-373-456-20 (1-1017)

Qy      156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      478 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 537

Qy      176 SerAlaGlu 178
            |||||||||
Db      538 TCTGCAGAG 546

RESULT 67
US-10-742-405-7
; Sequence 7, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
;  APPLICANT: Bowman, Edward P.
;  APPLICANT:  Chan, Jason R.
;  APPLICANT:  Moore, Kevin
;  APPLICANT:  Nguyen, Nhung
;  APPLICANT:  Churakova, Tatyana
;  APPLICANT:  Chen, Shi-Juan
;  APPLICANT:  Cua, Daniel J.
;  TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
;  FILE REFERENCE: DX01578K
;  CURRENT APPLICATION NUMBER: US/10/742,405
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 1580
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1569)
```

10-742-405-7

gnment Scores:
d. No.: 5.19e-13 Length: 1580
re: 23.00 Matches: 23
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 7.0% Indels: 0
9 Gaps: 0

10-821-670A-30 (1-329) x US-10-742-405-7 (1-1580)

156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
478 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 537

176 SerAlaGlu 178
|||||||||
538 TCTGCAGAG 546

ULT 68
10-373-456-2
equence 2, Application US/10373456
ublication No. US20040009146A1
ENERAL INFORMATION:
APPLICANT: Podhajcer, Osvaldo
TITLE OF INVENTION: Anti-Tumor Vaccine and Method
FILE REFERENCE: 1423P-US/101141-14
CURRENT APPLICATION NUMBER: US/10/373,456
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/359,836
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
EQ ID NO 2
LENGTH: 1828
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: p40-linker-p35 fragment cloned into MVL-hIL12lig vector (Fig. 11)
10-373-456-2

gnment Scores:
d. No.: 5.93e-13 Length: 1828
re: 23.00 Matches: 23
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 7.0% Indels: 0
7 Gaps: 0

10-821-670A-30 (1-329) x US-10-373-456-2 (1-1828)

156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
478 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 537

176 SerAlaGlu 178
|||||||||
538 TCTGCAGAG 546

ULT 69
10-228-811-4
equence 4, Application US/10228811
ublication No. US20030054392A1
ENERAL INFORMATION:
APPLICANT: Wittig, Prof. Burghardt
APPLICANT: Junghans, Claas
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
TITLE OF INVENTION: Therapy
FILE REFERENCE: XI 597/99
CURRENT APPLICATION NUMBER: US/10/228,811
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: DE 196 48 625.4
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1870)
; OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1869)..(1870)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
; OTHER INFORMATION: to 1870 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No
US-10-228-811-4

Alignment Scores:
Pred. No.: 6.06e-13 Length: 1870
Score: 23.00 Matches: 23
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 7.0% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-30 (1-329) x US-10-228-811-4 (1-1870)

Qy 156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1098 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1157

Qy 176 SerAlaGlu 178
|||||||||
Db 1158 TCTGCAGAG 1166

RESULT 70
US-10-172-399-7
; Sequence 7, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
; APPLICANT: Li, Chuan-Yuan
; APPLICANT: Dewhirst, Mark
; APPLICANT: Huang, Qian
; TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
; FILE REFERENCE: 180-129
; CURRENT APPLICATION NUMBER: US/10/172,399
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 2318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(1000)
US-10-172-399-7

Alignment Scores:
Pred. No.: 7.37e-13 Length: 2318
Score: 23.00 Matches: 23
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 7.0% Indels: 0

```
:                    6              Gaps:          0

-10-821-670A-30 (1-329) x US-10-172-399-7 (1-2318)

        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        479 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 538

        176 SerAlaGlu 178
            |||||||||
        539 TCTGCAGAG 547

SULT 71
-10-476-961-3
Sequence 3, Application US/10476961
Publication No. US20040241843A1
GENERAL INFORMATION:
 APPLICANT: Brenda F. Baker
 APPLICANT:  Susan M. Freier
 APPLICANT:  Isis Pharmaceuticals, Inc.
 TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
 FILE REFERENCE: RTSP-0393
 CURRENT APPLICATION NUMBER: US/10/476,961
 CURRENT FILING DATE:  2003-11-05
 PRIOR APPLICATION NUMBER: 2001-05-07
 PRIOR FILING DATE: 09/851,062
 NUMBER OF SEQ ID NOS: 87
SEQ ID NO 3
  LENGTH: 2318
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (14)...(1000)
-10-476-961-3

ignment Scores:
ed. No.:              7.37e-13       Length:        2318
ore:                  23.00          Matches:       23
cent Similarity:      100.0%         Conservative:  0
st Local Similarity:  100.0%         Mismatches:    0
ery Match:            7.0%           Indels:        0
:                     9              Gaps:          0

-10-821-670A-30 (1-329) x US-10-476-961-3 (1-2318)

        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        479 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 538

        176 SerAlaGlu 178
            |||||||||
        539 TCTGCAGAG 547

SULT 72
-10-373-456-1
Sequence 1, Application US/10373456
Publication No. US20040009146A1
GENERAL INFORMATION:
 APPLICANT: Podhajcer, Osvaldo
 TITLE OF INVENTION: Anti-Tumor Vaccine and Method
 FILE REFERENCE: 1423P-US/101141-14
 CURRENT APPLICATION NUMBER: US/10/373,456
 CURRENT FILING DATE:  2003-02-25
 PRIOR APPLICATION NUMBER: US 60/359,836
 PRIOR FILING DATE: 2002-02-26
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
  LENGTH: 2466
  TYPE: DNA
  ORGANISM: Artificial
  FEATURE:
;   OTHER INFORMATION: p35-IRES-p40 fragment cloned into MVL-hIL-12 and MVL-hIL-12-hIL-1
;   OTHER INFORMATION: 0 vectors (Fig 11)
US-10-373-456-1

Alignment Scores:
Pred. No.:              7.8e-13        Length:        2466
Score:                  23.00          Matches:       23
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            7.0%           Indels:        0
DB:                     7              Gaps:          0

US-10-821-670A-30 (1-329) x US-10-373-456-1 (1-2466)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1935 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1994

Qy        176 SerAlaGlu 178
              |||||||||
Db       1995 TCTGCAGAG 2003

RESULT 73
US-09-828-825-1
; Sequence 1, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV  IE
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA Promoter
;   NAME/KEY: mRNA
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: mRNA
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
;   OTHER INFORMATION: linker at 3624-3629)
;   NAME/KEY: promoter
;   LOCATION: (4352)..(4431)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4362)..(4583)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4678)..(5133)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5197)..(6564)
;   OTHER INFORMATION: Neo r expression cassette
```

```
 NAME/KEY: misc_feature
 LOCATION: (6975)..(7835)
 OTHER INFORMATION: Ampicillin resistance
 OTHER INFORMATION: Description of Artificial Sequence: Plasmid
 NAME/KEY: CDS
 LOCATION: (2640)..(4223)
 OTHER INFORMATION: IL 12.0 coding sequence - 2 amino acid linker at
 OTHER INFORMATION: 3624
09-828-825-1

gnment Scores:
d. No.:              2.44e-12       Length:        8578
re:                  23.00          Matches:       23
cent Similarity:     100.0%         Conservative:  0
t Local Similarity:  100.0%         Mismatches:    0
ry Match:            7.0%           Indels:        0
                     3              Gaps:          0

10-821-670A-30 (1-329) x US-09-828-825-1 (1-8578)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

       176 SerAlaGlu 178
           |||||||||
      3165 TCTGCAGAG 3173

ULT 74
09-828-825-3
equence 3, Application US/09828825
atent No. US20020018767A1
ENERAL INFORMATION:
APPLICANT: Lee, Seewoo
APPLICANT:  Kim, Han-soo
TITLE OF INVENTION: Anti-cancer Cellular Vaccine
FILE REFERENCE: 84906-102
CURRENT APPLICATION NUMBER: US/09/828,825
CURRENT FILING DATE:  2001-04-10
PRIOR APPLICATION NUMBER: KR00-43498
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 3
 LENGTH: 8578
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: plasmid
 NAME/KEY: enhancer
 LOCATION: (1)..(659)
 OTHER INFORMATION: CMV IE Enhancer
 NAME/KEY: promoter
 LOCATION: (669)..(750)
 OTHER INFORMATION: CMV IE Promoter
 NAME/KEY: misc_feature
 LOCATION: (890)..(1002)
 OTHER INFORMATION: InTervening Sequence
 NAME/KEY: promoter
 LOCATION: (1067)..(1085)
 OTHER INFORMATION: T7 RNA polymerase promoter
 NAME/KEY: misc_feature
 LOCATION: (1090)..(1984)
 OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
 NAME/KEY: RBS
 LOCATION: (2013)..(2593)
 OTHER INFORMATION: IRES sequence
 NAME/KEY: misc_feature
 LOCATION: (2627)..(4263)
 OTHER INFORMATION: Human IL12.0 sequence (2640-4217 is coding
 OTHER INFORMATION: sequence)
 NAME/KEY: promoter
 LOCATION: (4346)..(4425)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4356)..(4577)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4672)..(5127)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5191)..(6558)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6969)..(7829)
;   OTHER INFORMATION: Ampicillin resistance
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4217)
;   OTHER INFORMATION: IL12.0 coding sequence - no linker
US-09-828-825-3

Alignment Scores:
Pred. No.:              2.44e-12       Length:        8578
Score:                  23.00          Matches:       23
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            7.0%           Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-30 (1-329) x US-09-828-825-3 (1-8578)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

Qy        176 SerAlaGlu 178
              |||||||||
Db       3165 TCTGCAGAG 3173

RESULT 75
US-09-828-825-7
; Sequence 7, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
```

```
  LOCATION: (2627)..(4263)
  OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
  OTHER INFORMATION: sequence, 13 amino acid flexible linker at
  OTHER INFORMATION: 3606-3676)
  NAME/KEY: CDS
  LOCATION: (2640)..(4253)
  OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
  NAME/KEY: promoter
  LOCATION: (4362)..(4383)
  OTHER INFORMATION: T3 RNA Polymerase promoter
  NAME/KEY: polyA_signal
  LOCATION: (4393)..(4614)
  OTHER INFORMATION: SV40 fragment containing polyadenylation signal
  NAME/KEY: rep_origin
  LOCATION: (4709)..(5164)
  OTHER INFORMATION: f1 origin of replication
  NAME/KEY: misc_feature
  LOCATION: (5228)..(6595)
  OTHER INFORMATION: Neo r expression cassette
  NAME/KEY: misc_feature
  LOCATION: (7006)..(7866)
  OTHER INFORMATION: Ampicillin resistance
-09-828-825-7

ignment Scores:
ed. No.:                2.45e-12        Length:         8608
ore:                    23.00           Matches:        23
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              7.0%            Indels:         0
:                       3               Gaps:           0

-10-821-670A-30 (1-329) x US-09-828-825-7 (1-8608)

        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

        176 SerAlaGlu 178
            |||||||||
       3165 TCTGCAGAG 3173

SULT 76
-09-828-825-5
Sequence 5, Application US/09828825
Patent No. US20020018767A1
GENERAL INFORMATION:
 APPLICANT: Lee, Seewoo
 APPLICANT:  Kim, Han-soo
 TITLE OF INVENTION: Anti-cancer Cellular Vaccine
 FILE REFERENCE: 84906-102
 CURRENT APPLICATION NUMBER: US/09/828,825
 CURRENT FILING DATE:  2001-04-10
 PRIOR APPLICATION NUMBER: KR00-43498
 PRIOR FILING DATE: 2000-07-27
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
  LENGTH: 8623
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  NAME/KEY: misc_feature
  LOCATION: (1)..(750)
  OTHER INFORMATION: CMV enhancer and promoter
  NAME/KEY: misc_feature
  LOCATION: (890)..(1002)
  OTHER INFORMATION: Intervening sequence
  NAME/KEY: promoter
  LOCATION: (1067)..(1085)
  OTHER INFORMATION: T7 RNA polymerase promoter
  NAME/KEY: misc_feature
  LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4278)
;   OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
;   OTHER INFORMATION: flexible linker from 3606-3690
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4268)
;   OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
;   OTHER INFORMATION: sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4407)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4408)..(4629)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4724)..(5179)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5243)..(6610)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7021)..(7881)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

Alignment Scores:
Pred. No.:              2.45e-12        Length:         8623
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-828-825-5 (1-8623)

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

Qy        176 SerAlaGlu 178
              |||||||||
Db       3165 TCTGCAGAG 3173

RESULT 77
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 8629
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
```

```
 LOCATION: (1067)..(1085)
 OTHER INFORMATION: T7 RNA polymerase promoter
 NAME/KEY: misc_feature
 LOCATION: (1090)..(2726)
 OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
 OTHER INFORMATION: amino acid linker at 2087-2116)
 NAME/KEY: CDS
 LOCATION: (1103)..(2716)
 OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
 NAME/KEY: RBS
 LOCATION: (2752)..(3332)
 OTHER INFORMATION: IRES sequence
 NAME/KEY: misc_feature
 LOCATION: (3369)..(4263)
 OTHER INFORMATION: Human B7.1 sequence
 NAME/KEY: promoter
 LOCATION: (4383)..(4404)
 OTHER INFORMATION: T3 RNA Polymerase promoter
 NAME/KEY: polyA_signal
 LOCATION: (4414)..(4635)
 OTHER INFORMATION: SV40 fragment containing polyadenylation signal
 NAME/KEY: rep_origin
 LOCATION: (4730)..(5185)
 OTHER INFORMATION: f1 origin of replication
 NAME/KEY: misc_feature
 LOCATION: (5249)..(6616)
 OTHER INFORMATION: Neo r expression cassette
 NAME/KEY: misc_feature
 LOCATION: (7027)..(7887)
 OTHER INFORMATION: Ampicillin resistance gene
09-828-825-15

gnment Scores:
d. No.:              2.45e-12       Length:         8629
re:                  23.00          Matches:        23
cent Similarity:     100.0%         Conservative:   0
t Local Similarity:  100.0%         Mismatches:     0
ry Match:            7.0%           Indels:         0
                     3              Gaps:           0

10-821-670A-30 (1-329) x US-09-828-825-15 (1-8629)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1568 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1627

       176 SerAlaGlu 178
           |||||||||
      1628 TCTGCAGAG 1636

ULT 78
09-828-825-9
equence 9, Application US/09828825
atent No. US20020018767A1
ENERAL INFORMATION:
APPLICANT: Lee, Seewoo
APPLICANT:  Kim, Han-soo
TITLE OF INVENTION: Anti-cancer Cellular Vaccine
FILE REFERENCE: 84906-102
CURRENT APPLICATION NUMBER: US/09/828,825
CURRENT FILING DATE:  2001-04-10
PRIOR APPLICATION NUMBER: KR00-43498
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 9
 LENGTH: 8638
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: plasmid
 NAME/KEY: misc_feature
 LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4293)
;   OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
;   OTHER INFORMATION: amino acid linker at 3606-3706)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4283)
;   OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4392)..(4413)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4423)..(4644)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4739)..(5194)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5258)..(6625)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7036)..(7896)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9

Alignment Scores:
Pred. No.:           2.46e-12       Length:         8638
Score:               23.00          Matches:        23
Percent Similarity:  100.0%         Conservative:   0
Best Local Similarity: 100.0%       Mismatches:     0
Query Match:         7.0%           Indels:         0
DB:                  3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-828-825-9 (1-8638)

Qy       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3105 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3164

Qy       176 SerAlaGlu 178
             |||||||||
Db      3165 TCTGCAGAG 3173

RESULT 79
US-09-828-825-13
; Sequence 13, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 8644
;   TYPE: DNA
```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid
NAME/KEY: misc_feature
LOCATION: (1)..(750)
OTHER INFORMATION: CMV enhancer and promoter
NAME/KEY: promoter
LOCATION: (1067)..(1085)
OTHER INFORMATION: T7 RNA polymerase promoter
NAME/KEY: misc_feature
LOCATION: (1090)..(2731)
OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
OTHER INFORMATION: amino acid linker at 2087-2131)
NAME/KEY: CDS
LOCATION: (1103)..(2731)
OTHER INFORMATION: IL12.3 (15 amino acid linker)
NAME/KEY: RBS
LOCATION: (2767)..(3347)
OTHER INFORMATION: IRES sequence
NAME/KEY: misc_feature
LOCATION: (3384)..(4278)
OTHER INFORMATION: Human B7.1 sequence
NAME/KEY: promoter
LOCATION: (4398)..(4419)
OTHER INFORMATION: T3 RNA polymerase promoter
NAME/KEY: polyA_signal
LOCATION: (4429)..(4650)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal
NAME/KEY: rep_origin
LOCATION: (4745)..(5200)
OTHER INFORMATION: f1 origin of replication
NAME/KEY: misc_feature
LOCATION: (5264)..(5681)
OTHER INFORMATION: Neo r expression cassette
NAME/KEY: misc_feature
LOCATION: (7042)..(7902)
OTHER INFORMATION: Ampicillin resistance gene
-09-828-825-13

ignment Scores:
ed. No.: 2.46e-12 Length: 8644
ore: 23.00 Matches: 23
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 7.0% Indels: 0
: 3 Gaps: 0

-10-821-670A-30 (1-329) x US-09-828-825-13 (1-8644)

156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1568 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1627

176 SerAlaGlu 178
|||||||||
1628 TCTGCAGAG 1636

SULT 80
-09-828-825-11
Sequence 11, Application US/09828825
Patent No. US20020018767A1
GENERAL INFORMATION:
APPLICANT: Lee, Seewoo
APPLICANT: Kim, Han-soo
TITLE OF INVENTION: Anti-cancer Cellular Vaccine
FILE REFERENCE: 84906-102
CURRENT APPLICATION NUMBER: US/09/828,825
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: KR00-43498
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11

; LENGTH: 8659
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(750)
; OTHER INFORMATION: CMV enhancer and promoter
; NAME/KEY: promoter
; LOCATION: (1067)..(1085)
; OTHER INFORMATION: T7 RNA polymerase promoter
; NAME/KEY: misc_feature
; LOCATION: (1090)..(2756)
; OTHER INFORMATION: Human IL12.4 (coding sequence 1103-2746, 19 amino
; OTHER INFORMATION: acid linker at 2087-2146)
; NAME/KEY: CDS
; LOCATION: (1103)..(2746)
; OTHER INFORMATION: Human IL12.4 (19 amino acid linker)
; NAME/KEY: RBS
; LOCATION: (2782)..(3362)
; OTHER INFORMATION: IRES sequence
; NAME/KEY: misc_feature
; LOCATION: (3399)..(4293)
; OTHER INFORMATION: Human B7.1 sequence
; NAME/KEY: promoter
; LOCATION: (4413)..(4434)
; OTHER INFORMATION: T3 RNA polymerase promoter
; NAME/KEY: polyA_signal
; LOCATION: (4444)..(4665)
; OTHER INFORMATION: SV40 fragment containing polyadenylation signal
; NAME/KEY: rep_origin
; LOCATION: (4760)..(5215)
; OTHER INFORMATION: f1 origin of replication
; NAME/KEY: misc_feature
; LOCATION: (5279)..(6646)
; OTHER INFORMATION: Neo r expression cassette
; NAME/KEY: misc_feature
; LOCATION: (7057)..(7917)
; OTHER INFORMATION: Ampicillin resistance gene
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-11

Alignment Scores:
Pred. No.: 2.46e-12 Length: 8659
Score: 23.00 Matches: 23
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 7.0% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-30 (1-329) x US-09-828-825-11 (1-8659)

Qy 156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1568 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 1627

Qy 176 SerAlaGlu 178
|||||||||
Db 1628 TCTGCAGAG 1636

RESULT 81
US-10-511-237-3
; Sequence 3, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
; APPLICANT: Block, Andreas
; TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
; TITLE OF INVENTION: Genes
; FILE REFERENCE: 66741-043
; CURRENT APPLICATION NUMBER: US/10/511,237
; CURRENT FILING DATE: 2004-10-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3

```
LENGTH: 11453
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Adenoviral expression plasmid pShuttle.3r.hscIL-12 for regulated
OTHER INFORMATION: expression of human IL-12 following virus generation using AdEasy
FEATURE:
NAME/KEY: gene
LOCATION: (327)..(713)
OTHER INFORMATION: VP16
FEATURE:
NAME/KEY: gene
LOCATION: (714)..(1352)
OTHER INFORMATION: TetR
FEATURE:
NAME/KEY: Intron
LOCATION: (1353)..(1912)
OTHER INFORMATION:
FEATURE:
NAME/KEY: promoter
LOCATION: (1864)..(1902)
OTHER INFORMATION: TK-min
FEATURE:
NAME/KEY: protein_bind
LOCATION: (1913)..(2212)
OTHER INFORMATION: TetO7
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2213)..(2709)
OTHER INFORMATION: CMV-min + Intron
FEATURE:
NAME/KEY: promoter
LOCATION: (2226)..(2264)
OTHER INFORMATION: CMV-min
FEATURE:
NAME/KEY: gene
LOCATION: (2710)..(4308)
OTHER INFORMATION: Human singe-chain IL-12
FEATURE:
NAME/KEY: mutation
LOCATION: (4020)..(4023)
OTHER INFORMATION: T/C, A/T, G/C, T/G
10-511-237-3

gnment Scores:
d. No.:                3.18e-12        Length:         11453
re:                    23.00           Matches:        23
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              7.0%            Indels:         0
                       10              Gaps:           0

10-821-670A-30 (1-329) x US-10-511-237-3 (1-11453)

       156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      3175 GTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTC 3234

       176 SerAlaGlu 178
           |||||||||
      3235 TCTGCAGAG 3243

ULT 82
10-240-376A-130
equence 130, Application US/10240376A
ublication No. US20040161747A1
ENERAL INFORMATION:
APPLICANT: Morahan, Grant
TITLE OF INVENTION: A METHOD FOR SCREENING FOR AUTOIMMUNE
TITLE OF INVENTION:  DISEASE BY IDENTIFYING POLYMORPHISMS IN IL-12 p40
FILE REFERENCE: DAVI186.001APC
CURRENT APPLICATION NUMBER: US/10/240,376A
CURRENT FILING DATE:  2002-09-27
;  PRIOR APPLICATION NUMBER: PCT/AU01/00340
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: PQ 6466
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 60/204,366
;  PRIOR FILING DATE: 2000-05-15
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 18340
;   TYPE: DNA
;   ORGANISM: mammalian
US-10-240-376A-130

Alignment Scores:
Pred. No.:             5.39e-11        Length:         18340
Score:                 22.00           Matches:        22
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           6.7%            Indels:         0
DB:                    8               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-240-376A-130 (1-18340)

Qy        253 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14078 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 14137

Qy        273 ThrPhe 274
              ||||||
Db      14138 ACATTC 14143

RESULT 83
US-10-029-386-16833/c
; Sequence 16833, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16833
;   LENGTH: 270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR5.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;   OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BF204907.1, EVALUE 9.20e-02
;   OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 4.00e-41
US-10-029-386-16833

Alignment Scores:
Pred. No.:             1.38e-10        Length:         270
Score:                 20.00           Matches:        20
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           6.1%            Indels:         0
DB:                    7               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-029-386-16833 (1-270)

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       167 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 108

SULT 84
-11-128-061-661
Sequence 661, Application US/11128061
Publication No. US20060003958A1
GENERAL INFORMATION:
 APPLICANT: Melville, Mark W.
 APPLICANT:  Charlebois, Timothy S.
 APPLICANT:  Mounts, William M.
 APPLICANT:  Hann, Louane E.
 APPLICANT:  Sinacore, Martin S.
 APPLICANT:  Leonard, Mark W.
 APPLICANT:  Brown, Eugene L.
 APPLICANT:  Miller, Christopher P.
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
 TITLE OF INVENTION:  TO MONITOR GENE EXPRESSION
 FILE REFERENCE: 01997.027701
 CURRENT APPLICATION NUMBER: US/11/128,061
 CURRENT FILING DATE:  2005-05-11
 PRIOR APPLICATION NUMBER: US 60/570,425
 PRIOR FILING DATE: 2004-05-11
 NUMBER OF SEQ ID NOS: 7285
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 661
  LENGTH: 399
  TYPE: DNA
  ORGANISM: Mesocricetus auratus
-11-128-061-661

ignment Scores:
ed. No.:              1.98e-10       Length:         399
ore:                  20.00          Matches:        20
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            6.1%           Indels:         0
:                     16             Gaps:           0

-10-821-670A-30 (1-329) x US-11-128-061-661 (1-399)

       135 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182

SULT 85
-11-128-061-4303
Sequence 4303, Application US/11128061
Publication No. US20060003958A1
GENERAL INFORMATION:
 APPLICANT: Melville, Mark W.
 APPLICANT:  Charlebois, Timothy S.
 APPLICANT:  Mounts, William M.
 APPLICANT:  Hann, Louane E.
 APPLICANT:  Sinacore, Martin S.
 APPLICANT:  Leonard, Mark W.
 APPLICANT:  Brown, Eugene L.
 APPLICANT:  Miller, Christopher P.
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
 TITLE OF INVENTION:  TO MONITOR GENE EXPRESSION
 FILE REFERENCE: 01997.027701
 CURRENT APPLICATION NUMBER: US/11/128,061
 CURRENT FILING DATE:  2005-05-11
 PRIOR APPLICATION NUMBER: US 60/570,425
 PRIOR FILING DATE: 2004-05-11
 NUMBER OF SEQ ID NOS: 7285
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 4303
  LENGTH: 399
  TYPE: DNA
  ORGANISM: Mesocricetus auratus
-11-128-061-4303

Alignment Scores:
Pred. No.:              1.98e-10       Length:         399
Score:                  20.00          Matches:        20
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            6.1%           Indels:         0
DB:                     16             Gaps:           0

US-10-821-670A-30 (1-329) x US-11-128-061-4303 (1-399)

Qy         135 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182

RESULT 86
US-11-128-049-661
; Sequence 661, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
;  TITLE OF INVENTION:  MAKING AND USING SAME
;  FILE REFERENCE: 01997.027700
;  CURRENT APPLICATION NUMBER: US/11/128,049
;  CURRENT FILING DATE:  2005-05-11
;  PRIOR APPLICATION NUMBER: US 60/570,425
;  PRIOR FILING DATE: 2004-05-11
;  NUMBER OF SEQ ID NOS: 7285
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 661
;   LENGTH: 399
;   TYPE: DNA
;   ORGANISM: Mesocricetus auratus
US-11-128-049-661

Alignment Scores:
Pred. No.:              1.98e-10       Length:         399
Score:                  20.00          Matches:        20
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            6.1%           Indels:         0
DB:                     16             Gaps:           0

US-10-821-670A-30 (1-329) x US-11-128-049-661 (1-399)

Qy         135 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182

RESULT 87
US-11-128-049-4303
; Sequence 4303, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
;  TITLE OF INVENTION:  MAKING AND USING SAME
;  FILE REFERENCE: 01997.027700
;  CURRENT APPLICATION NUMBER: US/11/128,049
```

CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
EQ ID NO 4303
LENGTH: 399
TYPE: DNA
ORGANISM: Mesocricetus auratus
11-128-049-4303

gnment Scores:

d. No.:	1.98e-10	Length:	399
re:	20.00	Matches:	20
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	6.1%	Indels:	0
	16	Gaps:	0

10-821-670A-30 (1-329) x US-11-128-049-4303 (1-399)

```
        135 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182
```

ULT 88
10-029-386-3133/c
equence 3133, Application US/10029386
ublication No. US20030194704A1
ENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
EQ ID NO 3133
LENGTH: 556
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR5.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 5.00e-43
OTHER INFORMATION: EST_HUMAN HIT: BG389008.1, EVALUE 2.00e-01
10-029-386-3133

gnment Scores:

d. No.:	2.68e-10	Length:	556
re:	20.00	Matches:	20
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	6.1%	Indels:	0
	7	Gaps:	0

10-821-670A-30 (1-329) x US-10-029-386-3133 (1-556)

```
         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        362 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 303
```

ULT 89
09-823-549-77
equence 77, Application US/09823549
ublication No. US20020147998A1
; GENERAL INFORMATION:
; APPLICANT: McConlogue, Lisa C
; APPLICANT: Games, Kate D.
; APPLICANT: Yednock, Theodore A.
; APPLICANT: Hua, Tan
; APPLICANT: Messersmith, Elizabeth
; APPLICANT: Bard, Frederique
; TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
; FILE REFERENCE: 015270-009110US
; CURRENT APPLICATION NUMBER: US/09/823,549
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,847
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-12 p40, #1 marker
US-09-823-549-77

Alignment Scores:

Pred. No.:	5.6e-08	Length:	73
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.2%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-30 (1-329) x US-09-823-549-77 (1-73)

```
Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59
```

RESULT 90
US-10-685-992-77
; Sequence 77, Application US/10685992
; Publication No. US20040213739A1
; GENERAL INFORMATION:
; APPLICANT: McConlogue, Lisa C
; APPLICANT: Games, Kate D.
; APPLICANT: Yednock, Theodore A.
; APPLICANT: Hua, Tan
; APPLICANT: Messersmith, Elizabeth
; APPLICANT: Bard, Frederique
; TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
; FILE REFERENCE: 015270-009110US
; CURRENT APPLICATION NUMBER: US/10/685,992
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US/09/823,549
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,847
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-12 p40, #1 marker
US-10-685-992-77

Alignment Scores:

Pred. No.:	5.6e-08	Length:	73
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.2%	Indels:	0
DB:	9	Gaps:	0

-10-821-670A-30 (1-329) x US-10-685-992-77 (1-73)

```
        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
          9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59
```

SULT 91
-11-136-527-4408
Sequence 4408, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4408
LENGTH: 600
TYPE: DNA
ORGANISM: Rattus norvegicus
-11-136-527-4408

ignment Scores:

ed. No.:	3.85e-07	Length:	600
ore:	17.00	Matches:	17
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	5.2%	Indels:	0
:	16	Gaps:	0

-10-821-670A-30 (1-329) x US-11-136-527-4408 (1-600)

```
        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
        262 AGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAG 312
```

SULT 92
-11-136-527-312
Sequence 312, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 312
LENGTH: 1024
TYPE: DNA
ORGANISM: Rattus norvegicus
-11-136-527-312

ignment Scores:

ed. No.:	6.28e-07	Length:	1024
ore:	17.00	Matches:	17
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	5.2%	Indels:	0
:	16	Gaps:	0

-10-821-670A-30 (1-329) x US-11-136-527-312 (1-1024)

```
Qy      227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      686 AGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAG 736
```

RESULT 93
US-10-603-064-3
; Sequence 3, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1409
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-10-603-064-3

Alignment Scores:

Pred. No.:	8.41e-07	Length:	1409
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.2%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-603-064-3 (1-1409)

```
Qy      227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740
```

RESULT 94
US-10-603-064-2
; Sequence 2, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-2

Alignment Scores:

Pred. No.:	8.75e-07	Length:	1472
Score:	17.00	Matches:	17

```
:cent Similarity:     100.0%          Conservative:  0
:t Local Similarity:  100.0%          Mismatches:    0
:ry Match:            5.2%            Indels:        0
                      8               Gaps:          0

:10-821-670A-30 (1-329) x US-10-603-064-2 (1-1472)

       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
       690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740

:ULT 95
 10-603-064-12
:equence 12, Application US/10603064
 ublication No. US20040072299A1
:ENERAL INFORMATION:
 APPLICANT: Gillies, Stephen
 APPLICANT:  Lo, Kin Ming
 TITLE OF INVENTION: Multiple Cytokine Protein Complexes
 FILE REFERENCE: LEX-010
 CURRENT APPLICATION NUMBER: US/10/603,064
 CURRENT FILING DATE:  2003-06-24
 PRIOR APPLICATION NUMBER: US/09/634,368
 PRIOR FILING DATE: 2000-08-09
 PRIOR APPLICATION NUMBER: 60/147,924
 PRIOR FILING DATE: 1999-08-09
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.0
:EQ ID NO 12
  LENGTH: 1569
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: murine
  OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
 10-603-064-12

 gnment Scores:
:d. No.:              9.27e-07        Length:        1569
:re:                  17.00           Matches:       17
:cent Similarity:     100.0%          Conservative:  0
:t Local Similarity:  100.0%          Mismatches:    0
:ry Match:            5.2%            Indels:        0
                      8               Gaps:          0

 10-821-670A-30 (1-329) x US-10-603-064-12 (1-1569)

       227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
      1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

:ULT 96
 10-742-405-5
:equence 5, Application US/10742405
:ublication No. US20040213761A1
:ENERAL INFORMATION:
 APPLICANT: Bowman, Edward P.
 APPLICANT:  Chan, Jason R.
 APPLICANT:  Moore, Kevin
 APPLICANT:  Nguyen, Nhung
 APPLICANT:  Churakova, Tatyana
 APPLICANT:  Chen, Shi-Juan
 APPLICANT:  Cua, Daniel J.
 TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
 FILE REFERENCE: DX01578K
 CURRENT APPLICATION NUMBER: US/10/742,405
 CURRENT FILING DATE:  2003-12-18
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn version 3.2
:EQ ID NO 5
  LENGTH: 1610
  TYPE: DNA
  ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1599)
US-10-742-405-5

Alignment Scores:
Pred. No.:              9.5e-07         Length:        1610
Score:                  17.00           Matches:       17
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            5.2%            Indels:        0
DB:                     9               Gaps:          0

US-10-821-670A-30 (1-329) x US-10-742-405-5 (1-1610)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 732

RESULT 97
US-10-172-399-3
; Sequence 3, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTHE
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1840
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (35)..(1042)
US-10-172-399-3

Alignment Scores:
Pred. No.:              1.07e-06        Length:        1840
Score:                  17.00           Matches:       17
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            5.2%            Indels:        0
DB:                     6               Gaps:          0

US-10-821-670A-30 (1-329) x US-10-172-399-3 (1-1840)

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 754

RESULT 98
US-10-603-064-11
; Sequence 11, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
```

SEQ ID NO 11
LENGTH: 2013
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
-10-603-064-11

ignment Scores:

ed. No.:	1.16e-06	Length:	2013
ore:	17.00	Matches:	17
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	5.2%	Indels:	0
:	8	Gaps:	0

-10-821-670A-30 (1-329) x US-10-603-064-11 (1-2013)

```
        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
       1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281
```

SULT 99
-10-603-064-13
Sequence 13, Application US/10603064
Publication No. US20040072299A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/10/603,064
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/634,368
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 2709
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
OTHER INFORMATION: sequence
-10-603-064-13

ignment Scores:

ed. No.:	1.53e-06	Length:	2709
ore:	17.00	Matches:	17
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	5.2%	Indels:	0
:	8	Gaps:	0

-10-821-670A-30 (1-329) x US-10-603-064-13 (1-2709)

```
        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
       1927 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1977
```

SULT 100
-10-136-837-3
Sequence 3, Application US/10136837
Publication No. US20030181405A1
GENERAL INFORMATION:
APPLICANT: NORDSTROM, Jeffrey L
APPLICANT: PERICLE, Federica
APPLICANT: ROLLAND, Alain
APPLICANT: RALSTON, Robert

; TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 273/082 (GM15-1USC1)
; CURRENT APPLICATION NUMBER: US/10/136,837
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/268,135
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5966
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse IL-12 pIN0961
US-10-136-837-3

Alignment Scores:

Pred. No.:	3.15e-06	Length:	5966
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.2%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-136-837-3 (1-5966)

```
Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5343 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 5393
```

Search completed: June 12, 2006, 17:16:27
Job time : 1613.84 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: June 10, 2006, 02:09:37 ; Search time 22.4223 Seconds
(without alignments)
2793.504 Million cell updates/sec

tle: US-10-821-670A-30
rfect score: 329
quence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

oring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

arched: 253354 seqs, 63461778 residues

rd size: 1

tal number of hits satisfying chosen parameters: 506227

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Listing first 200 summaries

mmand line parameters:
ODEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10821670/runat_07062006_110508_27905/app_query.fasta_1
B=Published_Applications_NA_New -QFMT=fastap
UFFIX=oligo.p2n.200scores.rnpbn -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
NITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
OCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
ORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
SER=US10821670_@CGN_1_1_62_@runat_07062006_110508_27905 -NCPU=6 -ICPU=3
O_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
GAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

tabase : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	9	2.7	3284	7	US-11-293-697-630	Sequence 630, App
2	8	2.4	2115	7	US-11-217-529-76502	Sequence 76502, A
3	8	2.4	5874	7	US-11-313-450-15	Sequence 15, Appl
4	7	2.1	334	6	US-10-560-723-28	Sequence 28, Appl
5	7	2.1	442	6	US-10-953-349-33510	Sequence 33510, A
6	7	2.1	522	7	US-11-217-529-78298	Sequence 78298, A
7	7	2.1	528	7	US-11-217-529-4334	Sequence 4334, Ap
8	7	2.1	595	6	US-10-953-349-6086	Sequence 6086, Ap
9	7	2.1	819	6	US-10-471-571A-635	Sequence 635, App
10	7	2.1	849	6	US-10-471-571A-5423	Sequence 5423, Ap
c 11	7	2.1	939	6	US-10-953-349-32992	Sequence 32992, A
c 12	7	2.1	975	7	US-11-217-529-79951	Sequence 79951, A
13	7	2.1	1005	6	US-10-953-349-802	Sequence 802, App
14	7	2.1	1035	6	US-10-953-349-8097	Sequence 8097, Ap
c 15	7	2.1	1043	6	US-10-953-349-28829	Sequence 28829, A
c 16	7	2.1	1092	7	US-11-217-529-4663	Sequence 4663, Ap
c 17	7	2.1	1158	7	US-11-217-529-77622	Sequence 77622, A
18	7	2.1	1161	7	US-11-297-134-9	Sequence 9, Appli
c 19	7	2.1	1176	6	US-10-953-349-8850	Sequence 8850, Ap
c 20	7	2.1	1184	6	US-10-953-349-20842	Sequence 20842, A
c 21	7	2.1	1209	7	US-11-217-529-4209	Sequence 4209, Ap
22	7	2.1	1237	6	US-10-953-349-21311	Sequence 21311, A
c 23	7	2.1	1273	6	US-10-953-349-21541	Sequence 21541, A
24	7	2.1	1584	7	US-11-217-529-75662	Sequence 75662, A
c 25	7	2.1	1636	6	US-10-953-349-17465	Sequence 17465, A
26	7	2.1	1651	7	US-11-145-307A-256	Sequence 256, App
c 27	7	2.1	1690	6	US-10-953-349-18501	Sequence 18501, A
28	7	2.1	1717	6	US-10-953-349-33266	Sequence 33266, A
c 29	7	2.1	1728	7	US-11-217-529-78959	Sequence 78959, A
c 30	7	2.1	1737	7	US-11-217-529-81980	Sequence 81980, A
31	7	2.1	1758	7	US-11-217-529-1188	Sequence 1188, Ap
c 32	7	2.1	1956	7	US-11-217-529-76747	Sequence 76747, A
33	7	2.1	2121	7	US-11-217-529-78482	Sequence 78482, A
34	7	2.1	2148	7	US-11-217-529-2300	Sequence 2300, Ap
35	7	2.1	2240	6	US-10-953-349-11671	Sequence 11671, A
c 36	7	2.1	2259	7	US-11-293-697-1478	Sequence 1478, Ap
37	7	2.1	2304	7	US-11-121-154-64	Sequence 64, Appl
c 38	7	2.1	2507	6	US-10-953-349-9838	Sequence 9838, Ap
c 39	7	2.1	2508	7	US-11-293-697-1575	Sequence 1575, Ap
c 40	7	2.1	2616	6	US-10-471-571A-4673	Sequence 4673, Ap
41	7	2.1	2787	6	US-10-471-571A-2597	Sequence 2597, Ap
c 42	7	2.1	2825	7	US-11-293-697-1497	Sequence 1497, Ap
43	7	2.1	2857	6	US-10-196-749-105	Sequence 105, App
c 44	7	2.1	2871	6	US-10-511-455-40	Sequence 40, Appl
c 45	7	2.1	3226	7	US-11-293-697-723	Sequence 723, App
c 46	7	2.1	3624	7	US-11-217-529-3816	Sequence 3816, Ap
c 47	7	2.1	3678	7	US-11-217-529-309	Sequence 309, App
c 48	7	2.1	5934	7	US-11-313-450-13	Sequence 13, Appl
c 49	7	2.1	6371	7	US-11-251-465-8	Sequence 8, Appli
c 50	7	2.1	39536	6	US-10-857-260-27	Sequence 27, Appl
c 51	7	2.1	56580	6	US-10-553-298-1	Sequence 1, Appli
c 52	7	2.1	394191	6	US-10-506-549-3	Sequence 3, Appli
c 53	6	1.8	20	7	US-11-266-409-12	Sequence 12, Appl
54	6	1.8	25	7	US-11-217-529-9246	Sequence 9246, Ap
55	6	1.8	25	7	US-11-217-529-18480	Sequence 18480, A
56	6	1.8	25	7	US-11-217-529-19397	Sequence 19397, A
c 57	6	1.8	25	7	US-11-217-529-31190	Sequence 31190, A
58	6	1.8	25	7	US-11-217-529-36523	Sequence 36523, A
c 59	6	1.8	25	7	US-11-217-529-36968	Sequence 36968, A
c 60	6	1.8	25	7	US-11-217-529-43878	Sequence 43878, A
61	6	1.8	25	7	US-11-217-529-48094	Sequence 48094, A
62	6	1.8	25	7	US-11-217-529-50534	Sequence 50534, A
c 63	6	1.8	25	7	US-11-217-529-71800	Sequence 71800, A
c 64	6	1.8	25	7	US-11-217-529-82993	Sequence 82993, A
65	6	1.8	25	7	US-11-217-529-88008	Sequence 88008, A
66	6	1.8	25	7	US-11-217-529-89000	Sequence 89000, A
67	6	1.8	25	7	US-11-217-529-106446	Sequence 106446,
c 68	6	1.8	25	7	US-11-217-529-107708	Sequence 107708,
c 69	6	1.8	25	7	US-11-217-529-112662	Sequence 112662,
c 70	6	1.8	25	7	US-11-217-529-123888	Sequence 123888,
c 71	6	1.8	25	7	US-11-217-529-134360	Sequence 134360,
72	6	1.8	25	7	US-11-217-529-142444	Sequence 142444,
73	6	1.8	25	7	US-11-217-529-144453	Sequence 144453,
c 74	6	1.8	25	7	US-11-217-529-152420	Sequence 152420,
75	6	1.8	72	7	US-11-267-871-456	Sequence 456, App
c 76	6	1.8	72	7	US-11-267-871-456	Sequence 456, App
c 77	6	1.8	177	7	US-11-217-529-79352	Sequence 79352, A
c 78	6	1.8	198	6	US-10-471-571A-5615	Sequence 5615, Ap
79	6	1.8	240	7	US-11-244-678-7	Sequence 7, Appli
c 80	6	1.8	243	7	US-11-217-529-147	Sequence 147, App
81	6	1.8	243	7	US-11-217-529-80845	Sequence 80845, A
82	6	1.8	267	7	US-11-217-529-166793	Sequence 166793,

83	6	1.8	273	6	US-10-471-571A-2941	Sequence 2941, Ap
84	6	1.8	279	6	US-10-512-190-1	Sequence 1, Appli
85	6	1.8	294	6	US-10-511-814-9	Sequence 9, Appli
86	6	1.8	294	6	US-10-511-814-10	Sequence 10, Appl
87	6	1.8	294	6	US-10-511-814-12	Sequence 12, Appl
88	6	1.8	294	6	US-10-511-814-13	Sequence 13, Appl
89	6	1.8	297	7	US-11-217-529-81028	Sequence 81028, A
90	6	1.8	303	7	US-11-217-529-5663	Sequence 5663, Ap
91	6	1.8	303	7	US-11-217-529-174215	Sequence 174215,
92	6	1.8	306	7	US-11-217-529-190938	Sequence 190938,
93	6	1.8	306	7	US-11-321-421-87	Sequence 87, Appl
94	6	1.8	309	7	US-11-217-529-81582	Sequence 81582, A
95	6	1.8	312	7	US-11-217-529-75899	Sequence 75899, A
96	6	1.8	315	6	US-10-488-619-794	Sequence 794, App
97	6	1.8	324	7	US-11-217-529-76199	Sequence 76199, A
98	6	1.8	324	7	US-11-023-959A-118	Sequence 118, App
99	6	1.8	332	6	US-10-488-619-375	Sequence 375, App
100	6	1.8	339	7	US-11-217-529-77451	Sequence 77451, A
101	6	1.8	339	7	US-11-217-529-166940	Sequence 166940,
102	6	1.8	348	6	US-10-488-619-499	Sequence 499, App
103	6	1.8	348	7	US-11-217-529-77235	Sequence 77235, A
104	6	1.8	357	7	US-11-217-529-6132	Sequence 6132, Ap
105	6	1.8	365	6	US-10-992-149-2	Sequence 2, Appli
106	6	1.8	369	6	US-10-499-266-11	Sequence 11, Appl
107	6	1.8	379	6	US-10-994-679-63	Sequence 63, Appl
108	6	1.8	386	7	US-11-301-554-442	Sequence 442, App
109	6	1.8	387	7	US-11-217-529-78662	Sequence 78662, A
110	6	1.8	387	7	US-11-217-529-80425	Sequence 80425, A
111	6	1.8	393	7	US-11-217-529-76946	Sequence 76946, A
112	6	1.8	396	7	US-11-217-529-82136	Sequence 82136, A
113	6	1.8	402	7	US-11-217-529-75995	Sequence 75995, A
114	6	1.8	406	7	US-11-301-554-381	Sequence 381, App
115	6	1.8	406	7	US-11-301-554-898	Sequence 898, App
116	6	1.8	420	7	US-11-255-980-6	Sequence 6, Appli
117	6	1.8	423	7	US-11-217-529-3397	Sequence 3397, Ap
118	6	1.8	427	6	US-10-488-619-1587	Sequence 1587, Ap
119	6	1.8	435	7	US-11-217-529-5980	Sequence 5980, Ap
120	6	1.8	436	6	US-10-488-619-552	Sequence 552, App
121	6	1.8	438	6	US-10-488-619-1590	Sequence 1590, Ap
122	6	1.8	441	6	US-10-468-193-6	Sequence 6, Appli
123	6	1.8	444	7	US-11-217-529-82599	Sequence 82599, A
124	6	1.8	447	7	US-11-217-529-166970	Sequence 166970,
125	6	1.8	449	6	US-10-511-937-2873	Sequence 2873, Ap
126	6	1.8	450	6	US-10-471-571A-3305	Sequence 3305, Ap
127	6	1.8	456	6	US-10-488-619-1794	Sequence 1794, Ap
128	6	1.8	461	7	US-11-301-554-965	Sequence 965, App
129	6	1.8	462	6	US-10-473-173-248	Sequence 248, App
130	6	1.8	465	7	US-11-322-999-14	Sequence 14, Appl
131	6	1.8	471	6	US-10-488-619-417	Sequence 417, App
132	6	1.8	471	7	US-11-217-529-5788	Sequence 5788, Ap
133	6	1.8	474	7	US-11-217-529-3216	Sequence 3216, Ap
134	6	1.8	478	6	US-10-505-928-542	Sequence 542, App
135	6	1.8	483	7	US-11-219-563-141	Sequence 141, App
136	6	1.8	483	7	US-11-301-554-1239	Sequence 1239, Ap
137	6	1.8	487	7	US-11-301-554-1263	Sequence 1263, Ap
138	6	1.8	492	7	US-11-301-554-928	Sequence 928, App
139	6	1.8	498	6	US-10-488-619-564	Sequence 564, App
140	6	1.8	498	7	US-11-217-529-5867	Sequence 5867, Ap
141	6	1.8	499	6	US-10-953-349-15009	Sequence 15009, A
142	6	1.8	500	7	US-11-249-305-1	Sequence 1, Appli
143	6	1.8	500	7	US-11-249-305-2	Sequence 2, Appli
144	6	1.8	500	7	US-11-249-305-3	Sequence 3, Appli
145	6	1.8	500	7	US-11-249-305-4	Sequence 4, Appli
146	6	1.8	501	7	US-11-136-524-79	Sequence 79, Appl
147	6	1.8	509	6	US-10-953-349-217	Sequence 217, App
148	6	1.8	510	7	US-11-136-524-37	Sequence 37, Appl
149	6	1.8	510	7	US-11-217-529-2274	Sequence 2274, Ap
150	6	1.8	510	7	US-11-217-529-78451	Sequence 78451, A
151	6	1.8	513	7	US-11-217-529-79024	Sequence 79024, A
152	6	1.8	518	7	US-11-301-554-371	Sequence 371, App
153	6	1.8	518	7	US-11-301-554-1203	Sequence 1203, Ap
154	6	1.8	526	7	US-11-301-554-1218	Sequence 1218, Ap
155	6	1.8	537	6	US-10-471-571A-2883	Sequence 2883, Ap
156	6	1.8	538	6	US-10-488-619-2515	Sequence 2515, Ap
c 157	6	1.8	541	6	US-10-560-723-113	Sequence 113, App
158	6	1.8	543	7	US-11-301-554-956	Sequence 956, App
159	6	1.8	543	7	US-11-217-529-5827	Sequence 5827, Ap
160	6	1.8	549	7	US-11-301-554-359	Sequence 359, App
c 161	6	1.8	555	6	US-10-471-571A-4635	Sequence 4635, Ap
c 162	6	1.8	555	7	US-11-217-529-79490	Sequence 79490, A
163	6	1.8	557	7	US-11-301-554-848	Sequence 848, App
c 164	6	1.8	562	6	US-10-488-619-1255	Sequence 1255, Ap
c 165	6	1.8	564	6	US-10-488-619-1992	Sequence 1992, Ap
c 166	6	1.8	579	6	US-10-473-173-108	Sequence 108, App
167	6	1.8	581	7	US-11-301-951-7	Sequence 7, Appli
168	6	1.8	584	6	US-10-953-349-1733	Sequence 1733, Ap
169	6	1.8	591	6	US-10-488-619-1230	Sequence 1230, Ap
c 170	6	1.8	591	7	US-11-301-554-1122	Sequence 1122, Ap
c 171	6	1.8	593	6	US-10-953-349-25340	Sequence 25340, A
172	6	1.8	594	7	US-11-301-554-1751	Sequence 1751, Ap
173	6	1.8	596	6	US-10-488-619-2778	Sequence 2778, Ap
174	6	1.8	597	6	US-10-488-619-1332	Sequence 1332, Ap
c 175	6	1.8	597	6	US-10-488-619-2832	Sequence 2832, Ap
176	6	1.8	597	6	US-10-471-571A-2843	Sequence 2843, Ap
177	6	1.8	597	7	US-11-217-529-77932	Sequence 77932, A
178	6	1.8	602	6	US-10-488-619-1740	Sequence 1740, Ap
179	6	1.8	606	6	US-10-953-349-27873	Sequence 27873, A
c 180	6	1.8	607	6	US-10-488-619-1738	Sequence 1738, Ap
c 181	6	1.8	610	6	US-10-488-619-2390	Sequence 2390, Ap
182	6	1.8	615	7	US-11-217-529-2766	Sequence 2766, Ap
183	6	1.8	618	6	US-10-953-349-5623	Sequence 5623, Ap
184	6	1.8	621	7	US-11-217-529-76434	Sequence 76434, A
185	6	1.8	625	6	US-10-953-349-2892	Sequence 2892, Ap
c 186	6	1.8	627	6	US-10-953-349-30134	Sequence 30134, A
c 187	6	1.8	627	6	US-10-471-571A-3259	Sequence 3259, Ap
188	6	1.8	633	6	US-10-953-349-8180	Sequence 8180, Ap
189	6	1.8	633	6	US-10-953-349-28624	Sequence 28624, A
190	6	1.8	634	7	US-11-301-554-23	Sequence 23, Appl
191	6	1.8	635	6	US-10-488-619-2164	Sequence 2164, Ap
c 192	6	1.8	636	6	US-10-953-349-6142	Sequence 6142, Ap
c 193	6	1.8	640	6	US-10-953-349-31246	Sequence 31246, A
c 194	6	1.8	641	6	US-10-488-619-1891	Sequence 1891, Ap
195	6	1.8	642	7	US-11-217-529-2277	Sequence 2277, Ap
196	6	1.8	657	7	US-11-217-529-173805	Sequence 173805,
197	6	1.8	660	7	US-11-217-529-80548	Sequence 80548, A
c 198	6	1.8	663	6	US-10-953-349-3111	Sequence 3111, Ap
c 199	6	1.8	668	6	US-10-953-349-39726	Sequence 39726, A
200	6	1.8	669	6	US-10-488-619-1764	Sequence 1764, Ap

ALIGNMENTS

RESULT 1
US-11-293-697-630/c
; Sequence 630, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 630
; LENGTH: 3284
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-630

Alignment Scores:

Pred. No.:	7.83	Length:	3284
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0

```
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            2.7%            Indels:        0
:                     7               Gaps:          0

-10-821-670A-30 (1-329) x US-11-293-697-630 (1-3284)

       101 PheLeuLeuIleHisLysLysGluAsp 109
           ||||||||||||||||||||||||||||
      1053 TTTTTACTGATTCACAAAAAGGAAGAC 1027

SULT 2
-11-217-529-76502
Sequence 76502, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 76502
  LENGTH: 2115
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
-11-217-529-76502

ignment Scores:
ed. No.:              54.9            Length:        2115
ore:                  8.00            Matches:       8
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            2.4%            Indels:        0
:                     7               Gaps:          0

-10-821-670A-30 (1-329) x US-11-217-529-76502 (1-2115)

       241 AsnLeuGlnLeuLysProLeuLys 248
           ||||||||||||||||||||||||||
       136 AATTTGCAACTTAAACCACTGAAA 159

SULT 3
-11-313-450-15/c
Sequence 15, Application US/11313450
Publication No. US20060110778A1
GENERAL INFORMATION:
 APPLICANT: Adorante, Joeseph S.
 APPLICANT:  Ehring, George R.
 TITLE OF INVENTION: High-Throughput Screens For Identifying
 TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
 FILE REFERENCE: 17407 CIP (AP)
 CURRENT APPLICATION NUMBER: US/11/313,450
 CURRENT FILING DATE:  2005-12-19
 PRIOR APPLICATION NUMBER: 09/989797
 PRIOR FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/252771
 PRIOR FILING DATE: 2000-11-22
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
  LENGTH: 5874
  TYPE: DNA
  ORGANISM: Homo sapiens
-11-313-450-15

Alignment Scores:
Pred. No.:            136             Length:        5874
Score:                8.00            Matches:       8
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          2.4%            Indels:        0
DB:                   7               Gaps:          0

US-10-821-670A-30 (1-329) x US-11-313-450-15 (1-5874)

Qy          12 SerLeuValLeuLeuAlaProPro 19
               |||||||||||||||||||||||
Db        1309 TCCCTAGTGCTGCTAGCACCTCCT 1286

RESULT 4
US-10-560-723-28
; Sequence 28, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
;  APPLICANT: EXONHIT THERAPEUTICALS
;  TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
;  TITLE OF INVENTION:  CANCER THERAPY AND DIAGNOSIS
;  FILE REFERENCE: B0213WO
;  CURRENT APPLICATION NUMBER: US/10/560,723
;  CURRENT FILING DATE:  2005-12-15
;  NUMBER OF SEQ ID NOS: 185
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 334
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-560-723-28

Alignment Scores:
Pred. No.:            111             Length:        334
Score:                7.00            Matches:       7
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          2.1%            Indels:        0
DB:                   6               Gaps:          0

US-10-821-670A-30 (1-329) x US-10-560-723-28 (1-334)

Qy         144 TrpLeuThrAlaIleSerThr 150
               |||||||||||||||||||||
Db          27 TGGCTCACTGCAATCTCCACC 47

RESULT 5
US-10-953-349-33510/c
; Sequence 33510, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33510
;   LENGTH: 442
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-33510

Alignment Scores:
Pred. No.:            142             Length:        442
Score:                7.00            Matches:       7
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          2.1%            Indels:        0
DB:                   6               Gaps:          0
```

10-821-670A-30 (1-329) x US-10-953-349-33510 (1-442)

```
        14 ValLeuLeuAlaProProLeu 20
           ||||||||||||||||||||
        77 GTGCTCCTTGCTCCTCCTCTT 57
```

ULT 6
11-217-529-78298/c
equence 78298, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 78298
LENGTH: 522
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-78298

gnment Scores:

d. No.:	164	Length:	522
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.1%	Indels:	0
	7	Gaps:	0

10-821-670A-30 (1-329) x US-11-217-529-78298 (1-522)

```
        11 PheSerLeuValLeuLeuAla 17
           ||||||||||||||||||||
        44 TTCTCTCTTGTACTATTAGCA 24
```

ULT 7
11-217-529-4334/c
equence 4334, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 4334
LENGTH: 528
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-4334

gnment Scores:

d. No.:	166	Length:	528
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-4334 (1-528)

```
Qy         12 SerLeuValLeuLeuAlaPro 18
              ||||||||||||||||||||
Db        392 TCATTGGTACTGCTAGCTCCG 372
```

RESULT 8
US-10-953-349-6086/c
; Sequence 6086, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6086
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6086

Alignment Scores:

Pred. No.:	185	Length:	595
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-953-349-6086 (1-595)

```
Qy        154 PheThrValLysSerSerArg 160
              |||||||||||||||||||||
Db        354 TTTACTGTGAAGTCTAGTCGT 334
```

RESULT 9
US-10-471-571A-635/c
; Sequence 635, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 635
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-635

Alignment Scores:

Pred. No.:	245	Length:	819
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

-10-821-670A-30 (1-329) x US-10-471-571A-635 (1-819)

```
       157 LysSerSerArgGlySerSer 163
           ||||||||||||||||||||
       359 AAATCTTCCCGTGGGTCATCA 339
```

SULT 10
-10-471-571A-5423
Sequence 5423, Application US/10471571A
Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 5423
LENGTH: 849
TYPE: DNA
ORGANISM: Staphylococcus aureus
-10-471-571A-5423

ignment Scores:			
ed. No.:	253	Length:	849
ore:	7.00	Matches:	7
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.1%	Indels:	0
:	6	Gaps:	0

-10-821-670A-30 (1-329) x US-10-471-571A-5423 (1-849)

```
       121 LysGluSerLysAsnLysIle 127
           ||||||||||||||||||||
       223 AAAGAATCTAAAAATAAGATT 243
```

SULT 11
-10-953-349-32992/c
Sequence 32992, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 32992
LENGTH: 939
TYPE: DNA
ORGANISM: Zea mays subsp. mays
-10-953-349-32992

ignment Scores:			
ed. No.:	277	Length:	939
ore:	7.00	Matches:	7
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.1%	Indels:	0
:	6	Gaps:	0

-10-821-670A-30 (1-329) x US-10-953-349-32992 (1-939)

```
       202 AlaAlaGluGluSerLeuPro 208
           ||||||||||||||||||||
       141 GCGGCTGAAGAGAGCCTGCCT 121
```

RESULT 12
US-11-217-529-79951/c
; Sequence 79951, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79951
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79951

Alignment Scores:			
Pred. No.:	286	Length:	975
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-79951 (1-975)

```
Qy          11 PheSerLeuValLeuLeuAla 17
               ||||||||||||||||||||
Db         424 TTTTCATTAGTGCTGCTGGCG 404
```

RESULT 13
US-10-953-349-802
; Sequence 802, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 802
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-802

Alignment Scores:			
Pred. No.:	294	Length:	1005
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-953-349-802 (1-1005)

```
Qy          96 ValLeuSerHisSerPheLeu 102
               ||||||||||||||||||||
Db         920 GTGTTATCACACTCTTTTCTT 940
```

RESULT 14

```
10-953-349-8097
equence 8097, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
EQ ID NO 8097
  LENGTH: 1035
  TYPE: DNA
  ORGANISM: Arabidopsis thaliana
 10-953-349-8097

gnment Scores:
d. No.:               302           Length:        1035
re:                   7.00          Matches:       7
cent Similarity:      100.0%        Conservative:  0
t Local Similarity:   100.0%        Mismatches:    0
ry Match:             2.1%          Indels:        0
                      6             Gaps:          0

10-821-670A-30 (1-329) x US-10-953-349-8097 (1-1035)

         66 SerGluValLeuGlySerGly 72
            ||||||||||||||||||||||
        142 TCTGAAGTCCTTGGAAGCGGC 162

ULT 15
10-953-349-28829/c
equence 28829, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
EQ ID NO 28829
  LENGTH: 1043
  TYPE: DNA
  ORGANISM: Triticum aestivum
 10-953-349-28829

gnment Scores:
d. No.:               304           Length:        1043
re:                   7.00          Matches:       7
cent Similarity:      100.0%        Conservative:  0
t Local Similarity:   100.0%        Mismatches:    0
ry Match:             2.1%          Indels:        0
                      6             Gaps:          0

 10-821-670A-30 (1-329) x US-10-953-349-28829 (1-1043)

         11 PheSerLeuValLeuLeuAla 17
            ||||||||||||||||||||
        220 TTCTCCTTGGTGCTCTTGGCG 200

ULT 16
 11-217-529-4663/c
equence 4663, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4663
;   LENGTH: 1092
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4663

Alignment Scores:
Pred. No.:               316           Length:        1092
Score:                   7.00          Matches:       7
Percent Similarity:      100.0%        Conservative:  0
Best Local Similarity:   100.0%        Mismatches:    0
Query Match:             2.1%          Indels:        0
DB:                      7             Gaps:          0

US-10-821-670A-30 (1-329) x US-11-217-529-4663 (1-1092)

Qy         317 SerSerSerTrpSerAsnTrp 323
               |||||||||||||||||||||
Db         323 TCCTCCTCTTGGTCAAACTGG 303

RESULT 17
US-11-217-529-77622/c
; Sequence 77622, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77622
;   LENGTH: 1158
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77622

Alignment Scores:
Pred. No.:               333           Length:        1158
Score:                   7.00          Matches:       7
Percent Similarity:      100.0%        Conservative:  0
Best Local Similarity:   100.0%        Mismatches:    0
Query Match:             2.1%          Indels:        0
DB:                      7             Gaps:          0

US-10-821-670A-30 (1-329) x US-11-217-529-77622 (1-1158)

Qy         317 SerSerSerTrpSerAsnTrp 323
               |||||||||||||||||||||
Db         398 TCCTCTTCTTGGTCGAATTGG 378

RESULT 18
US-11-297-134-9
; Sequence 9, Application US/11297134
```

```
Publication No. US20060111297A1
GENERAL INFORMATION:
 APPLICANT: Genzyme Corporation
 APPLICANT:  Roberts, Bruce
 TITLE OF INVENTION: BLOOD FACTOR DOMAINS
 FILE REFERENCE: 5270C
 CURRENT APPLICATION NUMBER: US/11/297,134
 CURRENT FILING DATE:  2005-12-08
 PRIOR APPLICATION NUMBER: PCT/US2005/018461
 PRIOR FILING DATE: 2004-06-09
 PRIOR APPLICATION NUMBER: US 60/477,291
 PRIOR FILING DATE: 2003-06-09
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
  LENGTH: 1161
  TYPE: DNA
  ORGANISM: Homo sapiens
-11-297-134-9

ignment Scores:
ed. No.:                334             Length:         1161
ore:                    7.00            Matches:        7
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              2.1%            Indels:         0
:                       7               Gaps:           0

-10-821-670A-30 (1-329) x US-11-297-134-9 (1-1161)

        233 IleIleLysProAspProPro 239
            ||||||||||||||||||||
        389 ATCATCAAGCCCGACCCTCCA 409

SULT 19
-10-953-349-8850/c
Sequence 8850, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 8850
  LENGTH: 1176
  TYPE: DNA
  ORGANISM: Arabidopsis thaliana
-10-953-349-8850

ignment Scores:
ed. No.:                338             Length:         1176
ore:                    7.00            Matches:        7
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              2.1%            Indels:         0
:                       6               Gaps:           0

-10-821-670A-30 (1-329) x US-10-953-349-8850 (1-1176)

        283 AsnArgGluLysLysAspArg 289
            |||||||||||||||||||
        801 AATCGAGAAAAGAAAGATCGA 781

SULT 20
-10-953-349-20842/c
Sequence 20842, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 20842
  LENGTH: 1184
  TYPE: DNA
  ORGANISM: Glycine max
US-10-953-349-20842

Alignment Scores:
Pred. No.:              340             Length:         1184
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.1%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-953-349-20842 (1-1184)

Qy          284 ArgGluLysLysAspArgLeu 290
                ||||||||||||||||||||
Db          585 AGAGAGAAAAAGGATAGGTTG 565

RESULT 21
US-11-217-529-4209/c
Sequence 4209, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
 APPLICANT: SUNTORY LIMITED
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 4209
  LENGTH: 1209
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
US-11-217-529-4209

Alignment Scores:
Pred. No.:              346             Length:         1209
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.1%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-30 (1-329) x US-11-217-529-4209 (1-1209)

Qy          284 ArgGluLysLysAspArgLeu 290
                ||||||||||||||||||||
Db          822 AGAGAAAAAAAAGACCGCCTT 802

RESULT 22
US-10-953-349-21311
Sequence 21311, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
```

```
TITLE OF INVENTION:  ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE:  2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 21311
 LENGTH: 1237
 TYPE: DNA
 ORGANISM: Glycine max
10-953-349-21311

gnment Scores:
d. No.:                353            Length:        1237
re:                    7.00           Matches:       7
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              2.1%           Indels:        0
                       6              Gaps:          0

10-821-670A-30 (1-329) x US-10-953-349-21311 (1-1237)

        97 LeuSerHisSerPheLeuLeu 103
           ||||||||||||||||||||||
        52 CTTTCTCATTCATTCTTATTA 72

ULT 23
10-953-349-21541/c
equence 21541, Application US/10953349
ublication No. US20060107345A1
ENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION:  ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE:  2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 21541
 LENGTH: 1273
 TYPE: DNA
 ORGANISM: Glycine max
10-953-349-21541

gnment Scores:
d. No.:                362            Length:        1273
re:                    7.00           Matches:       7
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              2.1%           Indels:        0
                       6              Gaps:          0

10-821-670A-30 (1-329) x US-10-953-349-21541 (1-1273)

        13 LeuValLeuLeuAlaProPro 19
           ||||||||||||||||||||||
       238 TTGGTCCTGCTGGCACCACCA 218

ULT 24
11-217-529-75662
equence 75662, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75662
;   LENGTH: 1584
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-75662

Alignment Scores:
Pred. No.:             440            Length:        1584
Score:                 7.00           Matches:       7
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           2.1%           Indels:        0
DB:                    7              Gaps:          0

US-10-821-670A-30 (1-329) x US-11-217-529-75662 (1-1584)

Qy        213 ValAspAlaIleHisLysLeu 219
              |||||||||||||||||||||
Db       1140 GTGGACGCAATTCATAAGCTA 1160

RESULT 25
US-10-953-349-17465/c
; Sequence 17465, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17465
;   LENGTH: 1636
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-17465

Alignment Scores:
Pred. No.:             452            Length:        1636
Score:                 7.00           Matches:       7
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           2.1%           Indels:        0
DB:                    6              Gaps:          0

US-10-821-670A-30 (1-329) x US-10-953-349-17465 (1-1636)

Qy        226 SerSerPhePheIleArgAsp 232
              |||||||||||||||||||||
Db       1352 TCATCTTTCTTCATAAGAGAT 1332

RESULT 26
US-11-145-307A-256
; Sequence 256, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
```

SOFTWARE: PatentIn version 3.1
SEQ ID NO 256
LENGTH: 1651
TYPE: DNA
ORGANISM: Homo sapiens
-11-145-307A-256

ignment Scores:

ed. No.:	456	Length:	1651
ore:	7.00	Matches:	7
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.1%	Indels:	0
:	7	Gaps:	0

-10-821-670A-30 (1-329) x US-11-145-307A-256 (1-1651)

```
       218 LysLeuLysTyrGluAsnTyr 224
           ||||||||||||||||||||
      1616 AAGTTGAAATATGAAAATTAT 1636
```

SULT 27
-10-953-349-18501/c
Sequence 18501, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18501
LENGTH: 1690
TYPE: DNA
ORGANISM: Glycine max
-10-953-349-18501

ignment Scores:

ed. No.:	466	Length:	1690
ore:	7.00	Matches:	7
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.1%	Indels:	0
:	6	Gaps:	0

-10-821-670A-30 (1-329) x US-10-953-349-18501 (1-1690)

```
       238 ProProLysAsnLeuGlnLeu 244
           ||||||||||||||||||||
      1257 CCACCTAAAAATCTACAGTTG 1237
```

SULT 28
-10-953-349-33266
Sequence 33266, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 33266
LENGTH: 1717
TYPE: DNA
ORGANISM: Zea mays subsp. mays
-10-953-349-33266

Alignment Scores:

Pred. No.:	472	Length:	1717
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-953-349-33266 (1-1717)

```
Qy        233 IleIleLysProAspProPro 239
              |||||||||||||||||||||
Db        205 ATCATCAAGCCCGACCCTCCC 225
```

RESULT 29
US-11-217-529-78959/c
; Sequence 78959, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78959
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78959

Alignment Scores:

Pred. No.:	475	Length:	1728
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-78959 (1-1728)

```
Qy         12 SerLeuValLeuLeuAlaPro 18
              |||||||||||||||||||
Db        122 TCTTTAGTACTGCTTGCCCCG 102
```

RESULT 30
US-11-217-529-81980/c
; Sequence 81980, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81980

LENGTH: 1737
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
FEATURE:
NAME/KEY: modified_base
LOCATION: (1678)..(1715)
OTHER INFORMATION: a, c, g, t, unknown, or other
11-217-529-81980

gnment Scores:

d. No.:	477	Length:	1737
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.1%	Indels:	0
	7	Gaps:	0

10-821-670A-30 (1-329) x US-11-217-529-81980 (1-1737)

```
        66 SerGluValLeuGlySerGly 72
           ||||||||||||||||||||||
        30 AGCGAAGTGTTGGGTAGCGGT 10
```

ULT 31
11-217-529-1188
equence 1188, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 1188
LENGTH: 1758
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-1188

gnment Scores:

d. No.:	482	Length:	1758
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.1%	Indels:	0
	7	Gaps:	0

10-821-670A-30 (1-329) x US-11-217-529-1188 (1-1758)

```
        12 SerLeuValLeuLeuAlaPro 18
           ||||||||||||||||||||||
       133 TCATTGGTACTGCTAGCTCCG 153
```

ULT 32
11-217-529-76747/c
equence 76747, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76747
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76747

Alignment Scores:

Pred. No.:	530	Length:	1956
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-76747 (1-1956)

```
Qy         12 SerLeuValLeuLeuAlaPro 18
              ||||||||||||||||||||||
Db        130 TCTTTAGTTCTTTTAGCTCCT 110
```

RESULT 33
US-11-217-529-78482
; Sequence 78482, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78482
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78482

Alignment Scores:

Pred. No.:	570	Length:	2121
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-78482 (1-2121)

```
Qy         70 GlySerGlyLysThrLeuThr 76
              ||||||||||||||||||||
Db         85 GGCTCAGGAAAAACGCTAACG 105
```

RESULT 34
US-11-217-529-2300
; Sequence 2300, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED

```
 APPLICANT:  NAKAO, YOSHIHIRO
 APPLICANT:  NAKAMURA, NORIHISA
 APPLICANT:  KODAMA, YUKIKO
 APPLICANT:  FUJIMURA, TOMOKO
 APPLICANT:  ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: S-38-285
 CURRENT APPLICATION NUMBER: US/11/217,529
 CURRENT FILING DATE:  2005-09-02
 PRIOR APPLICATION NUMBER: US 10/932,182
 PRIOR FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
EQ ID NO 2300
  LENGTH: 2148
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
-11-217-529-2300

ignment Scores:
ed. No.:              576          Length:        2148
ore:                  7.00         Matches:       7
rcent Similarity:     100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            2.1%         Indels:        0
:                     7            Gaps:          0

-10-821-670A-30 (1-329) x US-11-217-529-2300 (1-2148)

         70 GlySerGlyLysThrLeuThr 76
            ||||||||||||||||||||
         85 GGTTCAGGAAAAACGTTGACG 105

SULT 35
-10-953-349-11671
Sequence 11671, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION:  ENCONDED THERBY
 FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE:  2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
SEQ ID NO 11671
  LENGTH: 2240
  TYPE: DNA
  ORGANISM: Arabidopsis thaliana
-10-953-349-11671

ignment Scores:
ed. No.:              598          Length:        2240
ore:                  7.00         Matches:       7
rcent Similarity:     100.0%       Conservative:  0
st Local Similarity:  100.0%       Mismatches:    0
ery Match:            2.1%         Indels:        0
:                     6            Gaps:          0

-10-821-670A-30 (1-329) x US-10-953-349-11671 (1-2240)

        104 IleHisLysLysGluAspGly 110
            ||||||||||||||||||||
       1054 ATTCATAAGAAAGAAGATGGG 1074

SULT 36
-11-293-697-1478/c
Sequence 1478, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
 APPLICANT: HELIX RESEARCH INSTITUTE
 TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1478
;   LENGTH: 2259
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1478

Alignment Scores:
Pred. No.:              602          Length:        2259
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.1%         Indels:        0
DB:                     7            Gaps:          0

US-10-821-670A-30 (1-329) x US-11-293-697-1478 (1-2259)

Qy         100 SerPheLeuLeuIleHisLys 106
               ||||||||||||||||||||
Db        1074 AGTTTCCTTTTAATCCATAAG 1054

RESULT 37
US-11-121-154-64
; Sequence 64, Application US/11121154
; Publication No. US20060105914A1
; GENERAL INFORMATION:
;  APPLICANT: TAYLOR, LARRY EDMUND
;  APPLICANT:  WEINER, RONALD M.
;  APPLICANT:  HUTCHESON, STEVEN WAYNE
;  APPLICANT:  EKBORG, NATHAN A.
;  APPLICANT:  HOWARD, MICHAEL
;  TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
;  FILE REFERENCE: 108172-00121
;  CURRENT APPLICATION NUMBER: US/11/121,154
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,971
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 214
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
;   LENGTH: 2304
;   TYPE: DNA
;   ORGANISM: Microbulbifer degradans
US-11-121-154-64

Alignment Scores:
Pred. No.:              613          Length:        2304
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.1%         Indels:        0
DB:                     7            Gaps:          0

US-10-821-670A-30 (1-329) x US-11-121-154-64 (1-2304)

Qy         316 TyrSerSerSerTrpSerAsn 322
               ||||||||||||||||||||
Db         202 TACAGTTCATCGTGGAGCAAT 222

RESULT 38
US-10-953-349-9838/c
; Sequence 9838, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
```

FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EQ ID NO 9838
LENGTH: 2507
TYPE: DNA
ORGANISM: Arabidopsis thaliana
10-953-349-9838

gnment Scores:

d. No.:	661	Length:	2507
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.1%	Indels:	0
	6	Gaps:	0

10-821-670A-30 (1-329) x US-10-953-349-9838 (1-2507)

```
        97 LeuSerHisSerPheLeuLeu 103
           ||||||||||||||||||||
       261 CTTAGCCACAGCTTCCTTCTG 241
```

ULT 39
11-293-697-1575/c
equence 1575, Application US/11293697
ublication No. US20060105376A1
ENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 1575
LENGTH: 2508
TYPE: DNA
ORGANISM: Homo sapiens
11-293-697-1575

gnment Scores:

d. No.:	661	Length:	2508
re:	7.00	Matches:	7
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	2.1%	Indels:	0
	7	Gaps:	0

10-821-670A-30 (1-329) x US-11-293-697-1575 (1-2508)

```
       225 ThrSerSerPhePheIleArg 231
           ||||||||||||||||||||
      1322 ACCTCGTCATTTTTCATCAGA 1302
```

ULT 40
10-471-571A-4673/c
equence 4673, Application US/10471571A
ublication No. US20060115490A1
ENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4673
; LENGTH: 2616
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-4673

Alignment Scores:

Pred. No.:	686	Length:	2616
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-471-571A-4673 (1-2616)

```
Qy        157 LysSerSerArgGlySerSer 163
              ||||||||||||||||||||
Db       1160 AAATCATCAAGGGGTTCTAGT 1140
```

RESULT 41
US-10-471-571A-2597
; Sequence 2597, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2597
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-2597

Alignment Scores:

Pred. No.:	726	Length:	2787
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-471-571A-2597 (1-2787)

```
Qy         70 GlySerGlyLysThrLeuThr 76
              ||||||||||||||||||||
Db        808 GGAAGTGGTAAGACGTTGACT 828
```

RESULT 42
US-11-293-697-1497/c
; Sequence 1497, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1497
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1497

ignment Scores:
ed. No.: 734 Length: 2825
ore: 7.00 Matches: 7
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 2.1% Indels: 0
: 7 Gaps: 0

-10-821-670A-30 (1-329) x US-11-293-697-1497 (1-2825)

```
       155 ThrValLysSerSerArgGly 161
           ||||||||||||||||||||
      1956 ACAGTGAAAAGCTCCCGTGGC 1936
```

SULT 43
-10-196-749-105
Sequence 105, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
APPLICANT: Baker,Kevin P.
APPLICANT: Chen,Jian
APPLICANT: Desnoyers,Luc
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Pan,James
APPLICANT: Smith,Victoria
APPLICANT: Watanabe,Colin K.
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 105
LENGTH: 2857
TYPE: DNA
ORGANISM: Homo Sapien
-10-196-749-105

ignment Scores:
ed. No.: 742 Length: 2857
ore: 7.00 Matches: 7
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 2.1% Indels: 0
: 6 Gaps: 0

-10-821-670A-30 (1-329) x US-10-196-749-105 (1-2857)

```
Qy          73 LysThrLeuThrIleGlnVal 79
               |||||||||||||||||||
Db        1571 AAGACACTAACAATTCAAGTT 1591
```

RESULT 44
US-10-511-455-40/c
; Sequence 40, Application US/10511455
; Publication No. US20060088835A1
; GENERAL INFORMATION:
; APPLICANT: Pickard, Benjamin Simon
; APPLICANT: Blackwood, Douglas
; APPLICANT: Porteous, David
; APPLICANT: Muir, Walter John
; APPLICANT: Mors, Ole
; APPLICANT: Ewald, Henrik Lykke
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
; FILE REFERENCE: 9013.63
; CURRENT APPLICATION NUMBER: US/10/511,455
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/GB03/001543
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB0207902.8
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207904.4
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207900.2
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207901.0
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0227734.1
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 2871
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-455-40

Alignment Scores:
Pred. No.: 745 Length: 2871
Score: 7.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.1% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-30 (1-329) x US-10-511-455-40 (1-2871)

```
Qy         162 SerSerAspProGlnGlyVal 168
               |||||||||||||||||||
Db          87 AGCAGCGATCCTCAAGGAGTG 67
```

RESULT 45
US-11-293-697-723/c
; Sequence 723, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 723
; LENGTH: 3226
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-723

gnment Scores:
d. No.: 826 Length: 3226
re: 7.00 Matches: 7
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 2.1% Indels: 0
7 Gaps: 0

10-821-670A-30 (1-329) x US-11-293-697-723 (1-3226)

102 LeuLeuIleHisLysLysGlu 108
||||||||||||||||||||
2295 CTACTTATCCATAAAAAGGAA 2275

ULT 46
11-217-529-3816/c
equence 3816, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 3816
LENGTH: 3624
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-3816

gnment Scores:
d. No.: 916 Length: 3624
re: 7.00 Matches: 7
cent Similarity: 100.0% Conservative: 0
t Local Similarity: 100.0% Mismatches: 0
ry Match: 2.1% Indels: 0
7 Gaps: 0

10-821-670A-30 (1-329) x US-11-217-529-3816 (1-3624)

284 ArgGluLysLysAspArgLeu 290
||||||||||||||||||||
2190 AGAGAAAAGAAAGACCGTCTT 2170

ULT 47
11-217-529-309/c
equence 309, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3

; SEQ ID NO 309
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-309

Alignment Scores:
Pred. No.: 928 Length: 3678
Score: 7.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.1% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-30 (1-329) x US-11-217-529-309 (1-3678)

Qy 13 LeuValLeuLeuAlaProPro 19
||||||||||||||||||||
Db 2602 CTAGTTCTCTTGGCTCCTCCC 2582

RESULT 48
US-11-313-450-13/c
; Sequence 13, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
; APPLICANT: Adorante, Joeseph S.
; APPLICANT: Ehring, George R.
; TITLE OF INVENTION: High-Throughput Screens For Identifying
; TITLE OF INVENTION: Selective Persistent Sodium Channels Channel Blockers
; FILE REFERENCE: 17407 CIP (AP)
; CURRENT APPLICATION NUMBER: US/11/313,450
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/989797
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252771
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5934
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-313-450-13

Alignment Scores:
Pred. No.: 1.42e+03 Length: 5934
Score: 7.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.1% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-30 (1-329) x US-11-313-450-13 (1-5934)

Qy 64 GlnSerSerGluValLeuGly 70
||||||||||||||||||||
Db 37 CAAAGCTCTGAGGTCCTGGGG 17

RESULT 49
US-11-251-465-8/c
; Sequence 8, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14

PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8
LENGTH: 6371
TYPE: DNA
ORGANISM: Homo sapiens
-11-251-465-8

ignment Scores:

ed. No.:	1.51e+03	Length:	6371
ore:	7.00	Matches:	7
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.1%	Indels:	0
:	7	Gaps:	0

-10-821-670A-30 (1-329) x US-11-251-465-8 (1-6371)

64 GlnSerSerGluValLeuGly 70
||||||||||||||||||||
85 CAAAGCTCTGAGGTCCTGGGG 65

SULT 50
-10-857-260-27/c
Sequence 27, Application US/10857260
Publication No. US20060110742A1
GENERAL INFORMATION:
APPLICANT: Lyons, Leslie A.
APPLICANT: Grahn, Robert
APPLICANT: Erdman, Carolyn
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Carrier Tests for Polycystic Kidney Disease in the Cat
FILE REFERENCE: 02307O-146800US
CURRENT APPLICATION NUMBER: US/10/857,260
CURRENT FILING DATE: 2004-05-28
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 39536
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
OTHER INFORMATION: GenBank Accession No. AC145332.28 genomic DNA for
OTHER INFORMATION: PKD1 39536 bp contig
-10-857-260-27

ignment Scores:

ed. No.:	7.56e+03	Length:	39536
ore:	7.00	Matches:	7
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	2.1%	Indels:	0
:	6	Gaps:	0

-10-821-670A-30 (1-329) x US-10-857-260-27 (1-39536)

161 GlySerSerAspProGlnGly 167
||||||||||||||||||||
716 GGGAGCAGCGACCCCCAGGGG 696

SULT 51
-10-553-298-1/c
Sequence 1, Application US/10553298
Publication No. US20060110385A1
GENERAL INFORMATION:
APPLICANT: NeuroNova AG
TITLE OF INVENTION: A Method for Diagnosing and Treating Affective Disorders
FILE REFERENCE: XXX
CURRENT APPLICATION NUMBER: US/10/553,298
CURRENT FILING DATE: 2005-10-14
NUMBER OF SEQ ID NOS: 111

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 56580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon1
; LOCATION: (3000)..(3124)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon2
; LOCATION: (24841)..(25009)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon3
; LOCATION: (26134)..(26202)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon4
; LOCATION: (30958)..(31030)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon5
; LOCATION: (32481)..(32577)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon6
; LOCATION: (35416)..(35496)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon7
; LOCATION: (36113)..(36242)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon8
; LOCATION: (37541)..(37677)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon9
; LOCATION: (45470)..(45560)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon10
; LOCATION: (47229)..(47295)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon11
; LOCATION: (47380)..(47529)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon12
; LOCATION: (50438)..(50539)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon13
; LOCATION: (54392)..(54889)
; OTHER INFORMATION:
US-10-553-298-1

Alignment Scores:

Pred. No.:	1.04e+04	Length:	56580
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.1%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-553-298-1 (1-56580)

Qy 65 SerSerGluValLeuGlySer 71
||||||||||||||||||||
Db 21521 TCATCTGAGGTCCTGGGTTCG 21501

```
ULT 52
10-506-549-3/c
equence 3, Application US/10506549
ublication No. US20060100417A1
ENERAL INFORMATION:
APPLICANT: APPLERA CORPORATION
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION:  AND USES THEREOF
FILE REFERENCE: CL001361-US
CURRENT APPLICATION NUMBER: US/10/506,549
CURRENT FILING DATE:  2004-09-03
PRIOR APPLICATION NUMBER: 60/361,343
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 3
 LENGTH: 394191
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(394191)
 OTHER INFORMATION: n = A,T,C or G
10-506-549-3

gnment Scores:
d. No.:                5.52e+04        Length:         394191
re:                    7.00            Matches:        7
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              2.1%            Indels:         0
                       6               Gaps:           0

10-821-670A-30 (1-329) x US-10-506-549-3 (1-394191)

       144 TrpLeuThrAlaIleSerThr 150
           ||||||||||||||||||||
    331384 TGGCTCACTGCAATCTCCACC 331364

ULT 53
11-266-409-12/c
equence 12, Application US/11266409
ublication No. US20060093578A1
ENERAL INFORMATION:
APPLICANT: SUZUMURA, AKIO
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
FILE REFERENCE: 279847US40
CURRENT APPLICATION NUMBER: US/11/266,409
CURRENT FILING DATE:  2005-11-04
PRIOR APPLICATION NUMBER: US 60/624,851
PRIOR FILING DATE: 2004-11-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.3
EQ ID NO 12
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic DNA
11-266-409-12

gnment Scores:
d. No.:                94.4            Length:         20
re:                    6.00            Matches:        6
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              1.8%            Indels:         0
                       7               Gaps:           0

10-821-670A-30 (1-329) x US-11-266-409-12 (1-20)

       266 ProHisSerTyrPheSer 271
                   ||||||||||||||||||
Db          20 CCCCATTCCTACTTCTCC 3

RESULT 54
US-11-217-529-9246
; Sequence 9246, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9246
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-9246

Alignment Scores:
Pred. No.:             115             Length:         25
Score:                 6.00            Matches:        6
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           1.8%            Indels:         0
DB:                    7               Gaps:           0

US-10-821-670A-30 (1-329) x US-11-217-529-9246 (1-25)

Qy         158 SerSerArgGlySerSer 163
               ||||||||||||||||||
Db           8 TCATCGAGAGGCAGCAGT 25

RESULT 55
US-11-217-529-18480
; Sequence 18480, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18480
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-18480

Alignment Scores:
Pred. No.:             115             Length:         25
Score:                 6.00            Matches:        6
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           1.8%            Indels:         0
```

: 7 Gaps: 0

-10-821-670A-30 (1-329) x US-11-217-529-18480 (1-25)

204 GluGluSerLeuProIle 209
||||||||||||||||||||
2 GAGGAATCGTTGCCTATC 19

SULT 56
-11-217-529-19397
Sequence 19397, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19397
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-19397

ignment Scores:

ed. No.:	115	Length:	25
ore:	6.00	Matches:	6
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	1.8%	Indels:	0
:	7	Gaps:	0

-10-821-670A-30 (1-329) x US-11-217-529-19397 (1-25)

11 PheSerLeuValLeuLeu 16
||||||||||||||||||||
8 TTTTCACTGGTTCTCTTG 25

SULT 57
-11-217-529-31190/c
Sequence 31190, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31190
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-31190

ignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-31190 (1-25)

Qy 67 GluValLeuGlySerGly 72
||||||||||||||||||||
Db 22 GAAGTATTAGGTTCAGGG 5

RESULT 58
US-11-217-529-36523
; Sequence 36523, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36523
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-36523

Alignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-36523 (1-25)

Qy 31 TyrValValGluLeuAsp 36
||||||||||||||||||||
Db 2 TACGTCGTGGAGTTAGAT 19

RESULT 59
US-11-217-529-36968/c
; Sequence 36968, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36968
; LENGTH: 25

```
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
11-217-529-36968

gnment Scores:
d. No.:                115             Length:         25
re:                    6.00            Matches:        6
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              1.8%            Indels:         0
                       7               Gaps:           0

10-821-670A-30 (1-329) x US-11-217-529-36968 (1-25)

       147 AlaIleSerThrAspLeu 152
           |||||||||||||||||
        22 GCTATTAGTACAGATCTG 5

ULT 60
11-217-529-43878/c
equence 43878, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 43878
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-43878

gnment Scores:
d. No.:                115             Length:         25
re:                    6.00            Matches:        6
cent Similarity:       100.0%          Conservative:   0
t Local Similarity:    100.0%          Mismatches:     0
ry Match:              1.8%            Indels:         0
                       7               Gaps:           0

10-821-670A-30 (1-329) x US-11-217-529-43878 (1-25)

       158 SerSerArgGlySerSer 163
           |||||||||||||||||
        21 TCTTCAAGAGGTTCGTCT 4

ULT 61
11-217-529-48094
equence 48094, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
```

```
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48094
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-48094

Alignment Scores:
Pred. No.:                115             Length:         25
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              1.8%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-30 (1-329) x US-11-217-529-48094 (1-25)

Qy         113 SerThrAspIleLeuArg 118
               |||||||||||||||||
Db           2 AGTACGGATATTTTAAGG 19

RESULT 62
US-11-217-529-50534
; Sequence 50534, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50534
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-50534

Alignment Scores:
Pred. No.:                115             Length:         25
Score:                    6.00            Matches:        6
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              1.8%            Indels:         0
DB:                       7               Gaps:           0

US-10-821-670A-30 (1-329) x US-11-217-529-50534 (1-25)

Qy          80 LysGluPheAlaAspAla 85
               |||||||||||||||||
Db           6 AAGGAGTTCGCGGACGCA 23

RESULT 63
US-11-217-529-71800/c
; Sequence 71800, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
```

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 71800
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-71800

ignment Scores:

ed. No.:	115	Length:	25
ore:	6.00	Matches:	6
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	1.8%	Indels:	0
:	7	Gaps:	0

-10-821-670A-30 (1-329) x US-11-217-529-71800 (1-25)

```
        44 GluMetValValLeuThr 49
           ||||||||||||||||||
        18 GAGATGGTGGTACTGACC 1
```

SULT 64
-11-217-529-82993/c
Sequence 82993, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 82993
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-82993

ignment Scores:

ed. No.:	115	Length:	25
ore:	6.00	Matches:	6
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	1.8%	Indels:	0
:	7	Gaps:	0

-10-821-670A-30 (1-329) x US-11-217-529-82993 (1-25)

```
        93 GlyGlyGluValLeuSer 98
           ||||||||||||||||||
        20 GGTGGAGAAGTGCTATCT 3
```

SULT 65
-11-217-529-88008
Sequence 88008, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-88008

Alignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-88008 (1-25)

```
Qy        242 LeuGlnLeuLysProLeu 247
              ||||||||||||||||||
Db          2 CTGCAGCTCAAACCTCTG 19
```

RESULT 66
US-11-217-529-89000
; Sequence 89000, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89000
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-89000

Alignment Scores:

Pred. No.:	115	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-89000 (1-25)

```
Qy         12 SerLeuValLeuLeuAla 17
              ||||||||||||||||||
Db          5 TCCCTTGTCCTACTGGCT 22
```

RESULT 67

```
11-217-529-106446
equence 106446, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 106446
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-106446

gnment Scores:
d. No.:                115            Length:        25
re:                    6.00           Matches:       6
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              1.8%           Indels:        0
                       7              Gaps:          0

10-821-670A-30 (1-329) x US-11-217-529-106446 (1-25)

        73 LysThrLeuThrIleGln 78
           |||||||||||||||||
         3 AAGACGCTAACGATCCAG 20

ULT 68
11-217-529-107708/c
equence 107708, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 107708
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-107708

gnment Scores:
d. No.:                115            Length:        25
re:                    6.00           Matches:       6
cent Similarity:       100.0%         Conservative:  0
t Local Similarity:    100.0%         Mismatches:    0
ry Match:              1.8%           Indels:        0
                       7              Gaps:          0

10-821-670A-30 (1-329) x US-11-217-529-107708 (1-25)

Qy         295 ThrSerAlaLysValVal 300
               |||||||||||||||||
Db          22 ACGTCGGCAAAAGTTGTC 5

RESULT 69
US-11-217-529-112662/c
; Sequence 112662, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112662
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-112662

Alignment Scores:
Pred. No.:                115            Length:        25
Score:                    6.00           Matches:       6
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              1.8%           Indels:        0
DB:                       7              Gaps:          0

US-10-821-670A-30 (1-329) x US-11-217-529-112662 (1-25)

Qy         292 ValAspLysThrSerAla 297
               |||||||||||||||||
Db          24 GTCGACAAAACCAGCGCA 7

RESULT 70
US-11-217-529-123888/c
; Sequence 123888, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123888
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-123888

Alignment Scores:
Pred. No.:                115            Length:        25
Score:                    6.00           Matches:       6
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
```

ery Match: 1.8% Indels: 0
: 7 Gaps: 0

-10-821-670A-30 (1-329) x US-11-217-529-123888 (1-25)

279 GlnGlyLysAsnAsnArg 284
||||||||||||||||||
24 CAAGGAAAGAACAATCGA 7

SULT 71
-11-217-529-134360/c
Sequence 134360, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 134360
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-134360

ignment Scores:
ed. No.: 115 Length: 25
ore: 6.00 Matches: 6
cent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 1.8% Indels: 0
: 7 Gaps: 0

-10-821-670A-30 (1-329) x US-11-217-529-134360 (1-25)

12 SerLeuValLeuLeuAla 17
||||||||||||||||||
24 TCATTAGTGCTGCTGGCG 7

SULT 72
-11-217-529-142444
Sequence 142444, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 142444
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-142444

Alignment Scores:
Pred. No.: 115 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 1.8% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-30 (1-329) x US-11-217-529-142444 (1-25)

Qy 65 SerSerGluValLeuGly 70
||||||||||||||||||
Db 3 TCTTCGGAAGTACTGGGC 20

RESULT 73
US-11-217-529-144453
; Sequence 144453, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 144453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-144453

Alignment Scores:
Pred. No.: 115 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 1.8% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-30 (1-329) x US-11-217-529-144453 (1-25)

Qy 158 SerSerArgGlySerSer 163
||||||||||||||||||
Db 5 TCTAGTCGAGGGTCTTCA 22

RESULT 74
US-11-217-529-152420/c
; Sequence 152420, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152420

```
  LENGTH: 25
  TYPE: DNA
  ORGANISM: Saccharomyces pastorianus
11-217-529-152420

gnment Scores:
d. No.:                 115             Length:         25
re:                     6.00            Matches:        6
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               1.8%            Indels:         0
                        7               Gaps:           0

10-821-670A-30 (1-329) x US-11-217-529-152420 (1-25)

       324 AlaSerValSerCysSer 329
           |||||||||||||||||||
        20 GCTAGCGTATCCTGTTCC 3

ULT 75
11-267-871-456
equence 456, Application US/11267871
ublication No. US20060094655A1
ENERAL INFORMATION:
 APPLICANT: Guyon, Thierry
 APPLICANT:  Borrelly, Gilles
 APPLICANT:  Drittanti, Lila
 APPLICANT:  Vega, Manuel
 TITLE OF INVENTION: MODIFIED GROWTH HORMONES
 FILE REFERENCE: 17109-015001/925
 CURRENT APPLICATION NUMBER: US/11/267,871
 CURRENT FILING DATE:  2005-11-03
 PRIOR APPLICATION NUMBER: 60/706,697
 PRIOR FILING DATE: 2005-08-08
 PRIOR APPLICATION NUMBER: 60/625,652
 PRIOR FILING DATE: 2004-11-04
 NUMBER OF SEQ ID NOS: 719
 SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 456
  LENGTH: 72
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Primer
11-267-871-456

gnment Scores:
d. No.:                 294             Length:         72
re:                     6.00            Matches:        6
cent Similarity:        100.0%          Conservative:   0
t Local Similarity:     100.0%          Mismatches:     0
ry Match:               1.8%            Indels:         0
                        7               Gaps:           0

10-821-670A-30 (1-329) x US-11-267-871-456 (1-72)

       158 SerSerArgGlySerSer 163
           ||||||||||||||||||
        13 TCCAGTCGTGGATCGAGC 30

ULT 76
11-267-871-456/c
equence 456, Application US/11267871
ublication No. US20060094655A1
ENERAL INFORMATION:
 APPLICANT: Guyon, Thierry
 APPLICANT:  Borrelly, Gilles
 APPLICANT:  Drittanti, Lila
 APPLICANT:  Vega, Manuel
 TITLE OF INVENTION: MODIFIED GROWTH HORMONES
 FILE REFERENCE: 17109-015001/925
 CURRENT APPLICATION NUMBER: US/11/267,871
 CURRENT FILING DATE:  2005-11-03
 PRIOR APPLICATION NUMBER: 60/706,697
 PRIOR FILING DATE: 2005-08-08
 PRIOR APPLICATION NUMBER: 60/625,652
 PRIOR FILING DATE: 2004-11-04
 NUMBER OF SEQ ID NOS: 719
 SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 456
  LENGTH: 72
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Primer
US-11-267-871-456

Alignment Scores:
Pred. No.:              294             Length:         72
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            1.8%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-30 (1-329) x US-11-267-871-456 (1-72)

Qy         158 SerSerArgGlySerSer 163
               ||||||||||||||||||
Db          60 TCCAGTCGTGGATCGAGC 43

RESULT 77
US-11-217-529-79352/c
; Sequence 79352, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79352
;   LENGTH: 177
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79352

Alignment Scores:
Pred. No.:              652             Length:         177
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            1.8%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-30 (1-329) x US-11-217-529-79352 (1-177)

Qy         246 ProLeuLysAsnSerArg 251
               |||||||||||||||||
Db         119 CCCTTGAAAAATTCTAGA 102

RESULT 78
US-10-471-571A-5615/c
; Sequence 5615, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
```

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 5615
LENGTH: 198
TYPE: DNA
ORGANISM: Staphylococcus aureus
-10-471-571A-5615

ignment Scores:

ed. No.:	721	Length:	198
ore:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	1.8%	Indels:	0
	6	Gaps:	0

-10-821-670A-30 (1-329) x US-10-471-571A-5615 (1-198)

```
        102 LeuLeuIleHisLysLys 107
            ||||||||||||||||||
        154 TTACTAATACATAAAAAA 137
```

SULT 79
-11-244-678-7
Sequence 7, Application US/11244678
Publication No. US20060099206A1
GENERAL INFORMATION:
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark
APPLICANT: Laken, Haley A.
APPLICANT: Rouse, Jason
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMPROVING
TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION
FILE REFERENCE: 16158-052001
CURRENT APPLICATION NUMBER: US/11/244,678
CURRENT FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/616,474
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 240
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated oligonucleotide
-11-244-678-7

ignment Scores:

ed. No.:	855	Length:	240
ore:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	1.8%	Indels:	0
	7	Gaps:	0

-10-821-670A-30 (1-329) x US-11-244-678-7 (1-240)

```
        275 GlyValGlnValGlnGly 280
            ||||||||||||||||||
          6 GGAGTACAAGTGCAAGGT 23
```

SULT 80
-11-217-529-147/c
Sequence 147, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 147
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-147

Alignment Scores:

Pred. No.:	864	Length:	243
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-147 (1-243)

```
Qy        283 AsnArgGluLysLysAsp 288
              ||||||||||||||||||
Db        198 AATCGTGAGAAAAAAGAC 181
```

RESULT 81
US-11-217-529-80845
; Sequence 80845, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80845
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80845

Alignment Scores:

Pred. No.:	864	Length:	243
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-80845 (1-243)

```
Qy        158 SerSerArgGlySerSer 163
              ||||||||||||||||||
Db         37 TCTAGTCGAGGGTCTTCA 54
```

ULT 82
11-217-529-166793
equence 166793, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 166793
LENGTH: 267
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
11-217-529-166793

gnment Scores:

d. No.:	939	Length:	267
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	1.8%	Indels:	0
	7	Gaps:	0

10-821-670A-30 (1-329) x US-11-217-529-166793 (1-267)

```
       171 GlyAlaAlaThrLeuSer 176
           ||||||||||||||||||
       241 GGTGCTGCAACTTTATCC 258
```

ULT 83
10-471-571A-2941/c
equence 2941, Application US/10471571A
ublication No. US20060115490A1
ENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
EQ ID NO 2941
LENGTH: 273
TYPE: DNA
ORGANISM: Staphylococcus aureus
10-471-571A-2941

gnment Scores:

d. No.:	958	Length:	273
re:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	1.8%	Indels:	0
	6	Gaps:	0

10-821-670A-30 (1-329) x US-10-471-571A-2941 (1-273)

```
        17 AlaProProLeuMetAla 22
           ||||||||||||||||||
       155 GCACCACCACTGATGGCA 138
```

RESULT 84
US-10-512-190-1/c
; Sequence 1, Application US/10512190
; Publication No. US20060099219A1
; GENERAL INFORMATION:
; APPLICANT: Hallez, Sophie
; APPLICANT: Burny, Arsene
; APPLICANT: Jacquet, Alain
; APPLICANT: Bollen, Alex
; TITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: COMPRISING IT AND ITS PREPARATION PROCESS
; FILE REFERENCE: 9997.50USWO
; CURRENT APPLICATION NUMBER: US/10/512,190
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/BE03/000073
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/410,461
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: FR 0205173
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: FR 0304170
; PRIOR FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutated (recombinant) HPV-16 E7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(279)
US-10-512-190-1

Alignment Scores:

Pred. No.:	977	Length:	279
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x US-10-512-190-1 (1-279)

```
Qy        197 GlySerAlaCysProAla 202
              ||||||||||||||||||
Db        122 GGTTCTGCTTGTCCAGCT 105
```

RESULT 85
US-10-511-814-9/c
; Sequence 9, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
; APPLICANT: McCance, Dennis
; APPLICANT: Westbrook, III, Thomas F.
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
; FILE REFERENCE: 21108.0016U2
; CURRENT APPLICATION NUMBER: US/10/511,814
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US03/12667
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,245
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct

```
-10-511-814-9

ignment Scores:
ed. No.:                1.02e+03        Length:         294
ore:                    6.00            Matches:        6
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              1.8%            Indels:         0
:                       6               Gaps:           0

-10-821-670A-30 (1-329) x US-10-511-814-9 (1-294)

        197 GlySerAlaCysProAla 202
            ||||||||||||||||||
        140 GGTTCTGCTTGTCCAGCT 123

SULT 86
-10-511-814-10/c
Sequence 10, Application US/10511814
Publication No. US20060088472A1
GENERAL INFORMATION:
 APPLICANT: McCance, Dennis
 APPLICANT:  Westbrook, III, Thomas F.
 TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
 FILE REFERENCE: 21108.0016U2
 CURRENT APPLICATION NUMBER: US/10/511,814
 CURRENT FILING DATE:  2004-10-19
 PRIOR APPLICATION NUMBER: PCT/US03/12667
 PRIOR FILING DATE: 2003-04-21
 PRIOR APPLICATION NUMBER: 60/374,245
 PRIOR FILING DATE: 2002-04-19
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 10
  LENGTH: 294
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence:/Note =
  OTHER INFORMATION: Synthetic Construct
-10-511-814-10

ignment Scores:
ed. No.:                1.02e+03        Length:         294
ore:                    6.00            Matches:        6
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              1.8%            Indels:         0
:                       6               Gaps:           0

-10-821-670A-30 (1-329) x US-10-511-814-10 (1-294)

        197 GlySerAlaCysProAla 202
            ||||||||||||||||||
        140 GGTTCTGCTTGTCCAGCT 123

SULT 87
-10-511-814-12/c
Sequence 12, Application US/10511814
Publication No. US20060088472A1
GENERAL INFORMATION:
 APPLICANT: McCance, Dennis
 APPLICANT:  Westbrook, III, Thomas F.
 TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
 FILE REFERENCE: 21108.0016U2
 CURRENT APPLICATION NUMBER: US/10/511,814
 CURRENT FILING DATE:  2004-10-19
 PRIOR APPLICATION NUMBER: PCT/US03/12667
 PRIOR FILING DATE: 2003-04-21
 PRIOR APPLICATION NUMBER: 60/374,245
 PRIOR FILING DATE: 2002-04-19
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: Synthetic Construct
US-10-511-814-12

Alignment Scores:
Pred. No.:              1.02e+03        Length:         294
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            1.8%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-511-814-12 (1-294)

Qy          197 GlySerAlaCysProAla 202
                ||||||||||||||||||
Db          140 GGTTCTGCTTGTCCAGCT 123

RESULT 88
US-10-511-814-13/c
; Sequence 13, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
;  APPLICANT: McCance, Dennis
;  APPLICANT:  Westbrook, III, Thomas F.
;  TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
;  FILE REFERENCE: 21108.0016U2
;  CURRENT APPLICATION NUMBER: US/10/511,814
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US03/12667
;  PRIOR FILING DATE: 2003-04-21
;  PRIOR APPLICATION NUMBER: 60/374,245
;  PRIOR FILING DATE: 2002-04-19
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: Synthetic Construct
US-10-511-814-13

Alignment Scores:
Pred. No.:              1.02e+03        Length:         294
Score:                  6.00            Matches:        6
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            1.8%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-511-814-13 (1-294)

Qy          197 GlySerAlaCysProAla 202
                ||||||||||||||||||
Db          140 GGTTCTGCTTGTCCAGCT 123

RESULT 89
US-11-217-529-81028
; Sequence 81028, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
```

```
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 81028
 LENGTH: 297
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-81028

gnment Scores:
d. No.:               1.03e+03       Length:         297
re:                   6.00           Matches:        6
cent Similarity:      100.0%         Conservative:   0
t Local Similarity:   100.0%         Mismatches:     0
ry Match:             1.8%           Indels:         0
                      7              Gaps:           0

10-821-670A-30 (1-329) x US-11-217-529-81028 (1-297)

       117 LeuArgGluGlnLysGlu 122
           ||||||||||||||||||
        79 TTAAGAGAGCAGAAGGAA 96

ULT 90
11-217-529-5663
equence 5663, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 5663
 LENGTH: 303
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-5663

gnment Scores:
d. No.:               1.05e+03       Length:         303
re:                   6.00           Matches:        6
cent Similarity:      100.0%         Conservative:   0
t Local Similarity:   100.0%         Mismatches:     0
ry Match:             1.8%           Indels:         0
                      7              Gaps:           0

10-821-670A-30 (1-329) x US-11-217-529-5663 (1-303)

         8 IleAlaTrpPheSerLeu 13
           ||||||||||||||||||
        37 ATCGCCTGGTTTTCCCTG 54

ULT 91
11-217-529-174215
equence 174215, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174215
;   LENGTH: 303
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174215

Alignment Scores:
Pred. No.:            1.05e+03       Length:         303
Score:                6.00           Matches:        6
Percent Similarity:   100.0%         Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:          1.8%           Indels:         0
DB:                   7              Gaps:           0

US-10-821-670A-30 (1-329) x US-11-217-529-174215 (1-303)

Qy          15 LeuLeuAlaProProLeu 20
               ||||||||||||||||||
Db         142 CTTTTAGCTCCACCTTTA 159

RESULT 92
US-11-217-529-190938
; Sequence 190938, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190938
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190938

Alignment Scores:
Pred. No.:            1.06e+03       Length:         306
Score:                6.00           Matches:        6
Percent Similarity:   100.0%         Conservative:   0
Best Local Similarity: 100.0%        Mismatches:     0
Query Match:          1.8%           Indels:         0
DB:                   7              Gaps:           0

US-10-821-670A-30 (1-329) x US-11-217-529-190938 (1-306)

Qy         281 LysAsnAsnArgGluLys 286
               ||||||||||||||||||
Db         139 AAAAACAATCGTGAAAAG 156
```

SULT 93
-11-321-421-87
Sequence 87, Application US/11321421
Publication No. US20060115496A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
FILE REFERENCE: TX-1-C2-1
CURRENT APPLICATION NUMBER: US/11/321,421
CURRENT FILING DATE: 2005-12-29
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 87
LENGTH: 306
TYPE: DNA
ORGANISM: Toxoplasma gondii
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(306)
OTHER INFORMATION:
-11-321-421-87

ignment Scores:

ed. No.:	1.06e+03	Length:	306
ore:	6.00	Matches:	6
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	1.8%	Indels:	0
:	7	Gaps:	0

-10-821-670A-30 (1-329) x US-11-321-421-87 (1-306)

```
         39 ProAspAlaProGlyGlu 44
            ||||||||||||||||||
        204 CCTGACGCCCCAGGAGAG 221
```

SULT 94
-11-217-529-81582
Sequence 81582, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 81582
LENGTH: 309
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
-11-217-529-81582

ignment Scores:

ed. No.:	1.07e+03	Length:	309
ore:	6.00	Matches:	6
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	1.8%	Indels:	0
:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-81582 (1-309)

```
Qy          8 IleAlaTrpPheSerLeu 13
              |||||||||||||||||||
Db         37 ATTGCCTGGTTCTCCCTG 54
```

RESULT 95
US-11-217-529-75899
; Sequence 75899, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75899
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75899

Alignment Scores:

Pred. No.:	1.08e+03	Length:	312
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	1.8%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-30 (1-329) x US-11-217-529-75899 (1-312)

```
Qy         12 SerLeuValLeuLeuAla 17
              ||||||||||||||||||
Db        169 TCCCTTGTCCTACTGGCT 186
```

RESULT 96
US-10-488-619-794
; Sequence 794, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 794
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(315)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-794

Alignment Scores:

Pred. No.:	1.09e+03	Length:	315
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0

```
ry Match:            1.8%          Indels:        0
                     6             Gaps:          0

10-821-670A-30 (1-329) x US-10-488-619-794 (1-315)

        14 ValLeuLeuAlaProPro 19
           ||||||||||||||||||
        27 GTCCTCCTTGCTCCACCC 44

ULT 97
11-217-529-76199
equence 76199, Application US/11217529
ublication No. US20060099612A1
ENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT:  NAKAO, YOSHIHIRO
APPLICANT:  NAKAMURA, NORIHISA
APPLICANT:  KODAMA, YUKIKO
APPLICANT:  FUJIMURA, TOMOKO
APPLICANT:  ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE:  2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
EQ ID NO 76199
 LENGTH: 324
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
11-217-529-76199

gnment Scores:
d. No.:              1.11e+03      Length:        324
re:                  6.00          Matches:       6
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
ry Match:            1.8%          Indels:        0
                     7             Gaps:          0

10-821-670A-30 (1-329) x US-11-217-529-76199 (1-324)

       172 AlaAlaThrLeuSerAla 177
           ||||||||||||||||||
        37 GCAGCTACGCTGAGCGCA 54

ULT 98
11-023-959A-118
equence 118, Application US/11023959A
ublication No. US20060106203A1
ENERAL INFORMATION:
APPLICANT: Winter, Greg
TITLE OF INVENTION: Ligand
FILE REFERENCE: 8039/2142
CURRENT APPLICATION NUMBER: US/11/023,959A
CURRENT FILING DATE:  2004-12-28
PRIOR APPLICATION NUMBER: PCT/GB03/002804
PRIOR FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 187
SOFTWARE: PatentIn version 3.3
EQ ID NO 118
 LENGTH: 324
 TYPE: DNA
 ORGANISM: Homo sapiens
11-023-959A-118

gnment Scores:
d. No.:              1.11e+03      Length:        324
re:                  6.00          Matches:       6
cent Similarity:     100.0%        Conservative:  0
t Local Similarity:  100.0%        Mismatches:    0
Query Match:         1.8%          Indels:        0
DB:                  7             Gaps:          0

US-10-821-670A-30 (1-329) x US-11-023-959A-118 (1-324)

Qy          11 PheSerLeuValLeuLeu 16
               ||||||||||||||||||
Db          75 TTCAGTCTCGTATTGCTT 92

RESULT 99
US-10-488-619-375/c
; Sequence 375, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 375
;   LENGTH: 332
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(332)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-375

Alignment Scores:
Pred. No.:           1.14e+03      Length:        332
Score:               6.00          Matches:       6
Percent Similarity:  100.0%        Conservative:  0
Best Local Similarity: 100.0%      Mismatches:    0
Query Match:         1.8%          Indels:        0
DB:                  6             Gaps:          0

US-10-821-670A-30 (1-329) x US-10-488-619-375 (1-332)

Qy          11 PheSerLeuValLeuLeu 16
               ||||||||||||||||||
Db         289 TTTTCTTTGGTCTTGCTC 272

RESULT 100
US-11-217-529-77451/c
; Sequence 77451, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77451
;   LENGTH: 339
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77451

Alignment Scores:
Pred. No.:           1.16e+03      Length:        339
```

ore:	6.00	Matches:	6
cent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	1.8%	Indels:	0
:	7	Gaps:	0

-10-821-670A-30 (1-329) x US-11-217-529-77451 (1-339)

```
         15 LeuLeuAlaProProLeu 20
            ||||||||||||||||||
        224 CTATTAGCGCCCCCTTTA 207
```

arch completed: June 10, 2006, 02:17:13
b time : 158.422 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

)M protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:33:29 ; Search time 6994.12 Seconds
(without alignments)
4210.361 Million cell updates/sec

Title: US-10-821-670A-27
Perfect score: 307
Sequence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size: 1

Total number of hits satisfying chosen parameters: 12722146

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110449_27523/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rge -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss08
-USER=US10821670_@CGN_1_1_6646_@runat_07062006_110449_27523 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	307	100.0	921	2	AR595948	AR595948 Sequence
c	2	307	100.0	921	2	AR595949	AR595949 Sequence
	3	307	100.0	1006	14	FCIL12P40	Y07762 Felis catus
	4	307	100.0	1533	2	AR595959	AR595959 Sequence
c	5	307	100.0	1533	2	AR595960	AR595960 Sequence
	6	307	100.0	1599	2	AR595956	AR595956 Sequence
c	7	307	100.0	1599	2	AR595957	AR595957 Sequence
	8	206	67.1	921	2	AR242436	AR242436 Sequence
	9	206	67.1	921	2	AR242437	AR242437 Sequence
	10	206	67.1	921	2	AR280204	AR280204 Sequence
	11	206	67.1	921	2	AR280205	AR280205 Sequence
	12	206	67.1	921	2	AR322419	AR322419 Sequence
	13	206	67.1	921	2	AR322420	AR322420 Sequence
	14	206	67.1	987	2	AR595950	AR595950 Sequence
c	15	206	67.1	987	2	AR595951	AR595951 Sequence
	16	206	67.1	990	2	AX076200	AX076200 Sequence
	17	206	67.1	990	2	AX076482	AX076482 Sequence
	18	206	67.1	2193	2	AR242435	AR242435 Sequence
	19	206	67.1	2193	2	AR280203	AR280203 Sequence
	20	206	67.1	2193	2	AR322418	AR322418 Sequence
	21	206	67.1	4522	2	AX076209	AX076209 Sequence
	22	206	67.1	4522	2	AX076476	AX076476 Sequence
	23	205	66.8	985	2	AR595967	AR595967 Sequence
c	24	205	66.8	985	2	AR595968	AR595968 Sequence
	25	177	57.7	990	14	FCU83184	U83184 Felis catus
	26	65	21.2	431	14	AF054607	AF054607 Felis cat
	27	52	16.9	990	2	AX154603	AX154603 Sequence
	28	43	14.0	984	2	AX154600	AX154600 Sequence
	29	42	13.7	984	2	AX154599	AX154599 Sequence
	30	41	13.4	972	8	AY191829	AY191829 Synthetic
	31	41	13.4	975	2	AX154597	AX154597 Sequence
	32	39	12.7	993	14	AB107654	AB107654 Lama glam
	33	39	12.7	1005	5	AY234218	AY234218 Papio anu
	34	39	12.7	1005	5	CTU19834	U19834 Cercocebus
	35	39	12.7	1080	5	MMU19841	U19841 Macaca mula
	36	37	12.1	921	2	AR595965	AR595965 Sequence
c	37	37	12.1	921	2	AR595966	AR595966 Sequence
	38	37	12.1	924	2	BD171282	BD171282 Novel can
	39	37	12.1	987	2	AR595969	AR595969 Sequence
c	40	37	12.1	987	2	AR595970	AR595970 Sequence
	41	37	12.1	990	2	AR151061	AR151061 Sequence
	42	37	12.1	990	2	AR151071	AR151071 Sequence
	43	37	12.1	990	2	BD014653	BD014653 Process f
	44	37	12.1	990	2	BD014663	BD014663 Process f
	45	37	12.1	990	2	E15017	E15017 Canine mRNA
	46	37	12.1	990	2	AR316460	AR316460 Sequence
	47	37	12.1	990	2	AR316470	AR316470 Sequence
	48	37	12.1	1015	14	CFU49100	U49100 Canis famil
	49	37	12.1	1533	2	AR595973	AR595973 Sequence
c	50	37	12.1	1533	2	AR595974	AR595974 Sequence
	51	37	12.1	1599	2	AR595971	AR595971 Sequence
c	52	37	12.1	1599	2	AR595972	AR595972 Sequence
	53	37	12.1	2154	2	BD171281	BD171281 Novel can
	54	37	12.1	2267	2	AR596011	AR596011 Sequence
c	55	37	12.1	2267	2	AR596012	AR596012 Sequence
	56	36	11.7	446	14	AF091134	AF091134 Canis fam
	57	36	11.7	452	14	AF333121	AF333121 Canis fam
	58	36	11.7	588	14	AF349536	AF349536 Canis fam
	59	35	11.4	906	2	BD021808	BD021808 Natural k
	60	35	11.4	906	2	BD021809	BD021809 Natural k
	61	35	11.4	975	2	AX154602	AX154602 Sequence
	62	35	11.4	987	2	AR008950	AR008950 Sequence
	63	35	11.4	987	2	BD007070	BD007070 IL-12 gen
	64	35	11.4	987	2	BD007076	BD007076 Gene expr
	65	35	11.4	987	2	BD007077	BD007077 Gene expr
	66	35	11.4	987	2	BD007078	BD007078 Gene expr
	67	35	11.4	987	2	BD136034	BD136034 Interfero
	68	35	11.4	987	2	BD136035	BD136035 Interfero
	69	35	11.4	987	2	BD136036	BD136036 Interfero
	70	35	11.4	987	2	CQ803342	CQ803342 Sequence
	71	35	11.4	987	2	CS131491	CS131491 Sequence
	72	35	11.4	987	2	I28591	I28591 Sequence 1
	73	35	11.4	987	2	AX154633	AX154633 Sequence
	74	35	11.4	1007	5	AF180563	AF180563 Homo sapi
	75	35	11.4	1008	14	AB246353	AB246353 Bubalus b

	76	35	11.4	1012	14	AY198121 AY198121 Bubalus b
	77	35	11.4	1018	2	AR052857 AR052857 Sequence
	78	35	11.4	1018	2	AR288169 AR288169 Sequence
	79	35	11.4	1018	2	AR567156 AR567156 Sequence
	80	35	11.4	1029	2	CQ829448 CQ829448 Sequence
	81	35	11.4	1046	5	BC074723 BC074723 Homo sapi
	82	35	11.4	1073	5	BC067498 BC067498 Homo sapi
	83	35	11.4	1073	5	BC067499 BC067499 Homo sapi
	84	35	11.4	1073	5	BC067500 BC067500 Homo sapi
	85	35	11.4	1073	5	BC067501 BC067501 Homo sapi
	86	35	11.4	1073	5	BC067502 BC067502 Homo sapi
	87	35	11.4	1389	2	AR393788 AR393788 Sequence
	88	35	11.4	1389	2	AX084106 AX084106 Sequence
	89	35	11.4	1397	2	BD165800 BD165800 Antibody
	90	35	11.4	1399	2	AR091391 AR091391 Sequence
	91	35	11.4	1399	5	HUMCLMF40 M65272 Human cytot
	92	35	11.4	1560	2	AR091395 AR091395 Sequence
	93	35	11.4	1623	2	AR091394 AR091394 Sequence
	94	35	11.4	2307	2	CQ715179 CQ715179 Sequence
	95	35	11.4	2362	2	AR082684 AR082684 Sequence
	96	35	11.4	2362	2	AR122960 AR122960 Sequence
	97	35	11.4	2362	2	I28325 I28325 Sequence 1
	98	35	11.4	2362	2	AR309636 AR309636 Sequence
	99	35	11.4	2362	2	I89770 I89770 Sequence 1
	100	35	11.4	5686	2	BD136048 BD136048 Interfero
	101	35	11.4	6139	2	AR091393 AR091393 Sequence
c	102	33	10.7	681	7	BV440664 BV440664 S237P6324
	103	30	9.8	621	7	BV242752 BV242752 S234P6134
	104	28	9.1	224	14	DQ152965 DQ152965 Ovis arie
	105	28	9.1	525	14	CEU10160 U10160 Cervus elap
	106	28	9.1	969	2	AX154601 AX154601 Sequence
	107	28	9.1	984	2	AX154598 AX154598 Sequence
	108	28	9.1	984	14	AF004024 AF004024 Ovis arie
	109	28	9.1	984	14	AF209435 AF209435 Ovis arie
	110	28	9.1	993	14	AY603406 AY603406 Capra hir
	111	28	9.1	993	14	CEU57752 U57752 Cervus elap
	112	28	9.1	1008	14	AB246273 AB246273 Bubalus c
	113	28	9.1	1008	14	AB246358 AB246358 Bubalus b
	114	28	9.1	1012	14	AF007576 AF007576 Capra hir
	115	28	9.1	1012	14	BTU11815 U11815 Bos taurus
	116	28	9.1	1019	2	E35794 E35794 Process for
	117	28	9.1	2090	14	SSU08317 U08317 Sus scrofa
	118	27	8.8	932	14	AY686641S1 AY686641 Equus cab
	119	27	8.8	1058	14	ECIL12P40 Y11129 Equus cabal
	120	27	8.8	1626	8	AF401989 AF401989 Synthetic
	121	23	7.5	987	2	BD105974 BD105974 Animal mo
	122	23	7.5	987	2	AR533404 AR533404 Sequence
	123	23	7.5	1870	2	A92079 A92079 Sequence 3
	124	23	7.5	1870	2	AR230691 AR230691 Sequence
	125	23	7.5	2318	2	AR228993 AR228993 Sequence
	126	23	7.5	2318	5	HUMNKSFP40 M65290 Human natur
	127	22	7.2	200	5	AY591921 AY591921 Macaca fa
	128	22	7.2	999	6	AB025724 AB025724 Cavia por
	129	22	7.2	15648	5	AF512686 AF512686 Homo sapi
	130	22	7.2	18340	5	AY008847 AY008847 Homo sapi
	131	22	7.2	108511	5	AC011418 AC011418 Homo sapi
	132	21	6.8	528	6	AF082494 AF082494 Marmota m
	133	21	6.8	984	6	AF288519 AF288519 Marmota m
	134	21	6.8	984	6	MMIL12P40 X97019 M.monax mRN
	135	21	6.8	1425	6	AF421395 AF421395 Sigmodon
	136	20	6.5	399	2	CS211342 CS211342 Sequence
	137	20	6.5	399	2	CS214984 CS214984 Sequence
	138	20	6.5	399	6	AF046211 AF046211 Mesocrice
	139	20	6.5	2276	6	AB085792 AB085792 Mesocrice
	140	19	6.2	928	11	MGA564203 AJ564203 Meleagris
	141	19	6.2	948	2	CQ760887 CQ760887 Sequence
	142	19	6.2	948	2	CQ760890 CQ760890 Sequence
	143	19	6.2	948	2	CQ760892 CQ760892 Sequence
	144	19	6.2	948	11	DQ202328 DQ202328 Gallus ga
	145	19	6.2	948	11	AY262752 AY262752 Gallus ga
	146	17	5.5	73	2	AR439759 AR439759 Sequence
	147	17	5.5	73	2	AX268996 AX268996 Sequence
	148	17	5.5	508	6	AF097507 AF097507 Cavia por
	149	17	5.5	600	2	E26663 E26663 Improved me
	150	17	5.5	821	6	RNU16674 U16674 Rattus norv
	151	17	5.5	1008	6	AF133197 AF133197 Rattus no
	152	17	5.5	1061	2	AR069654 AR069654 Sequence
	153	17	5.5	1143	6	AF128214 AF128214 Mus muscu
	154	17	5.5	1143	6	AF128215 AF128215 Mus muscu
	155	17	5.5	1381	6	BC103608 BC103608 Mus muscu
	156	17	5.5	1381	6	BC103609 BC103609 Mus muscu
	157	17	5.5	1381	6	BC103610 BC103610 Mus muscu
	158	17	5.5	1381	6	BC103614 BC103614 Mus muscu
	159	17	5.5	1409	2	AR393787 AR393787 Sequence
	160	17	5.5	1409	2	AX084105 AX084105 Sequence
	161	17	5.5	1472	2	AR393786 AR393786 Sequence
	162	17	5.5	1472	2	AX084104 AX084104 Sequence
	163	17	5.5	1569	2	AR393796 AR393796 Sequence
	164	17	5.5	1569	2	AX084114 AX084114 Sequence
	165	17	5.5	1582	14	AY686641S2 AY686644 Equus cab
	166	17	5.5	1669	8	AF411293 AF411293 Synthetic
	167	17	5.5	1840	6	MUSIL40A M86671 Mus musculu
	168	17	5.5	2013	2	AR393795 AR393795 Sequence
	169	17	5.5	2013	2	AX084113 AX084113 Sequence
	170	17	5.5	2438	2	CQ812173 CQ812173 Sequence
	171	17	5.5	2709	2	AR393797 AR393797 Sequence
	172	17	5.5	2709	2	AX084115 AX084115 Sequence
	173	17	5.5	5252	2	CQ803341 CQ803341 Sequence
	174	17	5.5	5966	2	BD136050 BD136050 Interfero
	175	17	5.5	9049	2	CQ803350 CQ803350 Sequence
	176	17	5.5	10633	2	CQ803349 CQ803349 Sequence
	177	17	5.5	11746	2	CQ803348 CQ803348 Sequence
	178	17	5.5	38246	2	CQ803351 CQ803351 Sequence
	179	13	4.2	987	2	BD136055 BD136055 Interfero
	180	13	4.2	1000	6	S82420S3 S82422 interleukin
	181	13	4.2	76047	6	AL669944 AL669944 Mouse DNA
	182	13	4.2	110000	12	AC073744_2 Continuation (3 of
	183	13	4.2	110000	12	AC073744_3 Continuation (4 of
	184	13	4.2	189236	6	AL607030 AL607030 Mouse DNA
c	185	13	4.2	268294	12	AC020885 AC020885 Mus muscu
	186	13	4.2	287927	12	AC079530 AC079530 Mus muscu
	187	12	3.9	38	2	AR242440 AR242440 Sequence
	188	12	3.9	38	2	AR280208 AR280208 Sequence
	189	12	3.9	38	2	AR322423 AR322423 Sequence
	190	12	3.9	1062	6	AF288612 AF288612 Meriones
	191	12	3.9	1897	11	GGA564201 AJ564201 Gallus ga
	192	12	3.9	285389	12	AC096348 AC096348 Rattus no
	193	11	3.6	9821	11	GGA564202 AJ564202 Gallus ga
c	194	10	3.3	30	2	AX027245 AX027245 Sequence
	195	10	3.3	500	6	S82420S5 S82424 interleukin
c	196	10	3.3	2553	10	AF394057 AF394057 Porcine c
c	197	10	3.3	5668	10	AF268041 AF268041 Porcine c
c	198	10	3.3	6249	10	AF268039 AF268039 Porcine c
	199	10	3.3	21925	2	AX647863 AX647863 Sequence
	200	10	3.3	26184	2	AX647497 AX647497 Sequence

ALIGNMENTS

```
RESULT 1
AR595948
LOCUS       AR595948                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 26 from patent US 6818444.
ACCESSION   AR595948
VERSION     AR595948.1  GI:56646929
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 26 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
```

```
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          921
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR595948 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 2
AR595949/c
LOCUS       AR595949                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 28 from patent US 6818444.
ACCESSION   AR595949
VERSION     AR595949.1  GI:56646930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 28 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          921
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR595949 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

y         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

y         221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

y         241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

y         261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

y         281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

y         301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||||
b          21 TGGGCATCCGTGTCCTGCAGT 1

ESULT 3
CIL12P40
OCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
EFINITION  Felis catus mRNA for interleukin-12 p40 chain.
CCESSION   Y07762
ERSION     Y07762.1  GI:2102664
EYWORDS    interleukin-12 p40.
OURCE      Felis catus (cat)
 ORGANISM  Felis catus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
           Felinae; Felis.
EFERENCE   1
 AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
 TITLE     Molecular cloning of cat interleukin-12
 JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  PUBMED   9089110
EFERENCE   2  (bases 1 to 1006)
 AUTHORS   Schijns,V.E.C.J.
 TITLE     Direct Submission
 JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
           Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
           Utrecht, NETHERLANDS
EATURES             Location/Qualifiers
    source          1. .1006
                    /organism="Felis catus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9685"
                    /cell_type="lymphocyte"
                    /tissue_type="peripheral blood"
    gene            1. .1006
                    /gene="IL-12.p40"
    CDS             1. .990
                    /gene="IL-12.p40"
                    /note="heterodimer with IL-12 p35 chain"
                    /codon_start=1
                    /product="interleukin-12 p40 chain"
                    /protein_id="CAA69068.1"
                    /db_xref="GI:2102665"
                    /db_xref="GOA:O02744"
                    /db_xref="InterPro:IPR002996"
                    /db_xref="InterPro:IPR003530"
                    /db_xref="InterPro:IPR003961"
                    /db_xref="InterPro:IPR007110"
                    /db_xref="InterPro:IPR008957"
                    /db_xref="UniProtKB/Swiss-Prot:O02744"
                    /translation="MHPQQLVIAWLSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                    MVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                    LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                    GSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                    LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                    QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:              0               Length:         1006
Score:                  307.00          Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-27 (1-307) x FCIL12P40 (1-1006)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
```

```
Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 4
AR595959
LOCUS       AR595959               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0             Length:          1533
Score:                    307.00        Matches:         307
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              100.0%        Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-27 (1-307) x AR595959 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 5
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                0             Length:          1533
Score:                    307.00        Matches:         307
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              100.0%        Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-27 (1-307) x AR595960 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354
```

```
y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b        633 TGGGCATCCGTGTCCTGCAGT 613
```

```
ESULT 6
R595956
OCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 38 from patent US 6818444.
CCESSION   AR595956
ERSION     AR595956.1  GI:56646937
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 1599)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
    source          1. .1599
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN
```

```
Alignment Scores:
Pred. No.:                0              Length:          1599
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR595956 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
```

```
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 7
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                  0             Length:         1599
Score:                      307.00        Matches:        307
Percent Similarity:         100.0%        Conservative:   0
Best Local Similarity:      100.0%        Mismatches:     0
Query Match:                100.0%        Indels:         0
DB:                         2             Gaps:           0

US-10-821-670A-27 (1-307) x AR595957 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 8
AR242436
LOCUS       AR242436               921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6472509.
ACCESSION   AR242436
VERSION     AR242436.1  GI:27288853
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 6 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                  1.99e-229     Length:         921
Score:                      206.00        Matches:        306
Percent Similarity:         99.7%         Conservative:   0
Best Local Similarity:      99.7%         Mismatches:     1
Query Match:                67.1%         Indels:         0
DB:                         2             Gaps:           0

US-10-821-670A-27 (1-307) x AR242436 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
```

```
y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
b        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b        901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 9
R242437
OCUS       AR242437                 921 bp    mRNA    linear   PAT 20-DEC-2002
EFINITION  Sequence 7 from patent US 6472509.
CCESSION   AR242437
ERSION     AR242437.1  GI:27288854
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 921)
 AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
 TITLE     Feline cytokine protein
 JOURNAL   Patent: US 6472509-A 7 29-OCT-2002;
           Juridical Foundation: The Chemo-Seso-Therapeutic Research
           Institute; Kumamoto;
           EPX;
EATURES              Location/Qualifiers
    source           1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
RIGIN

lignment Scores:
red. No.:              1.99e-229      Length:        921

Score:                    206.00       Matches:       306
Percent Similarity:       99.7%        Conservative:  0
Best Local Similarity:    99.7%        Mismatches:    1
Query Match:              67.1%        Indels:        0
DB:                       2            Gaps:          0

US-10-821-670A-27 (1-307) x AR242437 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 10
```

```
AR280204
LOCUS       AR280204                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6518045.
ACCESSION   AR280204
VERSION     AR280204.1  GI:29715594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 6 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.99e-229      Length:          921
Score:                    206.00         Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              67.1%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR280204 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 11
AR280205
LOCUS       AR280205                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 7 from patent US 6518045.
ACCESSION   AR280205
VERSION     AR280205.1  GI:29715595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 7 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.99e-229      Length:          921
Score:                    206.00         Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              67.1%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR280205 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
```

```
b        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

b        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

b        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

b        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

b        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

b        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

b        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

b        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

b        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

b        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

y        301 TrpAlaSerValSerCysSer 307

b        901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 12
R322419
OCUS       AR322419                 921 bp    mRNA    linear   PAT 17-AUG-2003
EFINITION  Sequence 6 from patent US 6566097.
CCESSION   AR322419
ERSION     AR322419.1  GI:33708172
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 921)
 AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
 TITLE     Feline cytokine protein
 JOURNAL   Patent: US 6566097-A 6 20-MAY-2003;
           Juridical Foundation The Chemo-Sero-Therapeutic Research
           Institute;;
           EPX;
EATURES             Location/Qualifiers
    source          1. .921
                    /organism="unknown"
                    /mol_type="mRNA"
RIGIN

lignment Scores:
red. No.:              1.99e-229      Length:        921
core:                  206.00         Matches:       306
```

```
Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            67.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-27 (1-307) x AR322419 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307

Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 13
AR322420
```

```
LOCUS       AR322420                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 7 from patent US 6566097.
ACCESSION   AR322420
VERSION     AR322420.1  GI:33708173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 7 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                 1.99e-229     Length:          921
Score:                     206.00        Matches:         306
Percent Similarity:        99.7%         Conservative:    0
Best Local Similarity:     99.7%         Mismatches:      1
Query Match:               67.1%         Indels:          0
DB:                        2             Gaps:            0

US-10-821-670A-27 (1-307) x AR322420 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 14
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                 2.12e-229     Length:          987
Score:                     206.00        Matches:         306
Percent Similarity:        99.7%         Conservative:    0
Best Local Similarity:     99.7%         Mismatches:      1
Query Match:               67.1%         Indels:          0
DB:                        2             Gaps:            0

US-10-821-670A-27 (1-307) x AR595950 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
```

```
y       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

y       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

y       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
            ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
b       487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

y       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

y       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

y       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

y       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

y       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

y       301 TrpAlaSerValSerCysSer 307
            |||||||||||||||||||||
b       967 TGGGCATCCGTGTCCTGCAGT 987

ESULT 15
R595951/c
OCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 31 from patent US 6818444.
CCESSION   AR595951
ERSION     AR595951.1  GI:56646932
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 987)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
    source          1. .987
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
red. No.:               2.12e-229       Length:         987
core:                   206.00          Matches:        306
ercent Similarity:      99.7%           Conservative:   0
est Local Similarity:   99.7%           Mismatches:     1
uery Match:             67.1%           Indels:         0
B:                      2               Gaps:           0
```

```
US-10-821-670A-27 (1-307) x AR595951 (1-987)

Qy        1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy       21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy       41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy       61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy       81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy      101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy      121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy      141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
            ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db      501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy      161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy      241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy      261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy      301 TrpAlaSerValSerCysSer 307
            |||||||||||||||||||||
Db       21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 16
AX076200
LOCUS       AX076200                 990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
```

```
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:                2.13e-229      Length:         990
Score:                    206.00         Matches:        306
Percent Similarity:       99.7%          Conservative:   0
Best Local Similarity:    99.7%          Mismatches:     1
Query Match:              67.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x AX076200 (1-990)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 17
AX076482
LOCUS       AX076482                 990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:                2.13e-229      Length:         990
Score:                    206.00         Matches:        306
Percent Similarity:       99.7%          Conservative:   0
Best Local Similarity:    99.7%          Mismatches:     1
Query Match:              67.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x AX076482 (1-990)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
```

```
y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
b        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b        967 TGGGCATCCGTGTCCTGCAGT 987
```

```
ESULT 18
R242435
OCUS       AR242435               2193 bp    mRNA    linear   PAT 20-DEC-2002
EFINITION  Sequence 5 from patent US 6472509.
CCESSION   AR242435
ERSION     AR242435.1  GI:27288852
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 2193)
 AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
 TITLE     Feline cytokine protein
 JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
           Juridical Foundation: The Chemo-Seso-Therapeutic Research
           Institute; Kumamoto;
           EPX;
EATURES             Location/Qualifiers
    source          1. .2193
                    /organism="unknown"
                    /mol_type="mRNA"
RIGIN

lignment Scores:
red. No.:              4.5e-229       Length:        2193
core:                  206.00         Matches:       306
ercent Similarity:     99.7%          Conservative:  0
est Local Similarity:  99.7%          Mismatches:    1
```

```
Query Match:           67.1%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-27 (1-307) x AR242435 (1-2193)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db      1030 TGGGCATCCGTGTCCTGCAGT 1050
```

```
RESULT 19
AR280203
LOCUS       AR280203               2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
```

```
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                4.5e-229      Length:          2193
Score:                    206.00        Matches:         306
Percent Similarity:       99.7%         Conservative:    0
Best Local Similarity:    99.7%         Mismatches:      1
Query Match:              67.1%         Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-27 (1-307) x AR280203 (1-2193)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050

RESULT 20
AR322418
LOCUS       AR322418                2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                4.5e-229      Length:          2193
Score:                    206.00        Matches:         306
Percent Similarity:       99.7%         Conservative:    0
Best Local Similarity:    99.7%         Mismatches:      1
Query Match:              67.1%         Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-27 (1-307) x AR322418 (1-2193)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429
```

```
y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
b        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b       1030 TGGGCATCCGTGTCCTGCAGT 1050
```

ESULT 21
.X076209
OCUS AX076209 4522 bp DNA linear PAT 06-FEB-2001
EFINITION Sequence 10 from Patent WO0104155.
CCESSION AX076209
'ERSION AX076209.1 GI:12710834
EYWORDS .
OURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
EFERENCE 1
AUTHORS Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
TITLE Feline interleukin-12 as an immune stimulant
JOURNAL Patent: WO 0104155-A 10 18-JAN-2001;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
CALIFORNIA (US)
EATURES Location/Qualifiers
source 1. .4522
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Plasmid pMol-fil12p40"
RIGIN

lignment Scores:
red. No.: 8.89e-229 Length: 4522
core: 206.00 Matches: 306
ercent Similarity: 99.7% Conservative: 0

Best Local Similarity: 99.7% Mismatches: 1
Query Match: 67.1% Indels: 0
DB: 2 Gaps: 0

US-10-821-670A-27 (1-307) x AX076209 (1-4522)

```
Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db      3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db      4013 TGGGCATCCGTGTCCTGCAGT 4033
```

RESULT 22
AX076476
LOCUS AX076476 4522 bp DNA linear PAT 06-FEB-2001

```
)EFINITION  Sequence 2 from Patent WO0104280.
\CCESSION   AX076476
/ERSION     AX076476.1  GI:12711028
(EYWORDS    .
;OURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
<EFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
)RIGIN

Alignment Scores:
Pred. No.:                 8.89e-229       Length:          4522
Score:                     206.00          Matches:         306
Percent Similarity:        99.7%           Conservative:    0
Best Local Similarity:     99.7%           Mismatches:      1
Query Match:               67.1%           Indels:          0
DB:                        2               Gaps:            0

US-10-821-670A-27 (1-307) x AX076476 (1-4522)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db       4013 TGGGCATCCGTGTCCTGCAGT 4033

RESULT 23
AR595967
LOCUS       AR595967                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 55 from patent US 6818444.
ACCESSION   AR595967
VERSION     AR595967.1  GI:56646948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 55 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                 3.1e-228        Length:          985
Score:                     205.00          Matches:         305
Percent Similarity:        99.7%           Conservative:    0
Best Local Similarity:     99.7%           Mismatches:      1
Query Match:               66.8%           Indels:          0
DB:                        2               Gaps:            0

US-10-821-670A-27 (1-307) x AR595967 (1-985)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
```

```
y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
b        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

y        301 TrpAlaSerValSerCys 306
             ||||||||||||||||||
b        967 TGGGCATCCGTGTCCTGC 984

ESULT 24
.R595968/c
OCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 57 from patent US 6818444.
CCESSION   AR595968
ERSION     AR595968.1  GI:56646949
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 985)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
    source          1. .985
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

.lignment Scores:
red. No.:              3.1e-228       Length:        985
core:                  205.00         Matches:       305
ercent Similarity:     99.7%          Conservative:  0
est Local Similarity:  99.7%          Mismatches:    1
uery Match:            66.8%          Indels:        0
B:                     2              Gaps:          0
```

```
US-10-821-670A-27 (1-307) x AR595968 (1-985)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAAATTT 740

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db       499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy       301 TrpAlaSerValSerCys 306
             ||||||||||||||||||
Db        19 TGGGCATCCGTGTCCTGC 2

RESULT 25
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
```

```
(EYWORDS    .
)OURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
(EFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
    PUBMED  9522125
(EFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
'EATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCDTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
)RIGIN

\lignment Scores:
?red. No.:              1.37e-195       Length:         990
Score:                  177.00          Matches:        277
Percent Similarity:     99.6%           Conservative:   0
Best Local Similarity:  99.6%           Mismatches:     1
Query Match:            57.7%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-27 (1-307) x FCU83184 (1-990)

Qy         30 ThrProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySer 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ACGCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCT 213

Qy         50 GlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHis 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCAT 273

Qy         70 LysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATT 333

Qy         90 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGT 393

Qy        110 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGAT 453

Qy        130 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCysGly 149
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db        454 TTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGA 513

Qy        150 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACA 573

Qy        170 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633

Qy        190 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693

Qy        210 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Qy        230 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCC 813

Qy        250 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCC 873

Qy        270 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCC 933

Qy        290 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 307
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 AGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 26
AF054607
LOCUS       AF054607                 431 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p40 subunit mRNA, partial cds.
ACCESSION   AF054607
VERSION     AF054607.1  GI:3126822
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
    PUBMED  10391845
REFERENCE   2  (bases 1 to 431)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>431
                     /codon_start=1
                     /product="interleukin 12 p40 subunit"
                     /protein_id="AAC15980.1"
                     /db_xref="GI:3126823"
                     /translation="CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEA
                     KNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYT
                     VECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRD"
```

```
RIGIN

lignment Scores:
red. No.:              2.31e-65       Length:        431
core:                  65.00          Matches:       65
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            21.2%          Indels:        0
B:                     14             Gaps:          0

S-10-821-670A-27 (1-307) x AF054607 (1-431)

y       146 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       235 GTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTAT 294

y       166 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       295 AAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTA 354

y       186 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       355 CCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGC 414

y       206 PhePheIleArgAsp 210
            ||||||||||||||||
b       415 TTCTTCATCAGGGAC 429

ESULT 27
X154603
OCUS       AX154603                 990 bp    DNA     linear   PAT 22-JUN-2001
EFINITION  Sequence 7 from Patent WO0140257.
CCESSION   AX154603
ERSION     AX154603.1  GI:14536186
EYWORDS    .
OURCE      synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
EFERENCE   1
 AUTHORS   Leong,S.R. and Punnonen,J.
 TITLE     Cytokine polypeptides and nucleic acids
 JOURNAL   Patent: WO 0140257-A 7 07-JUN-2001;
           Maxygen, Inc. (US)
EATURES             Location/Qualifiers
    source          1. .990
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
RIGIN

lignment Scores:
red. No.:              7.21e-50       Length:        990
core:                  52.00          Matches:       52
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            16.9%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x AX154603 (1-990)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCTGACCCACCCAAGAACTTG 726

y       221 GlnLeuLysProLeuLysAsnSerArgHisValGlu 232
            ||||||||||||||||||||||||||||||||||||
b       727 CAGCTGAAGCCATTAAAGAATTCTCGACACGTGGAG 762

RESULT 28
AX154600
LOCUS       AX154600                 984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0140257.
ACCESSION   AX154600
VERSION     AX154600.1  GI:14536183
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 4 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:             2.23e-39       Length:        984
Score:                 43.00          Matches:       43
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           14.0%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-27 (1-307) x AX154600 (1-984)

Qy      102 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      370 AAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGG 429

Qy      122 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 141
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      430 TGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCT 489

Qy      142 AspProGln 144
            ||||||||
Db      490 GACCCCCAA 498

RESULT 29
AX154599
LOCUS       AX154599                 984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3 from Patent WO0140257.
ACCESSION   AX154599
VERSION     AX154599.1  GI:14536182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 3 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:             3.26e-38       Length:        984
Score:                 42.00          Matches:       42
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
```

```
Query Match:            13.7%       Indels:        0
DB:                     2           Gaps:          0

US-10-821-670A-27 (1-307) x AX154599 (1-984)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACTTG 726

Qy        221 GlnLeu 222
              ||||||
Db        727 CAGCTG 732

RESULT 30
AY191829
LOCUS       AY191829                 972 bp    mRNA    linear   SYN 04-FEB-2003
DEFINITION  Synthetic construct evolved IL-12 p40 precursor, mRNA, partial cds.
ACCESSION   AY191829
VERSION     AY191829.1  GI:27729525
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 972)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Optimized expression and specific activity of IL-12 by directed
            molecular evolution
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
   PUBMED   12529500
REFERENCE   2  (bases 1 to 972)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
            Drive, Redwood City, CA 94063, USA
FEATURES             Location/Qualifiers
     source          1. .972
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .>972
                     /codon_start=1
                     /transl_table=11
                     /product="evolved IL-12 p40 precursor"
                     /protein_id="AAO19112.1"
                     /db_xref="GI:27729526"
                     /translation="MCHQQLVISWFSLVLLASPLMAIWELKKDVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKNKSFLKCEAKNYSGRFTCWWLTTISTDLKFSVKSSR
                     GSTDPRGVTCGTATLSEDLGEYKKYRVECQEGSACPAAEESLPIEVVLEAVHKLKYEN
                     YTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWGYPDTWSTPHSYFSLTFCIQVQGK
                     SKREKKDRIFTDKTSATVICRKNAKIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide     1. .66
     mat_peptide     67. .972
                     /product="evolved IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:              4.72e-37        Length:         972
Score:                  41.00           Matches:        41
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.4%           Indels:         0
DB:                     8               Gaps:           0

US-10-821-670A-27 (1-307) x AY191829 (1-972)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

Qy        235 Trp 235
              |||
Db        754 TGG 756

RESULT 31
AX154597
LOCUS       AX154597                 975 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0140257.
ACCESSION   AX154597
VERSION     AX154597.1  GI:14536180
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 1 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .975
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

Alignment Scores:
Pred. No.:              4.74e-37        Length:         975
Score:                  41.00           Matches:        41
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AX154597 (1-975)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

Qy        235 Trp 235
              |||
Db        754 TGG 756

RESULT 32
AB107654
LOCUS       AB107654                 993 bp    mRNA    linear   MAM 29-APR-2004
DEFINITION  Lama glama IL-12 p40 mRNA for interleukin 12 p40 subunit, complete
            cds.
ACCESSION   AB107654
VERSION     AB107654.1  GI:29603618
KEYWORDS    .
SOURCE      Lama glama (llama)
  ORGANISM  Lama glama
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
            Camelidae; Lama.
REFERENCE   1
  AUTHORS   Odbileg,R., Lee,S.I., Yoshida,R., Chang,K.S., Ohashi,K.,
            Sugimoto,C. and Onuma,M.
  TITLE     Cloning and sequence analysis of llama cytokines related to
```

```
          cell-mediated immunity
 JOURNAL  Vet. Immunol. Immunopathol. 99 (1-2), 1-10 (2004)
  PUBMED  15113649
EFERENCE  2  (bases 1 to 993)
 AUTHORS  Ohashi,K., Raadan,O. and Lee,S.
 TITLE    Direct Submission
 JOURNAL  Submitted (04-APR-2003) Kazuhiko Ohashi, Graduate School of
          Veterinary Medicine, Hokkaido University, Department of Disease
          Control; Kita-ku Kita 18 Nishi 9, Sapporo, Hokkaido 060-0818, Japan
          (E-mail:okazu@vetmed.hokudai.ac.jp, Tel:81-11-706-5216,
          Fax:81-11-706-5217)
EATURES             Location/Qualifiers
    source          1. .993
                    /organism="Lama glama"
                    /mol_type="mRNA"
                    /db_xref="taxon:9844"
                    /sex="Female"
                    /cell_type="PBMC"
                    /country="Japan"
    gene            1. .993
                    /gene="IL-12 p40"
    CDS             1. .993
                    /gene="IL-12 p40"
                    /codon_start=1
                    /product="interleukin 12 p40 subunit"
                    /protein_id="BAC75391.1"
                    /db_xref="GI:29603619"
                    /translation="MHPQQLVVSWFSLVLLASPIMAIWELEKNVYVVELDWYPDAPGE
                    TVVLTCDTPEEDGITWTSDHSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                    LLHKKEDGVWSTDILKKDQKEPKSKTFLKCEAKNYSGHFTCWWLTAVSTDLKFSVKSS
                    RGSSDPRGVTCGAATLSAERVGVEHRDSWKYTVECQEGSSCPAAEESLPIELVVEAVH
                    KLKYENYSSSFFIRDIIRPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFC
                    VQVQGKHKREKKDKLFVDQTSAKVTCPKDASIRVQARDRYYSSSWSEWASVSCS"
RIGIN

lignment Scores:
red. No.:               1.03e-34        Length:         993
core:                   39.00           Matches:        39
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             12.7%           Indels:         0
B:                      14              Gaps:           0

S-10-821-670A-27 (1-307) x AB107654 (1-993)

y       214 ProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluVal 233
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       709 CCAGACCCACCCAAGAATCTGCAGCTGAAGCCATTGAAGAATTCTCGGCACGTGGAGGTC 768

y       234 SerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPhe 252
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       769 AGCTGGGAGTACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACGTTT 825

ESULT 33
Y234218
OCUS        AY234218               1005 bp    mRNA    linear   PRI 07-APR-2003
EFINITION   Papio anubis interleukin-12 alpha p40 subunit precursor (IL12a)
            mRNA, complete cds.
CCESSION    AY234218
ERSION      AY234218.1  GI:29569754
EYWORDS     .
OURCE       Papio anubis (olive baboon)
 ORGANISM   Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
EFERENCE    1  (bases 1 to 1005)
 AUTHORS    Villinger,F.
 TITLE      Nonhuman primate cytokines
 JOURNAL    Unpublished
EFERENCE    2  (bases 1 to 1005)
 AUTHORS    Villinger,F.
 TITLE      Direct Submission
 JOURNAL    Submitted (12-FEB-2003) Pathology & Laboratory Medicine, Emory
            University School of Medicine, Woodruff Memorial Building Rm 2339,
            1639 Pierce Drive, Atlanta, GA 30322, USA
EATURES             Location/Qualifiers
    source          1. .1005
                    /organism="Papio anubis"
                    /mol_type="mRNA"
                    /db_xref="taxon:9555"
    gene            1. .1005
                    /gene="IL12a"
    CDS             9. .995
                    /gene="IL12a"
                    /codon_start=1
                    /product="interleukin-12 alpha p40 subunit precursor"
                    /protein_id="AAO85331.1"
                    /db_xref="GI:29569755"
                    /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                    MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                    LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                    GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                    KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQAEVSWEYPDTWSTPHSYFSLTFCIQ
                    VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
    sig_peptide     9. .74
                    /gene="IL12a"
    mat_peptide     75. .992
                    /gene="IL12a"
                    /product="interleukin-12 alpha p40 subunit"
ORIGIN

Alignment Scores:
Pred. No.:              1.05e-34        Length:         1005
Score:                  39.00           Matches:        39
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.7%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-27 (1-307) x AY234218 (1-1005)

Qy      191 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 210
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      642 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 701

Qy      211 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      702 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 758

RESULT 34
CTU19834
LOCUS       CTU19834               1005 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Cercocebus torquatus interleukin-12 alpha p40 subunit (IL-12a)
            mRNA, complete cds.
ACCESSION   U19834
VERSION     U19834.1  GI:644785
KEYWORDS    .
SOURCE      Cercocebus torquatus (red-crowned mangabey)
  ORGANISM  Cercocebus torquatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Cercocebus.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES            Location/Qualifiers
    source          1. .1005
```

```
                     /organism="Cercocebus torquatus"
                     /mol_type="mRNA"
                     /sub_species="atys"
                     /db_xref="taxon:9530"
                     /clone="FPn IL-12a"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .1005
                     /gene="IL-12a"
     CDS             9. .995
                     /gene="IL-12a"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit"
                     /protein_id="AAA86701.1"
                     /db_xref="GI:644786"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LPHKKEDGIWSTDILKDQKEPKNETFLRCEAKNYSGRITCWWLSTISTDLTFSIISSR
                     GSSNPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWNEWTSVPCS"
)RIGIN

\lignment Scores:
'red. No.:              1.05e-34       Length:         1005
;core:                  39.00          Matches:        39
'ercent Similarity:     100.0%         Conservative:   0
;est Local Similarity:  100.0%         Mismatches:     0
)uery Match:            12.7%          Indels:         0
)B:                     5              Gaps:           0

)S-10-821-670A-27 (1-307) x CTU19834 (1-1005)

)y        191 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        642 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 701

)y        211 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        702 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 758

!ESULT 35
!MU19841
;OCUS       MMU19841               1080 bp    mRNA    linear   PRI 03-FEB-1996
)EFINITION  Macaca mulatta interleukin-12 alpha (IL-12a) mRNA, complete cds.
\CCESSION   U19841
/ERSION     U19841.1  GI:644799
<EYWORDS    .
;OURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
!EFERENCE   1  (bases 1 to 1080)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
    PUBMED  7561102
!EFERENCE   2  (bases 1 to 1080)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
'EATURES             Location/Qualifiers
     source          1. .1080
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /clone="RSo IL-12a clone 4"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .1080
                     /gene="IL-12a"
     CDS             13. .999
                     /gene="IL-12a"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 alpha"
                     /protein_id="AAB60397.1"
                     /db_xref="GI:644800"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
     variation       329
                     /gene="IL-12a"
                     /replace="t"
     variation       405
                     /gene="IL-12a"
                     /replace="c"
     variation       519
                     /gene="IL-12a"
                     /replace="a"
     variation       629
                     /gene="IL-12a"
                     /note="Leu to Pro"
                     /replace="c"
     variation       665
                     /gene="IL-12a"
                     /note="Leu to Pro"
                     /replace="c"
     variation       714
                     /gene="IL-12a"
                     /replace="g"
     variation       878
                     /gene="IL-12a"
                     /note="Ile to Thr"
                     /replace="c"
     variation       895
                     /gene="IL-12a"
                     /note="Ser to Pro"
                     /replace="c"
ORIGIN

Alignment Scores:
Pred. No.:              1.12e-34       Length:         1080
Score:                  39.00          Matches:        39
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            12.7%          Indels:         0
DB:                     5              Gaps:           0

US-10-821-670A-27 (1-307) x MMU19841 (1-1080)

Qy        191 ValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAsp 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GTGGATGCCATTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 705

Qy        211 IleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 ATCATCAAACCCGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 762

RESULT 36
AR595965
LOCUS       AR595965               921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 52 from patent US 6818444.
ACCESSION   AR595965
VERSION     AR595965.1  GI:56646946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
EFERENCE   1  (bases 1 to 921)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 52 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
    source          1. .921
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
red. No.:              2.07e-32       Length:        921
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            12.1%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x AR595965 (1-921)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b       601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

ESULT 37
R595966/c
OCUS       AR595966                921 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 54 from patent US 6818444.
CCESSION   AR595966
ERSION     AR595966.1  GI:56646947
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 921)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 54 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
    source          1. .921
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
red. No.:              2.07e-32       Length:        921
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            12.1%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x AR595966 (1-921)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b       321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

ESULT 38
D171282
OCUS       BD171282                924 bp    DNA     linear   PAT 18-FEB-2003
EFINITION  Novel canine cytokine protein.
CCESSION   BD171282
VERSION    BD171282.1  GI:28412572
KEYWORDS   JP 2002241398-A/2.
SOURCE     unidentified
  ORGANISM unidentified
           unclassified sequences.
REFERENCE  1  (bases 1 to 924)
  AUTHORS  Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE    Novel canine cytokine protein
  JOURNAL  Patent: JP 2002241398-A 2 28-AUG-2002;
           CHEMO SERO THERAPEUT RES INST
COMMENT    OS   Canine splenocyte
           PN   JP 2002241398-A/2
           PD   28-AUG-2002
           PF   03-JUN-1997 JP 1997161936
           PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
             C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
           C12P21/02//
           PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
             Strandedness: Double;
           CC   Topology: Linear;
           FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .924
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:             2.07e-32       Length:        924
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           12.1%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-27 (1-307) x BD171282 (1-924)

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      544 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 603

Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      604 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 654

RESULT 39
AR595969
LOCUS      AR595969                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION Sequence 58 from patent US 6818444.
ACCESSION  AR595969
VERSION    AR595969.1  GI:56646950
KEYWORDS   .
SOURCE     Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 987)
  AUTHORS  Wonderling,R.S. and Boroughs,K.L.
  TITLE    Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL  Patent: US 6818444-A 58 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .987
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:             2.21e-32       Length:        987
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           12.1%          Indels:        0
```

```
)B:                    2             Gaps:          0

)S-10-821-670A-27 (1-307) x AR595969 (1-987)

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
)b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

{ESULT 40
AR595970/c
)OCUS       AR595970               987 bp    DNA     linear   PAT 15-DEC-2004
)EFINITION  Sequence 60 from patent US 6818444.
\CCESSION   AR595970
/ERSION     AR595970.1  GI:56646951
{EYWORDS    .
;OURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
{EFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 60 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
'EATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
)RIGIN

\lignment Scores:
'red. No.:                2.21e-32       Length:         987
;core:                    37.00          Matches:        37
'ercent Similarity:       100.0%         Conservative:   0
}est Local Similarity:    100.0%         Mismatches:     0
}uery Match:              12.1%          Indels:         0
)B:                       2              Gaps:           0

)S-10-821-670A-27 (1-307) x AR595970 (1-987)

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
)b        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

{ESULT 41
\R151061
)OCUS       AR151061               990 bp    DNA     linear   PAT 08-AUG-2001
)EFINITION  Sequence 1 from patent US 6231850.
\CCESSION   AR151061
/ERSION     AR151061.1  GI:15117111
{EYWORDS    .
;OURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
{EFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
'EATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="unassigned DNA"
)RIGIN

\lignment Scores:
'red. No.:                2.21e-32       Length:         990
Score:                    37.00          Matches:        37
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              12.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x AR151061 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 42
AR151071
LOCUS       AR151071               990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6231850.
ACCESSION   AR151071
VERSION     AR151071.1  GI:15117121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 11 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.21e-32       Length:         990
Score:                    37.00          Matches:        37
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              12.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x AR151071 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 43
BD014653
LOCUS       BD014653               990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014653
VERSION     BD014653.1  GI:22555436
KEYWORDS    JP 2001161378-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
```

```
 JOURNAL   Patent: JP 2001161378-A 1 19-JUN-2001;
           TORAY INDUSTRIES INC
OMMENT     OS   Canis sp. (dog)
           PN   JP 2001161378-A/1
           PD   19-JUN-2001
           PF   26-SEP-2000 JP 2000292946
           PI   FUMIYOSHI OKANO
           PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
           PC   A61P35/00,
           PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
           PC   C12R1:91),
           PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
           CC   Process for producing highly pure protein, interleukin 12,  CC
                    protein
           CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                    immunopathy and
           CC   method of treating immunopathy
           FH   Key             Location/Qualifiers
           FT   CDS             (1). .(987)
           FT   mat_peptide     (67). .(987).
EATURES              Location/Qualifiers
    source           1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
RIGIN

lignment Scores:
red. No.:              2.21e-32       Length:        990
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            12.1%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x BD014653 (1-990)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 44
D014663
OCUS       BD014663                 990 bp    DNA     linear   PAT 27-AUG-2002
EFINITION  Process for producing highly pure protein, interleukin 12, protein
           inhibiting interleukin-12 activity, remedies for mammalian
           immunopathy and method of treating immunopathy.
CCESSION   BD014663
ERSION     BD014663.1  GI:22555446
EYWORDS    JP 2001161378-A/11.
OURCE      Canis sp.
 ORGANISM  Canis sp.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
           Canis.
EFERENCE   1  (bases 1 to 990)
 AUTHORS   Okano,F.
 TITLE     Process for producing highly pure protein, interleukin 12, protein
           inhibiting interleukin-12 activity, remedies for mammalian
           immunopathy and method of treating immunopathy
 JOURNAL   Patent: JP 2001161378-A 11 19-JUN-2001;
           TORAY INDUSTRIES INC
OMMENT     OS   Canis sp. (dog)
           PN   JP 2001161378-A/11
           PD   19-JUN-2001
           PF   26-SEP-2000 JP 2000292946
           PI   FUMIYOSHI OKANO
           PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
           PC   A61P35/00,
           PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
           PC   C12R1:91),
           PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
           CC   Process for producing highly pure protein, interleukin 12,  CC
                    protein
           CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                    immunopathy and
           CC   method of treating immunopathy
           FH   Key             Location/Qualifiers
           FT   CDS             (1). .(987)
           FT   mat_peptide     (67). .(987).
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:             2.21e-32       Length:        990
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           12.1%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-27 (1-307) x BD014663 (1-990)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 45
E15017
LOCUS       E15017                   990 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 40kDa subunit,complete cds.
ACCESSION   E15017
VERSION     E15017.1  GI:5709700
KEYWORDS    JP 1998036397-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 1 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/1
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .990
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .990
            FT                   /product='interleukin 12 40kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .990
```

```
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

Alignment Scores:
Pred. No.:                2.21e-32       Length:         990
Score:                    37.00          Matches:        37
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              12.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x E15017 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 46
AR316460
LOCUS       AR316460                990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6562334.
ACCESSION   AR316460
VERSION     AR316460.1  GI:33695288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 1 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.21e-32       Length:         990
Score:                    37.00          Matches:        37
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              12.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x AR316460 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 47
AR316470
LOCUS       AR316470                990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6562334.
ACCESSION   AR316470
VERSION     AR316470.1  GI:33695298
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 11 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.21e-32       Length:         990
Score:                    37.00          Matches:        37
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              12.1%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x AR316470 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 48
CFU49100
LOCUS       CFU49100                1015 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U49100
VERSION     U49100.1  GI:1223907
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .1015
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .990
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAA92059.1"
                     /db_xref="GI:1223908"
                     /translation="MHPQQLVISWFSLVLLASSLMTIWELEKDVYVVELDWHPDAPGE
                     MVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLL
                     LIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCV
                     QAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:                2.27e-32       Length:         1015
Score:                    37.00          Matches:        37
```

```
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            12.1%           Indels:        0
B:                     14              Gaps:          0

S-10-821-670A-27 (1-307) x CFU49100 (1-1015)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 49
R595973
OCUS       AR595973               1533 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 66 from patent US 6818444.
CCESSION   AR595973
ERSION     AR595973.1  GI:56646954
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 1533)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
    source          1. .1533
                    /organism="unknown"
                    /mol_type="genomic DNA"
RIGIN

lignment Scores:
red. No.:              3.34e-32        Length:        1533
core:                  37.00           Matches:       37
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            12.1%           Indels:        0
B:                     2               Gaps:          0

S-10-821-670A-27 (1-307) x AR595973 (1-1533)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

ESULT 50
R595974/c
OCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
EFINITION  Sequence 68 from patent US 6818444.
CCESSION   AR595974
ERSION     AR595974.1  GI:56646955
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 1533)
 AUTHORS   Wonderling,R.S. and Boroughs,K.L.
 TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
 JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
EATURES             Location/Qualifiers
    source          1. .1533
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:             3.34e-32        Length:        1533
Score:                 37.00           Matches:       37
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           12.1%           Indels:        0
DB:                    2               Gaps:          0

US-10-821-670A-27 (1-307) x AR595974 (1-1533)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 51
AR595971
LOCUS      AR595971               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION Sequence 61 from patent US 6818444.
ACCESSION  AR595971
VERSION    AR595971.1  GI:56646952
KEYWORDS   .
SOURCE     Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 1599)
  AUTHORS  Wonderling,R.S. and Boroughs,K.L.
  TITLE    Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL  Patent: US 6818444-A 61 16-NOV-2004;
           Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:             3.47e-32        Length:        1599
Score:                 37.00           Matches:       37
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           12.1%           Indels:        0
DB:                    2               Gaps:          0

US-10-821-670A-27 (1-307) x AR595971 (1-1599)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 52
AR595972/c
LOCUS      AR595972               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION Sequence 63 from patent US 6818444.
ACCESSION  AR595972
VERSION    AR595972.1  GI:56646953
KEYWORDS   .
SOURCE     Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 1599)
  AUTHORS  Wonderling,R.S. and Boroughs,K.L.
  TITLE    Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL  Patent: US 6818444-A 63 16-NOV-2004;
```

```
          Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.47e-32        Length:         1599
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR595972 (1-1599)

Qy         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 53
BD171281
LOCUS       BD171281                2154 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171281
VERSION     BD171281.1  GI:28412571
KEYWORDS    JP 2002241398-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 2154)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 1 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/1
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .2154
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              4.6e-32         Length:         2154
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x BD171281 (1-2154)

Qy         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 720

Qy         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 771

RESULT 54
AR596011
LOCUS       AR596011                2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 107 from patent US 6818444.
ACCESSION   AR596011
VERSION     AR596011.1  GI:56646992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 107 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .2267
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.83e-32        Length:         2267
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR596011 (1-2267)

Qy         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 55
AR596012/c
LOCUS       AR596012                2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 109 from patent US 6818444.
ACCESSION   AR596012
VERSION     AR596012.1  GI:56646993
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 109 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .2267
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.83e-32        Length:         2267
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR596012 (1-2267)
```

```
y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

ESULT 56
F091134
OCUS       AF091134                 446 bp    mRNA    linear   MAM 04-AUG-1999
EFINITION  Canis familiaris interleukin-12 p40 mRNA, partial cds.
CCESSION   AF091134
ERSION     AF091134.1  GI:5690205
EYWORDS    .
OURCE      Canis familiaris (dog)
 ORGANISM  Canis familiaris
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
           Canis.
EFERENCE   1  (bases 1 to 446)
 AUTHORS   German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J.
 TITLE     Cloning and sequencing of canine IL-12 p40 mRNA
 JOURNAL   Unpublished
EFERENCE   2  (bases 1 to 446)
 AUTHORS   German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J.
 TITLE     Direct Submission
 JOURNAL   Submitted (12-SEP-1998) Department of Clinical Veterinary Science,
           University of Bristol, Langford House, Langford, Bristol, North
           Somerset BS40 5DU, United Kingdom
EATURES             Location/Qualifiers
    source          1. .446
                    /organism="Canis familiaris"
                    /mol_type="mRNA"
                    /db_xref="taxon:9615"
    CDS             <1. .>446
                    /note="Il-12 p40"
                    /codon_start=1
                    /product="interleukin-12 p40"
                    /protein_id="AAD46992.1"
                    /db_xref="GI:5690206"
                    /translation="LGAGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIW
                    STDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTC
                    GAVTLSAERVRVDNRDYNKYTVECQEGSACPSAEESLPIEVVVDAIP"
RIGIN

lignment Scores:
red. No.:              1.53e-31       Length:        446
core:                  36.00          Matches:       36
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.7%          Indels:        0
B:                     14             Gaps:          0

S-10-821-670A-27 (1-307) x AF091134 (1-446)

y         97 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 116
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        151 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 210

y        117 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
             ||||||||||||||||||||||||||||||||||||||||||||||||
b        211 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 258

ESULT 57
F333121
OCUS       AF333121                 452 bp    mRNA    linear   MAM 06-FEB-2001
EFINITION  Canis familiaris interleukin 12 subunit p40 mRNA, partial cds.
CCESSION   AF333121
ERSION     AF333121.1  GI:12667429
EYWORDS    .
OURCE      Canis familiaris (dog)
 ORGANISM  Canis familiaris
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
           Canis.
EFERENCE   1  (bases 1 to 452)
 AUTHORS   Markus,S. and Baumgaertner,W.
 TITLE     Expression of canine interleukin-12 subunit p40 mRNA in a
           continuous macrophage cell line
 JOURNAL   Unpublished
EFERENCE   2  (bases 1 to 452)
 AUTHORS   Markus,S. and Baumgaertner,W.
 TITLE     Direct Submission
 JOURNAL   Submitted (03-JAN-2001) Department of Veterinary Pathology,
           Justus-Liebig-University of Giessen, Frankfurter Strasse 96,
           Giessen 35392, Germany
EATURES             Location/Qualifiers
    source          1. .452
                    /organism="Canis familiaris"
                    /mol_type="mRNA"
                    /db_xref="taxon:9615"
                    /cell_line="DH 82"
                    /cell_type="macrophage"
                    /note="amplified using primer pair p77s/p34as"
    CDS             <1. .>452
                    /codon_start=2
                    /product="interleukin 12 subunit p40"
                    /protein_id="AAK01441.1"
                    /db_xref="GI:12667430"
                    /translation="TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK
                    GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST
                    DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
RIGIN

Alignment Scores:
Pred. No.:              1.55e-31       Length:        452
Score:                  36.00          Matches:       36
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.7%          Indels:        0
DB:                     14             Gaps:          0

US-10-821-670A-27 (1-307) x AF333121 (1-452)

Qy         97 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 271

Qy        117 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 319

RESULT 58
AF349536
LOCUS       AF349536                 588 bp    mRNA    linear   MAM 17-MAY-2001
DEFINITION  Canis familiaris interleukin-12 subunit p40 mRNA, partial cds.
ACCESSION   AF349536
VERSION     AF349536.1  GI:14133584
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
  TITLE     Sequence of canine interleukin-12-p40 mRNA in DH82-cells
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 588)
  AUTHORS   Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2001) Institute of Pathology,
            Justus-Liebig-University, Frankfurter Str. 96, Giessen 35392,
            Germany
FEATURES              Location/Qualifiers
```

```
     source          1. .588
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /cell_line="DH82"
     CDS             <1. .>588
                     /codon_start=3
                     /product="interleukin-12 subunit p40"
                     /protein_id="AAK54070.1"
                     /db_xref="GI:14133585"
                     /translation="QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVV
                     LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIH
                     KKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFS
                     DPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
)RIGIN

\lignment Scores:
)red. No.:              1.98e-31        Length:         588
;core:                  36.00           Matches:        36
)ercent Similarity:     100.0%          Conservative:   0
}est Local Similarity:  100.0%          Mismatches:     0
}uery Match:            11.7%           Indels:         0
)B:                     14              Gaps:           0

)S-10-821-670A-27 (1-307) x AF349536 (1-588)

)y          97 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 116
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         348 GAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGA 407

)y         117 ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
               ||||||||||||||||||||||||||||||||||||||||||||||||
)b         408 CGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTC 455

{ESULT 59
}D021808
\OCUS       BD021808                906 bp    DNA     linear   PAT 27-AUG-2002
)EFINITION  Natural killer stimulatory factor.
\CCESSION   BD021808
/ERSION     BD021808.1  GI:22563031
{EYWORDS    JP 2001245678-A/1.
}OURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
!EFERENCE   1  (bases 1 to 906)
  AUTHORS   Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
            Hewick,R.M.
  TITLE     Natural killer stimulatory factor
  JOURNAL   Patent: JP 2001245678-A 1 11-SEP-2001;
            GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
:OMMENT     OS   Unidentified
            PN   JP 2001245678-A/1
            PD   11-SEP-2001
            PF   10-JAN-2001 JP 2001002839
            PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
            GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
            CLARK,
            PI   GORDON G WONG,RODNEY M HEWICK
            PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
            PC   A61P43/00,
            PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
            Natural killer stimulatory factor
            FH   Key             Location/Qualifiers
            FT   source          1. .906
            FT                   /organism='Unidentified'.
'EATURES             Location/Qualifiers
     source          1. .906
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
)RIGIN

\lignment Scores:
```

```
Pred. No.:              4.37e-30        Length:         906
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x BD021808 (1-906)

Qy         195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy         215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
               |||||||||||||||||||||||||||||||||||||||||||||
Db         738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 60
BD021809
LOCUS       BD021809                906 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Natural killer stimulatory factor.
ACCESSION   BD021809
VERSION     BD021809.1  GI:22563032
KEYWORDS    JP 2001245678-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
            Hewick,R.M.
  TITLE     Natural killer stimulatory factor
  JOURNAL   Patent: JP 2001245678-A 2 11-SEP-2001;
            GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2001245678-A/2
            PD   11-SEP-2001
            PF   10-JAN-2001 JP 2001002839
            PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
            GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
            CLARK,
            PI   GORDON G WONG,RODNEY M HEWICK
            PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
            PC   A61P43/00,
            PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
            Natural killer stimulatory factor
            FH   Key             Location/Qualifiers
            FT   source          1. .906
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              4.37e-30        Length:         906
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x BD021809 (1-906)

Qy         195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy         215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
               |||||||||||||||||||||||||||||||||||||||||||||
Db         738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782
```

```
ESULT 61
X154602
OCUS       AX154602                 975 bp    DNA     linear   PAT 22-JUN-2001
EFINITION  Sequence 6 from Patent WO0140257.
CCESSION   AX154602
ERSION     AX154602.1  GI:14536185
EYWORDS    .
OURCE      synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
EFERENCE   1
 AUTHORS   Leong,S.R. and Punnonen,J.
 TITLE     Cytokine polypeptides and nucleic acids
 JOURNAL   Patent: WO 0140257-A 6 07-JUN-2001;
           Maxygen, Inc. (US)
EATURES             Location/Qualifiers
    source          1. .975
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Synthetic Sequence"
RIGIN

lignment Scores:
red. No.:              4.68e-30       Length:         975
core:                  35.00          Matches:        35
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            11.4%          Indels:         0
B:                     2              Gaps:           0

S-10-821-670A-27 (1-307) x AX154602 (1-975)

y        106 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        382 TTTCTAAAGTGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGGTGGCTGACGGCA 441

y        126 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             |||||||||||||||||||||||||||||||||||||||||||||
b        442 ATCAGTACTGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

ESULT 62
R008950
OCUS       AR008950                 987 bp    DNA     linear   PAT 04-DEC-1998
EFINITION  Sequence 1 from patent US 5756085.
CCESSION   AR008950
ERSION     AR008950.1  GI:3967755
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 987)
 AUTHORS   Sykes,M. and Wolf,S.F.
 TITLE     Use of interleukin-12 to prevent graft versus host disease
 JOURNAL   Patent: US 5756085-A 1 26-MAY-1998;
EATURES             Location/Qualifiers
    source          1. .987
                    /organism="unknown"
                    /mol_type="unassigned DNA"
RIGIN

lignment Scores:
red. No.:              4.73e-30       Length:         987
core:                  35.00          Matches:        35
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            11.4%          Indels:         0
B:                     2              Gaps:           0

S-10-821-670A-27 (1-307) x AR008950 (1-987)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 63
BD007070
LOCUS       BD007070                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007070
VERSION     BD007070.1  GI:18635441
KEYWORDS    JP 2001503257-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 1 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .987
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:             4.73e-30       Length:         987
Score:                 35.00          Matches:        35
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           11.4%          Indels:         0
DB:                    2              Gaps:           0

US-10-821-670A-27 (1-307) x BD007070 (1-987)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 64
BD007076
LOCUS       BD007076                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007076
VERSION     BD007076.1  GI:18635447
KEYWORDS    JP 2001503258-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
```

```
  JOURNAL   Patent: JP 2001503258-A 1 13-MAR-2001;
            BARENTISU INC
:OMMENT     OS   Unidentified
            PN   JP 2001503258-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
'EATURES              Location/Qualifiers
     source           1. .987
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
)RIGIN

\lignment Scores:
'red. No.:              4.73e-30        Length:         987
;core:                  35.00           Matches:        35
'ercent Similarity:     100.0%          Conservative:   0
}est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            11.4%           Indels:         0
)B:                     2               Gaps:           0

)S-10-821-670A-27 (1-307) x BD007076 (1-987)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
)b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

:ESULT 65
)D007077
;OCUS       BD007077                 987 bp    DNA     linear   PAT 31-JAN-2002
)EFINITION  Gene expression and delivery systems and uses.
\CCESSION   BD007077
'ERSION     BD007077.1  GI:18635448
:EYWORDS    JP 2001503258-A/2.
;OURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
:EFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 2 13-MAR-2001;
            BARENTISU INC
:OMMENT     OS   Unidentified
            PN   JP 2001503258-A/2
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
'EATURES              Location/Qualifiers
     source           1. .987
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              4.73e-30        Length:         987
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x BD007077 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 66
BD007078
LOCUS       BD007078                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007078
VERSION     BD007078.1  GI:18635449
KEYWORDS    JP 2001503258-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 3 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/3
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .987
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              4.73e-30        Length:         987
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x BD007078 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750
```

```
ESULT 67
D136034
OCUS       BD136034                 987 bp    DNA     linear   PAT 18-SEP-2002
EFINITION  Interferon alpha plasmid and delivery system and method of
           preparing and using the same.
CCESSION   BD136034
ERSION     BD136034.1  GI:23230979
EYWORDS    JP 2002506647-A/1.
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
EFERENCE   1  (bases 1 to 987)
 AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
 TITLE     Interferon alpha plasmid and delivery system and method of
           preparing and using the same
 JOURNAL   Patent: JP 2002506647-A 1 05-MAR-2002;
           VALENTIS INC
OMMENT     OS   Homo sapiens (human)
           PN   JP 2002506647-A/1
           PD   05-MAR-2002
           PF   12-MAR-1999 JP 2000536861
           PR   19-MAR-1998 US    60/078654
           PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
           PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
           PC   C12N1/15,
           PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
            C12N5/00
           CC   Interferon alpha plasmid and delivery system and method of  CC
                    preparing and
           CC   using the same
           FH   Key             Location/Qualifiers
           FT   source          1. .987
           FT                   /organism='Homo sapiens (human)'.
EATURES              Location/Qualifiers
    source           1. .987
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
RIGIN

lignment Scores:
red. No.:              4.73e-30       Length:        987
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x BD136034 (1-987)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 68
D136035
OCUS       BD136035                 987 bp    DNA     linear   PAT 18-SEP-2002
EFINITION  Interferon alpha plasmid and delivery system and method of
           preparing and using the same.
CCESSION   BD136035
ERSION     BD136035.1  GI:23230980
EYWORDS    JP 2002506647-A/2.
OURCE      synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
EFERENCE   1  (bases 1 to 987)
 AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
 TITLE     Interferon alpha plasmid and delivery system and method of
           preparing and using the same
 JOURNAL   Patent: JP 2002506647-A 2 05-MAR-2002;
           VALENTIS INC
COMMENT    OS   Artificial Sequence
           PN   JP 2002506647-A/2
           PD   05-MAR-2002
           PF   12-MAR-1999 JP 2000536861
           PR   19-MAR-1998 US    60/078654
           PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
           PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
           PC   C12N1/15,
           PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
            C12N5/00
           CC   Sequence source: all codons optimized
           FH   Key             Location/Qualifiers
           FT   source          1. .987
           FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:             4.73e-30       Length:        987
Score:                 35.00          Matches:       35
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           11.4%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-27 (1-307) x BD136035 (1-987)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 69
BD136036
LOCUS      BD136036                 987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION Interferon alpha plasmid and delivery system and method of
           preparing and using the same.
ACCESSION  BD136036
VERSION    BD136036.1  GI:23230981
KEYWORDS   JP 2002506647-A/3.
SOURCE     synthetic construct
  ORGANISM synthetic construct
           other sequences; artificial sequences.
REFERENCE  1  (bases 1 to 987)
  AUTHORS  Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE    Interferon alpha plasmid and delivery system and method of
           preparing and using the same
  JOURNAL  Patent: JP 2002506647-A 3 05-MAR-2002;
           VALENTIS INC
COMMENT    OS   Artificial Sequence
           PN   JP 2002506647-A/3
           PD   05-MAR-2002
           PF   12-MAR-1999 JP 2000536861
           PR   19-MAR-1998 US    60/078654
           PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
           PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
           PC   C12N1/15,
           PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
            C12N5/00
           CC   Sequence source: most codons optimized
           FH   Key             Location/Qualifiers
           FT   source          1. .987
```

```
          FT                   /organism='Artificial Sequence'.
'EATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
)RIGIN

\lignment Scores:
'red. No.:                4.73e-30       Length:         987
;core:                    35.00          Matches:        35
'ercent Similarity:       100.0%         Conservative:   0
;est Local Similarity:    100.0%         Mismatches:     0
}uery Match:              11.4%          Indels:         0
)B:                       2              Gaps:           0

)S-10-821-670A-27 (1-307) x BD136036 (1-987)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
)b        706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

!ESULT 70
:Q803342
.OCUS       CQ803342                 987 bp    DNA     linear   PAT 10-MAY-2004
)EFINITION  Sequence 2 from Patent WO2004035799.
\CCESSION   CQ803342
/ERSION     CQ803342.1  GI:47110208
:EYWORDS    .
;OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
!EFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 2 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
'EATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
)RIGIN

\lignment Scores:
'red. No.:                4.73e-30       Length:         987
;core:                    35.00          Matches:        35
'ercent Similarity:       100.0%         Conservative:   0
;est Local Similarity:    100.0%         Mismatches:     0
}uery Match:              11.4%          Indels:         0
)B:                       2              Gaps:           0

)S-10-821-670A-27 (1-307) x CQ803342 (1-987)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
)b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

!ESULT 71
:S131491
.OCUS       CS131491                 987 bp    DNA     linear   PAT 02-AUG-2005
)EFINITION  Sequence 10 from Patent WO2005066348.
\CCESSION   CS131491
VERSION     CS131491.1  GI:71794159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 10 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HuIL12 p40 subunit"
ORIGIN

Alignment Scores:
Pred. No.:                4.73e-30       Length:         987
Score:                    35.00          Matches:        35
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              11.4%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x CS131491 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 72
I28591
LOCUS       I28591                   987 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5573764.
ACCESSION   I28591
VERSION     I28591.1  GI:1819367
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 1 12-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                4.73e-30       Length:         987
Score:                    35.00          Matches:        35
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              11.4%          Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-27 (1-307) x I28591 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

```
ESULT 73
X154633
OCUS       AX154633               987 bp    DNA     linear   PAT 22-JUN-2001
EFINITION  Sequence 37 from Patent WO0140257.
CCESSION   AX154633
ERSION     AX154633.1  GI:14536197
EYWORDS    .
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
EFERENCE   1
 AUTHORS   Leong,S.R. and Punnonen,J.
 TITLE     Cytokine polypeptides and nucleic acids
 JOURNAL   Patent: WO 0140257-A 37 07-JUN-2001;
           Maxygen, Inc. (US)
EATURES             Location/Qualifiers
     source         1. .987
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
RIGIN

lignment Scores:
red. No.:              4.73e-30       Length:        987
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x AX154633 (1-987)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 74
F180563
OCUS       AF180563               1007 bp    mRNA    linear   PRI 26-SEP-1999
EFINITION  Homo sapiens interleukin 12, P40 mRNA, complete cds.
CCESSION   AF180563
ERSION     AF180563.1  GI:5923854
EYWORDS    .
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
EFERENCE   1  (bases 1 to 1007)
 AUTHORS   Hongyuan,J. and Meiyun,Z.
 TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
 JOURNAL   Unpublished
EFERENCE   2  (bases 1 to 1007)
 AUTHORS   Hongyuan,J. and Meiyun,Z.
 TITLE     Direct Submission
 JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
           Yingxinjie, Xuanwuqu, Beijing 100052, China
EATURES             Location/Qualifiers
     source         1. .1007
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /cell_type="peripheral mononuclear"
     CDS            7. .993
                    /note="NKSF/CLMF; IL12p40; 40kD"
                    /codon_start=1
                    /product="interleukin 12, P40"
                    /protein_id="AAD56386.1"
                    /db_xref="GI:5923855"
                    /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                    MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                    LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                    GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                    KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                    VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:              4.82e-30       Length:        1007
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-27 (1-307) x AF180563 (1-1007)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
Db       712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756

RESULT 75
AB246353
LOCUS       AB246353               1008 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus bubalis IL-12p40 mRNA for interleukin-12p40, complete cds.
ACCESSION   AB246353
VERSION     AB246353.1  GI:84871717
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
                     /sex="female"
                     /cell_type="PBMC"
                     /note="Bulgarian Murrah buffalo - crossbreed between
                     Mediterranean and Indian buffalo both are Riverine type
                     water buffalo"
     gene            1. .1008
                     /gene="IL-12p40"
     CDS             1. .984
                     /gene="IL-12p40"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="BAE75858.1"
                     /db_xref="GI:84871718"
```

```
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCEAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
)RIGIN

\lignment Scores:
)red. No.:                4.83e-30        Length:         1008
;core:                    35.00           Matches:        35
)ercent Similarity:       100.0%          Conservative:   0
}est Local Similarity:    100.0%          Mismatches:     0
]uery Match:              11.4%           Indels:         0
)B:                       14              Gaps:           0

]S-10-821-670A-27 (1-307) x AB246353 (1-1008)

]y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        649 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCA 708

]y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
)b        709 GACCCACCCAAGAACCTGCAACTGAAACCATTAAAGAATTCTCGG 753

:ESULT 76
\Y198121
;OCUS       AY198121               1012 bp    mRNA    linear   MAM 09-JUN-2005
)EFINITION  Bubalus bubalis interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
\CCESSION   AY198121
'ERSION     AY198121.1  GI:28192687
:EYWORDS    .
;OURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
:EFERENCE   1  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
  TITLE     Interleukin-12 subunits p35 and p40 of Indian water buffalo
            (Bubalus bubalis) maintain high sequence homology with those of
            other ruminants
  JOURNAL   Eur. J. Immunogenet. 32 (3), 179-186 (2005)
:EFERENCE   2  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E. and Rasool,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-2002) Animal Biotechnology, Rajiv Gandhi Center
            for Biotechnology, Jagathy, Thycaud PO, Trivandrum, Kerala 695014,
            India
'EATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
     CDS             1. .984
                     /note="cytokine; 40 kDa subunit"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAO25629.1"
                     /db_xref="GI:28192688"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSADPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
)RIGIN

\lignment Scores:
)red. No.:                4.85e-30        Length:         1012
;core:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-27 (1-307) x AY198121 (1-1012)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCA 708

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        709 GACCCACCCAAGAACCTGCAACTGAAACCATTAAAGAATTCTCGG 753

RESULT 77
AR052857
LOCUS       AR052857               1018 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 194 from patent US 5833975.
ACCESSION   AR052857
VERSION     AR052857.1  GI:5977719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 194 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                4.87e-30        Length:         1018
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-27 (1-307) x AR052857 (1-1018)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 78
AR288169
LOCUS       AR288169               1018 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 194 from patent US 6537594.
ACCESSION   AR288169
VERSION     AR288169.1  GI:31675448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
            genes
  JOURNAL   Patent: US 6537594-A 194 25-MAR-2003;
            Virogenetics Corporation; Troy, NY
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
```

```
                     /mol_type="mRNA"
RIGIN

lignment Scores:
red. No.:                4.87e-30        Length:         1018
core:                    35.00           Matches:        35
ercent Similarity:       100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              11.4%           Indels:         0
B:                       2               Gaps:           0

S-10-821-670A-27 (1-307) x AR288169 (1-1018)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

ESULT 79
R567156
OCUS       AR567156               1018 bp    mRNA    linear   PAT 08-OCT-2004
EFINITION  Sequence 194 from patent US 6780407.
CCESSION   AR567156
ERSION     AR567156.1  GI:53984798
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 1018)
 AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
 TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
 JOURNAL   Patent: US 6780407-A 194 24-AUG-2004;
           Aventis Pasteur; Swiftwater, PA
EATURES             Location/Qualifiers
    source          1. .1018
                    /organism="unknown"
                    /mol_type="mRNA"
RIGIN

lignment Scores:
red. No.:                4.87e-30        Length:         1018
core:                    35.00           Matches:        35
ercent Similarity:       100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              11.4%           Indels:         0
B:                       2               Gaps:           0

S-10-821-670A-27 (1-307) x AR567156 (1-1018)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

ESULT 80
Q829448
OCUS       CQ829448               1029 bp    DNA     linear   PAT 05-JUL-2004
EFINITION  Sequence 7 from Patent WO2004052929.
CCESSION   CQ829448
ERSION     CQ829448.1  GI:49732784
EYWORDS    .
OURCE      synthetic construct
 ORGANISM  synthetic construct
           other sequences; artificial sequences.
EFERENCE   1
 AUTHORS   Vandenbroeck,K. and Alloza,I.
 TITLE     Recombinant cell line
 JOURNAL   Patent: WO 2004052929-A 7 24-JUN-2004;
           The Queen's University of Belfast (GB)
EATURES             Location/Qualifiers
    source          1. .1029
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="cDNA for beta chain of IL-12"
RIGIN

lignment Scores:
red. No.:                4.92e-30        Length:         1029
core:                    35.00           Matches:        35
ercent Similarity:       100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              11.4%           Indels:         0
B:                       2               Gaps:           0

S-10-821-670A-27 (1-307) x CQ829448 (1-1029)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        661 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 720

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b        721 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 765

ESULT 81
C074723
OCUS       BC074723               1046 bp    mRNA    linear   PRI 28-JUL-2005
EFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
           factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
           (cDNA clone MGC:103792 IMAGE:30915173), complete cds.
CCESSION   BC074723
ERSION     BC074723.2  GI:50960609
EYWORDS    MGC.
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
EFERENCE   1  (bases 1 to 1046)
 AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
           Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
           Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
           Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
           Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
           Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
           Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
           Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
           Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
           McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
           Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
           Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
           Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
           Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
           Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
           Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
           Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
           Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 CONSRTM   Mammalian Gene Collection Program Team
 TITLE     Generation and initial analysis of more than 15,000 full-length
           human and mouse cDNA sequences
 JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED   12477932
EFERENCE   2  (bases 1 to 1046)
 AUTHORS   .
 CONSRTM   NIH MGC Project
 TITLE     Direct Submission
 JOURNAL   Submitted (25-JUN-2004) National Institutes of Health, Mammalian
           Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
```

```
COMMENT     On Aug 4, 2004 this sequence version replaced gi:49901500.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
            Center
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBU Plate: 1 Row: A Column: 6.
FEATURES              Location/Qualifiers
     source           1. .1046
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="MGC:103792 IMAGE:30915173"
                      /tissue_type="Brain, PCR rescued clones"
                      /clone_lib="NIH_MGC_272"
                      /lab_host="DH10B"
                      /note="Vector: pCR4 Topo TA with reversed insert"
     gene             1. .1046
                      /gene="IL12B"
                      /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                      /db_xref="GeneID:3593"
                      /db_xref="MIM:161561"
     CDS              32. .1018
                      /gene="IL12B"
                      /codon_start=1
                      /product="interleukin 12B, precursor"
                      /protein_id="AAH74723.1"
                      /db_xref="GI:50960610"
                      /db_xref="GeneID:3593"
                      /db_xref="MIM:161561"
                      /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                      MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                      LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                      GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                      KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                      VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:              5e-30          Length:        1046
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-27 (1-307) x BC074723 (1-1046)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 82
BC067498
LOCUS       BC067498                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79355 IMAGE:6971868), complete cds.
ACCESSION   BC067498
VERSION     BC067498.1  GI:45768642
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED    12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 13
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES              Location/Qualifiers
     source           1. .1073
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="MGC:79355 IMAGE:6971868"
                      /tissue_type="PCR rescued clones"
                      /clone_lib="NIH_MGC_195"
                      /lab_host="DH10B"
                      /note="Vector: pDNR-Dual"
     gene             1. .1073
                      /gene="IL12B"
```

```
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67498.1"
                     /db_xref="GI:45768643"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
RIGIN

lignment Scores:
red. No.:              5.12e-30        Length:         1073
core:                  35.00           Matches:        35
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            11.4%           Indels:         0
B:                     5               Gaps:           0

S-10-821-670A-27 (1-307) x BC067498 (1-1073)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
b        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

ESULT 83
C067499
OCUS       BC067499               1073 bp    mRNA    linear   PRI 28-JUL-2005
EFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
           factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
           (cDNA clone MGC:79356 IMAGE:6971869), complete cds.
CCESSION   BC067499
ERSION     BC067499.1  GI:45768645
EYWORDS    MGC.
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
EFERENCE   1  (bases 1 to 1073)
 AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
           Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
           Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
           Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
           Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
           Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
           Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
           Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
           Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
           McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
           Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
           Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
           Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
           Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
           Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
           Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
           Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
           Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 CONSRTM   Mammalian Gene Collection Program Team
 TITLE     Generation and initial analysis of more than 15,000 full-length
           human and mouse cDNA sequences
  JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED  12477932
REFERENCE  2  (bases 1 to 1073)
  AUTHORS  .
  CONSRTM  NIH MGC Project
  TITLE    Direct Submission
  JOURNAL  Submitted (19-MAR-2004) National Institutes of Health, Mammalian
           Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT    Contact: MGC help desk
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Sequencing Group at the Stanford Human Genome
           Center, Stanford University School of Medicine, Stanford, CA  94305
           Web site:       http://www-shgc.stanford.edu
           Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
           Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
           R. M.

           Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Series: IRAK Plate: 172 Row: d Column: 12
           This clone was selected for full length sequencing because it
           passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79356 IMAGE:6971869"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67499.1"
                     /db_xref="GI:45768646"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:             5.12e-30        Length:         1073
Score:                 35.00           Matches:        35
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           11.4%           Indels:         0
DB:                    5               Gaps:           0

US-10-821-670A-27 (1-307) x BC067499 (1-1073)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
```

```
)b        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

(ESULT 84
)C067500
.OCUS       BC067500               1073 bp    mRNA    linear   PRI 28-JUL-2005
)EFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79358 IMAGE:6971872), complete cds.
\CCESSION   BC067500
/ERSION     BC067500.1  GI:45768649
(EYWORDS    MGC.
;OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
(EFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
(EFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
:OMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
'EATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79358 IMAGE:6971872"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67500.1"
                     /db_xref="GI:45768650"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:                5.12e-30        Length:          1073
Score:                    35.00           Matches:         35
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              11.4%           Indels:          0
DB:                       5               Gaps:            0

US-10-821-670A-27 (1-307) x BC067500 (1-1073)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 85
BC067501
LOCUS       BC067501               1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79359 IMAGE:6971873), complete cds.
ACCESSION   BC067501
VERSION     BC067501.1  GI:45767736
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
```

```
  CONSRTM    Mammalian Gene Collection Program Team
  TITLE      Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
  JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED    12477932
EFERENCE     2  (bases 1 to 1073)
  AUTHORS    .
  CONSRTM    NIH MGC Project
  TITLE      Direct Submission
  JOURNAL    Submitted (19-MAR-2004) National Institutes of Health, Mammalian
             Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
OMMENT       Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Sequencing Group at the Stanford Human Genome
             Center, Stanford University School of Medicine, Stanford, CA  94305
             Web site:       http://www-shgc.stanford.edu
             Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
             Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
             R. M.

             Clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRAK Plate: 172 Row: d Column: 22
             This clone was selected for full length sequencing because it
             passed the following selection criteria: matched mRNA gi: 24497437.
EATURES              Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79359 IMAGE:6971873"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67501.1"
                     /db_xref="GI:45767737"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
RIGIN

lignment Scores:
red. No.:              5.12e-30       Length:        1073
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     5              Gaps:          0

S-10-821-670A-27 (1-307) x BC067501 (1-1073)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
Db       710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 86
BC067502
LOCUS       BC067502               1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79360 IMAGE:6971874), complete cds.
ACCESSION   BC067502
VERSION     BC067502.1  GI:45768652
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 23
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79360 IMAGE:6971874"
```

```
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67502.1"
                     /db_xref="GI:45768653"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
)RIGIN

Alignment Scores:
Pred. No.:                5.12e-30        Length:         1073
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       5               Gaps:           0

US-10-821-670A-27 (1-307) x BC067502 (1-1073)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 709

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        710 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 754

RESULT 87
AR393788
LOCUS       AR393788                1389 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6617135.
ACCESSION   AR393788
VERSION     AR393788.1  GI:40120790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1389)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 4 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
     source          1. .1389
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                6.53e-30        Length:         1389
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-27 (1-307) x AR393788 (1-1389)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 88
AX084106
LOCUS       AX084106                1389 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 4 from Patent WO0110912.
ACCESSION   AX084106
VERSION     AX084106.1  GI:13185656
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 4 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .1389
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="human p40-IL-2 fusion protein coding sequence"
ORIGIN

Alignment Scores:
Pred. No.:                6.53e-30        Length:         1389
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-27 (1-307) x AX084106 (1-1389)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 89
BD165800
LOCUS       BD165800                1397 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165800
VERSION     BD165800.1  GI:27871612
KEYWORDS    JP 2002167400-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1397)
  AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
  TITLE     Antibody against cytotoxic lymphocyte maturing factors
  JOURNAL   Patent: JP 2002167400-A 1 11-JUN-2002;
            PROTEIN DESIGN LABS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002167400-A/1
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
```

```
          PI   GUBLER,
          PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
          PI   ALVIN SETH STERN
          PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
            Antibody against cytotoxic lymphocyte maturing factors FH   Key
                    Location/Qualifiers
          FT   CDS              (41). .(1024).
EATURES             Location/Qualifiers
    source          1. .1397
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
RIGIN

lignment Scores:
red. No.:              6.57e-30       Length:        1397
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x BD165800 (1-1397)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

ESULT 90
R091391
OCUS       AR091391              1399 bp    DNA     linear   PAT 07-SEP-2000
EFINITION  Sequence 3 from patent US 5994104.
CCESSION   AR091391
ERSION     AR091391.1  GI:10018146
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 1399)
 AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
 TITLE     Interleukin-12 fusion protein
 JOURNAL   Patent: US 5994104-A 3 30-NOV-1999;
EATURES             Location/Qualifiers
    source          1. .1399
                    /organism="unknown"
                    /mol_type="unassigned DNA"
RIGIN

lignment Scores:
red. No.:              6.57e-30       Length:        1399
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x AR091391 (1-1399)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

ESULT 91
UMCLMF40
OCUS       HUMCLMF40             1399 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human cytotoxic lymphocyte maturation factor 40 kDa subunit mRNA,
            complete cds.
ACCESSION   M65272 M38443 M38444
VERSION     M65272.1  GI:180625
KEYWORDS    cytotoxic lymphocyte maturation factor 40 kDa subunit; interleukin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1399)
  AUTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
            Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
            and Gately,M.K.
  TITLE     Coexpression of two distinct genes is required to generate secreted
            bioactive cytotoxic lymphocyte maturation factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
   PUBMED   1674604
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .1399
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             43. .1029
                     /codon_start=1
                     /product="cytotoxic lymphocyte maturation factor 40 kDa
                     subunit"
                     /protein_id="AAA35695.1"
                     /db_xref="GI:180626"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Alignment Scores:
Pred. No.:             6.57e-30       Length:        1399
Score:                 35.00          Matches:       35
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           11.4%          Indels:        0
DB:                    5              Gaps:          0

US-10-821-670A-27 (1-307) x HUMCLMF40 (1-1399)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 92
AR091395
LOCUS       AR091395              1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
                     /organism="unknown"
```

```
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.28e-30        Length:         1560
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR091395 (1-1560)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 642

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        643 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 687

RESULT 93
AR091394
LOCUS       AR091394                1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES              Location/Qualifiers
     source           1. .1623
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.56e-30        Length:         1623
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR091394 (1-1623)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 94
CQ715179
LOCUS       CQ715179                2307 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 1113 from Patent WO02068579.
ACCESSION   CQ715179
VERSION     CQ715179.1  GI:42276036
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 1113 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES              Location/Qualifiers
     source           1. .2307
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.05e-29        Length:         2307
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x CQ715179 (1-2307)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 707

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        708 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 752

RESULT 95
AR082684
LOCUS       AR082684                2362 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 1 from patent US 5976539.
ACCESSION   AR082684
VERSION     AR082684.1  GI:10009474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2362)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5976539-A 1 02-NOV-1999;
FEATURES              Location/Qualifiers
     source           1. .2362
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.08e-29        Length:         2362
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR082684 (1-2362)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 96
AR122960
LOCUS       AR122960                2362 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6168923.
ACCESSION   AR122960
```

```
ERSION     AR122960.1  GI:14107926
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 2362)
 AUTHORS   Scott,P. and Trinchieri,G.
 TITLE     Compositions and methods for use of IL-12 as an adjuvant
 JOURNAL   Patent: US 6168923-A 1 02-JAN-2001;
EATURES             Location/Qualifiers
    source          1. .2362
                    /organism="unknown"
                    /mol_type="unassigned DNA"
RIGIN

lignment Scores:
red. No.:              1.08e-29       Length:        2362
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x AR122960 (1-2362)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

ESULT 97
28325
OCUS       I28325                  2362 bp    DNA     linear   PAT 06-FEB-1997
EFINITION  Sequence 1 from patent US 5571515.
CCESSION   I28325
ERSION     I28325.1  GI:1819101
EYWORDS    .
OURCE      Unknown.
 ORGANISM  Unknown.
           Unclassified.
EFERENCE   1  (bases 1 to 2362)
 AUTHORS   Scott,P. and Trinchieri,G.
 TITLE     Compositions and methods for use of IL-12 as an adjuvant
 JOURNAL   Patent: US 5571515-A 1 05-NOV-1996;
EATURES             Location/Qualifiers
    source          1. .2362
                    /organism="unknown"
                    /mol_type="unassigned DNA"
RIGIN

lignment Scores:
red. No.:              1.08e-29       Length:        2362
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x I28325 (1-2362)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

ESULT 98
R309636
```

```
LOCUS      AR309636                2362 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6555658.
ACCESSION  AR309636
VERSION    AR309636.1  GI:31701687
KEYWORDS   .
SOURCE     Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 2362)
  AUTHORS  Trinchieri,G., Perussia,B., Clark,S.C., Wong,G.G., Hewick,R. and
           Kobayashi,M.
  TITLE    Antibodies to natural killer stimulatory factor
  JOURNAL  Patent: US 6555658-A 3 29-APR-2003;
           Wyeth and The Wistar Institute; Madison, NJ
FEATURES             Location/Qualifiers
     source          1. .2362
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:             1.08e-29       Length:        2362
Score:                 35.00          Matches:       35
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           11.4%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-27 (1-307) x AR309636 (1-2362)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 99
I89770
LOCUS      I89770                  2362 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION Sequence 1 from patent US 5723127.
ACCESSION  I89770
VERSION    I89770.1  GI:3409710
KEYWORDS   .
SOURCE     Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 2362)
  AUTHORS  Scott,P. and Trinchieri,G.
  TITLE    Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL  Patent: US 5723127-A 1 03-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .2362
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:             1.08e-29       Length:        2362
Score:                 35.00          Matches:       35
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           11.4%          Indels:        0
DB:                    2              Gaps:          0

US-10-821-670A-27 (1-307) x I89770 (1-2362)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||
)b        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

(ESULT 100
3D136048
.OCUS       BD136048               5686 bp    DNA     linear   PAT 18-SEP-2002
)EFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
\CCESSION   BD136048
/ERSION     BD136048.1  GI:23230993
(EYWORDS    JP 2002506647-A/15.
3OURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
(EFERENCE   1  (bases 1 to 5686)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 15 05-MAR-2002;
            VALENTIS INC
:OMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/15
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: synthetic construct
            FH   Key             Location/Qualifiers
            FT   source          1. .5686
            FT                   /organism='Artificial Sequence'.
'EATURES             Location/Qualifiers
     source          1. .5686
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
)RIGIN

\lignment Scores:
'red. No.:                2.46e-29       Length:         5686
3core:                    35.00          Matches:        35
'ercent Similarity:       100.0%         Conservative:   0
3est Local Similarity:    100.0%         Mismatches:     0
)uery Match:              11.4%          Indels:         0
)B:                       2              Gaps:           0

!S-10-821-670A-27 (1-307) x BD136048 (1-5686)

)y         195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        3864 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3923

)y         215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
               |||||||||||||||||||||||||||||||||||||||||||||
)b        3924 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3968


3earch completed: June 10, 2006, 12:08:18
Job time : 7012.12 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

)M protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:23:11 ; Search time 743.839 Seconds
(without alignments)
4316.416 Million cell updates/sec

Title: US-10-821-670A-27
Perfect score: 307
Sequence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size: 1

Total number of hits satisfying chosen parameters: 10484873

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110446_27507/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rng -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US10821670_@CGN_1_1_1666_@runat_07062006_110446_27507 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	307	100.0	921	6	ABK98942	Abk98942 Feline in
c	2	307	100.0	921	6	ABK98943	Abk98943 Feline in
c	3	307	100.0	921	14	ADV34681	Adv34681 Feline si
	4	307	100.0	921	14	ADV34679	Adv34679 Feline si
c	5	307	100.0	1533	6	ABK98954	Abk98954 Feline in
	6	307	100.0	1533	6	ABK98953	Abk98953 Feline in
c	7	307	100.0	1533	14	ADV34697	Adv34697 Feline si
	8	307	100.0	1533	14	ADV34695	Adv34695 Feline si
	9	307	100.0	1599	6	ABK98950	Abk98950 Feline in
c	10	307	100.0	1599	6	ABK98951	Abk98951 Feline in
	11	307	100.0	1599	14	ADV34691	Adv34691 Feline si
c	12	307	100.0	1599	14	ADV34693	Adv34693 Feline si
	13	206	67.1	921	2	AAV56627	Aav56627 Feline FL
	14	206	67.1	921	2	AAV56626	Aav56626 Feline FL
	15	206	67.1	987	6	ABK98944	Abk98944 Feline in
c	16	206	67.1	987	6	ABK98945	Abk98945 Feline in
	17	206	67.1	987	14	ADV34682	Adv34682 Feline si
c	18	206	67.1	987	14	ADV34684	Adv34684 Feline si
	19	206	67.1	990	4	AAF26082	Aaf26082 Feline IL
	20	206	67.1	990	4	AAF26085	Aaf26085 Feline IL
	21	206	67.1	2193	2	AAV56625	Aav56625 Feline FL
	22	206	67.1	4522	4	AAF26076	Aaf26076 Feline IL
	23	206	67.1	4522	4	AAF26094	Aaf26094 Plasmid p
c	24	205	66.8	985	6	ABK98962	Abk98962 Feline in
	25	205	66.8	985	6	ABK98961	Abk98961 Feline in
	26	205	66.8	985	14	ADV34707	Adv34707 Feline N-
c	27	205	66.8	985	14	ADV34709	Adv34709 Feline N-
	28	52	16.9	990	5	AAD15209	Aad15209 Modified
	29	43	14.0	984	5	AAD15206	Aad15206 Modified
	30	42	13.7	984	5	AAD15205	Aad15205 Modified
	31	41	13.4	975	5	AAD15203	Aad15203 Modified
	32	37	12.1	921	6	ABK98959	Abk98959 Canine in
c	33	37	12.1	921	6	ABK98960	Abk98960 Canine in
c	34	37	12.1	921	14	ADV34706	Adv34706 Canine si
	35	37	12.1	921	14	ADV34704	Adv34704 Canine si
	36	37	12.1	924	2	AAX18177	Aax18177 Canine ma
	37	37	12.1	987	6	ABK98963	Abk98963 Canine in
c	38	37	12.1	987	6	ABK98964	Abk98964 Canine in
c	39	37	12.1	987	14	ADV34712	Adv34712 Canine si
	40	37	12.1	987	14	ADV34710	Adv34710 Canine si
	41	37	12.1	990	2	AAV13816	Aav13816 Canine IL
	42	37	12.1	990	2	AAV13817	Aav13817 Canine IL
	43	37	12.1	990	2	AAX03162	Aax03162 Nucleic a
	44	37	12.1	990	2	AAX03152	Aax03152 Nucleic a
	45	37	12.1	990	2	AAX35625	Aax35625 Nucleic a
	46	37	12.1	990	2	AAX35615	Aax35615 Nucleic a
	47	37	12.1	990	4	AAI64378	Aai64378 Canine co
	48	37	12.1	990	4	AAI64388	Aai64388 Canine co
	49	37	12.1	990	11	ADZ25698	Adz25698 Canine in
	50	37	12.1	1015	13	ADT04849	Adt04849 Canine in
	51	37	12.1	1533	6	ABK98967	Abk98967 Canine in
c	52	37	12.1	1533	6	ABK98968	Abk98968 Canine in
c	53	37	12.1	1533	14	ADV34718	Adv34718 Canine si
	54	37	12.1	1533	14	ADV34716	Adv34716 Canine si
	55	37	12.1	1599	6	ABK98965	Abk98965 Canine in
c	56	37	12.1	1599	6	ABK98966	Abk98966 Canine in
c	57	37	12.1	1599	14	ADV34715	Adv34715 Canine si
	58	37	12.1	1599	14	ADV34713	Adv34713 Canine si
	59	37	12.1	2154	2	AAX18176	Aax18176 Canine fu
c	60	37	12.1	2267	6	ABK99006	Abk99006 Canine in
	61	37	12.1	2267	6	ABK99005	Abk99005 Canine in
	62	37	12.1	2267	14	ADV34757	Adv34757 Canine si
c	63	37	12.1	2267	14	ADV34759	Adv34759 Canine si
	64	35	11.4	906	2	AAQ04701	Aaq04701 Sequence
	65	35	11.4	975	5	AAD15208	Aad15208 Modified
	66	35	11.4	979	2	AAQ12149	Aaq12149 Cytotoxic
	67	35	11.4	984	12	ADG39430	Adg39430 Human CLM
	68	35	11.4	987	2	AAQ97484	Aaq97484 Human int
	69	35	11.4	987	2	AAV07273	Aav07273 Human Int
	70	35	11.4	987	2	AAV07217	Aav07217 DNA encod
	71	35	11.4	987	2	AAZ40406	Aaz40406 Human int
	72	35	11.4	987	2	AAZ40404	Aaz40404 Human int
	73	35	11.4	987	2	AAZ40405	Aaz40405 Human int
	74	35	11.4	987	5	AAD15210	Aad15210 Human cyt
	75	35	11.4	987	12	ADF77278	Adf77278 Human IL-

76	35	11.4	987	12	ADF77263	Adf77263 Human IL-
77	35	11.4	987	12	ADF77277	Adf77277 Human IL-
78	35	11.4	987	12	ADF77276	Adf77276 Human IL-
79	35	11.4	987	12	ADO07653	Ado07653 Human int
80	35	11.4	987	13	ADS00006	Ads00006 Human int
81	35	11.4	987	14	ADV42753	Adv42753 Human psy
82	35	11.4	987	14	ADW97242	Adw97242 Human p40
83	35	11.4	987	14	AEB48822	Aeb48822 Human int
84	35	11.4	1007	5	AAD18585	Aad18585 Human int
85	35	11.4	1018	2	AAQ67879	Aaq67879 EPV 42 kD
86	35	11.4	1018	2	AAZ08510	Aaz08510 EPV 42 kD
87	35	11.4	1018	13	ADR21886	Adr21886 EPV 42kDa
88	35	11.4	1029	12	ADP88402	Adp88402 Human int
89	35	11.4	1389	4	AAF76880	Aaf76880 Human p40
90	35	11.4	1397	2	AAT77849	Aat77849 40 kDa su
91	35	11.4	1397	2	AAT97969	Aat97969 40 kDa su
92	35	11.4	1397	2	AAV00401	Aav00401 40 kDa su
93	35	11.4	1397	2	AAV37767	Aav37767 Cytotoxic
94	35	11.4	1397	12	ADG39387	Adg39387 Human cyt
95	35	11.4	1397	12	ADO03758	Ado03758 Human CLM
96	35	11.4	1399	3	AAZ40021	Aaz40021 Human p40
97	35	11.4	1399	14	ADY86632	Ady86632 Human int
98	35	11.4	2300	3	AAA92406	Aaa92406 Human int
99	35	11.4	2336	14	AEE03207	Aee03207 Human int
100	35	11.4	2347	12	ACF57534	Acf57534 Human IL1
101	35	11.4	2347	12	ADJ62892	Adj62892 Human int
102	35	11.4	2347	14	ADZ26728	Adz26728 Human IL1
103	35	11.4	2362	2	AAQ23586	Aaq23586 Natural k
104	35	11.4	2362	2	AAT48098	Aat48098 Human int
105	35	11.4	2362	2	AAV42535	Aav42535 Human int
106	35	11.4	2362	2	AAV15227	Aav15227 Heterodim
107	35	11.4	2362	3	AAZ28862	Aaz28862 Human int
108	35	11.4	2362	4	AAF56280	Aaf56280 IL-12 vac
109	35	11.4	5686	2	AAZ40415	Aaz40415 Plasmid p
110	35	11.4	5686	12	ADF77239	Adf77239 Human IL-
111	35	11.4	6139	3	AAZ40023	Aaz40023 Interleuk
112	35	11.4	11569	10	ADG25150	Adg25150 Vector pA
113	34	11.1	945	12	ADF77264	Adf77264 Human IL-
114	32	10.4	985	10	ADK98707	Adk98707 Human int
115	28	9.1	969	5	AAD15207	Aad15207 Modified
116	28	9.1	984	2	AAT50759	Aat50759 Sequence
117	28	9.1	984	5	AAD15204	Aad15204 Modified
118	28	9.1	1019	3	AAA70709	Aaa70709 Bovine in
119	28	9.1	2390	12	ADM29103	Adm29103 Human int
120	23	7.5	987	2	AAV83199	Aav83199 Interleuk
121	23	7.5	987	6	ACC47592	Acc47592 Human int
122	23	7.5	1580	12	ADQ14472	Adq14472 DNA encod
123	23	7.5	2318	8	ACA61267	Aca61267 DNA encod
124	23	7.5	2318	10	ABX33940	Abx33940 Human cDN
125	23	7.5	4727	14	AEA40942	Aea40942 T-DNA reg
126	23	7.5	8578	6	AAD31546	Aad31546 pIRES-hB7
127	23	7.5	8578	6	AAD31545	Aad31545 pIRES-hB7
128	23	7.5	8608	6	AAD31548	Aad31548 pIRES-hB7
129	23	7.5	8623	6	AAD31547	Aad31547 pIRES-hB7
130	23	7.5	8629	6	AAD31552	Aad31552 pIRES-IL1
131	23	7.5	8638	6	AAD31549	Aad31549 pIRES-hB7
132	23	7.5	8644	6	AAD31551	Aad31551 pIRES-IL1
133	23	7.5	8659	6	AAD31550	Aad31550 pIRES-IL1
134	23	7.5	11453	10	ADG25152	Adg25152 Vector pS
135	22	7.2	1007	10	ACD26421	Acd26421 cDNA enco
136	22	7.2	18110	6	ABK15357	Abk15357 Human int
137	22	7.2	18340	5	AAD19368	Aad19368 Mammalian
c 138	20	6.5	270	12	ACH83638	Ach83638 Human gen
139	20	6.5	399	14	AEE14792	Aee14792 Hamster S
140	20	6.5	399	14	AEE11150	Aee11150 Hamster c
c 141	20	6.5	556	12	ACH69938	Ach69938 Human gen
142	19	6.2	948	12	ADI28579	Adi28579 Duck inte
143	19	6.2	948	12	ADI28581	Adi28581 Turkey in
144	19	6.2	948	12	ADI28576	Adi28576 Chicken i
145	17	5.5	73	4	AAS15322	Aas15322 Mouse IL-
146	17	5.5	600	2	AAX78397	Aax78397 IL-12p40
147	17	5.5	600	2	AAX25947	Aax25947 Interleuk
148	17	5.5	1008	13	ADS00008	Ads00008 Murine in
149	17	5.5	1008	14	ADW97243	Adw97243 Murine p4
150	17	5.5	1056	2	AAV28472	Aav28472 Murine in
151	17	5.5	1061	2	AAT35200	Aat35200 Mouse int
152	17	5.5	1409	4	AAF76879	Aaf76879 Murine p4
153	17	5.5	1472	4	AAF76878	Aaf76878 Murine p4
154	17	5.5	1569	4	AAF76888	Aaf76888 Single-ch
155	17	5.5	1610	12	ADQ14470	Adq14470 DNA encod
156	17	5.5	1840	8	ACA61265	Aca61265 DNA encod
157	17	5.5	2013	4	AAF76887	Aaf76887 Murine p3
158	17	5.5	2334	14	AEE03206	Aee03206 Murine in
159	17	5.5	2438	12	ADO43004	Ado43004 DNA encod
160	17	5.5	2709	4	AAF76889	Aaf76889 Coding se
161	17	5.5	5252	12	ADO07652	Ado07652 Tricistro
162	17	5.5	5966	2	AAZ40417	Aaz40417 Plasmid p
163	17	5.5	5966	12	ADF77241	Adf77241 Mouse IL-
164	17	5.5	5985	12	ADQ82718	Adq82718 Anticance
165	17	5.5	6295	2	AAV02043	Aav02043 Plasmid p
166	17	5.5	7287	2	AAV02042	Aav02042 Plasmid p
167	17	5.5	9049	12	ADO07661	Ado07661 Viral vec
168	17	5.5	10633	12	ADO07660	Ado07660 Viral vec
169	17	5.5	11458	10	ADG25151	Adg25151 Vector pA
170	17	5.5	11746	12	ADO07659	Ado07659 Viral vec
171	17	5.5	28191	14	AEE03204	Aee03204 Adenovira
172	17	5.5	28892	14	AEE03202	Aee03202 Adenovira
173	17	5.5	38246	12	ADO07662	Ado07662 Viral vec
174	13	4.2	987	2	AAV31480	Aav31480 Human int
175	13	4.2	987	2	AAZ40422	Aaz40422 Human int
176	13	4.2	987	12	ADF77256	Adf77256 Human IL-
177	12	3.9	38	2	AAV56630	Aav56630 Feline FL
178	12	3.9	200	2	AAV03357	Aav03357 Homo sapi
c 179	10	3.3	30	3	AAA48905	Aaa48905 Probe 12.
180	10	3.3	21925	10	ADC87602	Adc87602 Human GPC
181	10	3.3	26184	10	ADC87236	Adc87236 Human GPC
182	9	2.9	30	5	AAD19247	Aad19247 Mammalian
183	9	2.9	353	5	ABV07469	Abv07469 Human pro
184	9	2.9	419	5	AAD19240	Aad19240 Mammalian
185	9	2.9	419	5	AAD19239	Aad19239 Mammalian
186	9	2.9	426	5	ABV37403	Abv37403 Human pro
c 187	9	2.9	463	4	AAH08718	Aah08718 Human cDN
188	9	2.9	532	3	AAC04020	Aac04020 Human sec
c 189	9	2.9	664	4	AAL25132	Aal25132 Human bre
190	9	2.9	858	11	ACN88481	Acn88481 Breast ca
191	9	2.9	1974	4	AAH13637	Aah13637 Human cDN
192	9	2.9	2162	10	ADC30563	Adc30563 Human nov
193	9	2.9	2256	5	ABV22512	Abv22512 Human pro
194	9	2.9	2256	5	ABV28327	Abv28327 Human pro
195	9	2.9	2256	5	ABV24801	Abv24801 Human pro
196	9	2.9	2322	12	ADQ63757	Adq63757 Novel hum
c 197	9	2.9	2433	13	ADS45732	Ads45732 Bacterial
198	9	2.9	2659	11	ACN92560	Acn92560 Breast ca
c 199	9	2.9	2805	10	ADC32387	Adc32387 Human nov
c 200	9	2.9	3284	11	ADM01945	Adm01945 Human cDN

ALIGNMENTS

```
RESULT 1
ABK98942
ID   ABK98942 standard; cDNA; 921 BP.
XX
AC   ABK98942;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
```

```
XX
DT   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69302.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 49-50; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.94e-303      Length:          921
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       6              Gaps:            0

US-10-821-670A-27 (1-307) x ABK98942 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 2
ABK98943/c
ID   ABK98943 standard; cDNA; 921 BP.
XX
AC   ABK98943;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
```

```
X
S   Disclosure; Page 51; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a feline interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

lignment Scores:
red. No.:              2.94e-303      Length:        921
core:                  307.00         Matches:       307
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     6              Gaps:          0

S-10-821-670A-27 (1-307) x ABK98943 (1-921)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db        21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 3
ADV34681/c
ID   ADV34681 standard; DNA; 921 BP.
XX
AC   ADV34681;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 complementary DNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 28; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.94e-303      Length:        921
Score:                  307.00         Matches:       307
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
```

```
)B:                    14            Gaps:          0

)S-10-821-670A-27 (1-307) x ADV34681 (1-921)

)y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

)y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

)y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

)y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

)y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

)y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

)y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

)y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

)y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

)y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

)y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

)y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

)y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

)y        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
)b         21 TGGGCATCCGTGTCCTGCAGT 1

!ESULT 4
\DV34679
:D   ADV34679 standard; cDNA; 921 BP.
:X
\C   ADV34679;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 protein cDNA, nPeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .921
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 307 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34680.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 26; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.94e-303       Length:         921
Score:                  307.00          Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-27 (1-307) x ADV34679 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
```

```
y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b        901 TGGGCATCCGTGTCCTGCAGT 921
```

```
ESULT 5
BK98954/c
D   ABK98954 standard; cDNA; 1533 BP.
X
C   ABK98954;
X
T   21-OCT-2002  (first entry)
X
E   Feline interleukin-12 nFeIL-12-1533 complementary strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; ss.
X
S   Felis catus.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                4.76e-303      Length:          1533
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       6              Gaps:            0

US-10-821-670A-27 (1-307) x ABK98954 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054
```

```
Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

```
RESULT 6
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69307.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 63-64; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                4.76e-303       Length:          1533
Score:                    307.00          Matches:         307
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       6               Gaps:            0

US-10-821-670A-27 (1-307) x ABK98953 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
```

```
b        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

b        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

y        301 TrpAlaSerValSerCysSer 307

b        901 TGGGCATCCGTGTCCTGCAGT 921
```

ESULT 7
DV34697/c
D ADV34697 standard; DNA; 1533 BP.
X
C ADV34697;
X
T 24-FEB-2005 (first entry)
X
E Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
X
W DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W infectious disease; antimicrobial; ds.
X
S Felis catus.
X
N US2004248261-A1.
X
D 09-DEC-2004.
X
F 09-APR-2004; 2004US-00821670.
X
R 04-AUG-2000; 2000US-0223016P.
R 27-JUL-2001; 2001US-00917265.
X
A (WOND/) WONDERLING R S.
A (BORO/) BOROUGHS K L.
X
I Wonderling RS, Boroughs KL;
X
R WPI; 2005-020565/02.
X
T New nucleic acid molecule comprising a sequence encoding a feline p35 or
T p40 subunit protein and a nucleic acid linker, useful in preparing a
T vaccine against infectious diseases in feline animals.
X
S Example 3; SEQ ID NO 45; 103pp; English.
X
C The present invention relates to the feline interleukin (IL)-12p35 or p40
C subunit protein and their encoding nucleic acid molecules and a nucleic
C acid linker. The invention also provides the feline caspase (casp)-1,
C feline IL-18 single chain and canine IL-12 single chain proteins and
C their nucleic acid molecules. The nucleic acid molecule is useful in
C preparing a vaccine against infectious diseases in feline animals. The
C present sequence is the feline single chain IL-12 complementary DNA.
X
Q Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

lignment Scores:

red. No.:	4.76e-303	Length:	1533
core:	307.00	Matches:	307
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	100.0%	Indels:	0
B:	14	Gaps:	0

S-10-821-670A-27 (1-307) x ADV34697 (1-1533)

```
y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       301 TrpAlaSerValSerCysSer 307

Db       633 TGGGCATCCGTGTCCTGCAGT 613
```

RESULT 8
ADV34695
ID ADV34695 standard; cDNA; 1533 BP.
XX
AC ADV34695;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX

```
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag= a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS, Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.76e-303      Length:          1533
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       14             Gaps:            0

US-10-821-670A-27 (1-307) x ADV34695 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 9
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
```

```
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2002-573554/61.
R   P-PSDB; ABG69306.
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Claim 6; Page 58-60; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a feline interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

lignment Scores:
red. No.:              4.95e-303      Length:        1599
core:                  307.00         Matches:       307
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     6              Gaps:          0

S-10-821-670A-27 (1-307) x ABK98950 (1-1599)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db       967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 10
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
```

```
:C   these proteins, can be used to treat or prevent autoimmune diseases,
:C   allergic reactions, infectious diseases, tumour development, inflammatory
:C   diseases and/or graft rejection in animals. The present nucleic acid
:C   sequence represents a feline interleukin 12 DNA sequence, as described in
:C   the invention
:X
:Q   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.95e-303      Length:         1599
Score:                  307.00         Matches:        307
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-27 (1-307) x ABK98951 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 11
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.95e-303      Length:         1599
Score:                  307.00         Matches:        307
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-27 (1-307) x ADV34691 (1-1599)
```

```
y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
b         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
b        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
b        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
b        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
b        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
b        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
b        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
b        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
b        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
b        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
b        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
b        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
b        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

y        301 TrpAlaSerValSerCysSer 307
b        967 TGGGCATCCGTGTCCTGCAGT 987

ESULT 12
DV34693/c
D   ADV34693 standard; DNA; 1599 BP.
X
C   ADV34693;
X
T   24-FEB-2005  (first entry)
X
DE  Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW  DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW  infectious disease; antimicrobial; ds.
XX
OS  Felis catus.
XX
PN  US2004248261-A1.
XX
PD  09-DEC-2004.
XX
PF  09-APR-2004; 2004US-00821670.
XX
PR  04-AUG-2000; 2000US-0223016P.
PR  27-JUL-2001; 2001US-00917265.
XX
PA  (WOND/) WONDERLING R S.
PA  (BORO/) BOROUGHS K L.
XX
PI  Wonderling RS,  Boroughs KL;
XX
DR  WPI; 2005-020565/02.
XX
PT  New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT  p40 subunit protein and a nucleic acid linker, useful in preparing a
PT  vaccine against infectious diseases in feline animals.
XX
PS  Example 3; SEQ ID NO 40; 103pp; English.
XX
CC  The present invention relates to the feline interleukin (IL)-12p35 or p40
CC  subunit protein and their encoding nucleic acid molecules and a nucleic
CC  acid linker. The invention also provides the feline caspase (casp)-1,
CC  feline IL-18 single chain and canine IL-12 single chain proteins and
CC  their nucleic acid molecules. The nucleic acid molecule is useful in
CC  preparing a vaccine against infectious diseases in feline animals. The
CC  present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ  Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.95e-303      Length:          1599
Score:                    307.00         Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       14             Gaps:            0

US-10-821-670A-27 (1-307) x ADV34693 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174
```

```
Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

```
RESULT 13
AAV56627
ID   AAV56627 standard; cDNA; 921 BP.
XX
AC   AAV56627;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #2.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 21; Page 56-57; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                3.6e-200      Length:          921
Score:                    206.00        Matches:         306
Percent Similarity:       99.7%         Conservative:    0
Best Local Similarity:    99.7%         Mismatches:      1
Query Match:              67.1%         Indels:          0
DB:                       2             Gaps:            0

US-10-821-670A-27 (1-307) x AAV56627 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
```

```
y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b        901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 14
AV56626
D   AAV56626 standard; cDNA; 921 BP.
X
C   AAV56626;
X
T   23-NOV-1998  (first entry)
X
E   Feline FLAFp40 cDNA mature transcript #1.
X
W   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
W   T lymphocyte cell; autoimmune disease; ds.
X
S   Felis catus.
X
N   WO9746583-A1.
X
D   11-DEC-1997.
X
F   29-MAY-1997;   97WO-JP001824.
X
R   04-JUN-1996;   96JP-00165249.
X
A   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
X
I   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
X
R   WPI; 1998-042118/04.
R   P-PSDB; AAW76174.
X
T   Novel feline cytokine protein - useful for treating feline auto:immune
T   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
X
S   Claim 20; Page 55; 94pp; Japanese.
X
C   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
C   This protein can be used in the production of a FLAFp35/FLAFp40
C   heterodimer which can potentiate the cytotoxic activity of feline
C   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
C   feline autoimmune diseases e.g. as caused by feline herpes virus or
C   feline calcivirus
X
Q   Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 U; 0 Other;

lignment Scores:
red. No.:              3.6e-200      Length:         921
core:                  206.00        Matches:        306
ercent Similarity:     99.7%         Conservative:   0
est Local Similarity:  99.7%         Mismatches:     1
uery Match:            67.1%         Indels:         0
B:                     2             Gaps:           0

S-10-821-670A-27 (1-307) x AAV56626 (1-921)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db       901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 15
ABK98944
ID   ABK98944 standard; cDNA; 987 BP.
XX
AC   ABK98944;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
```

```
)N   US2002052030-A1.
:X
)D   02-MAY-2002.
:X
)F   27-JUL-2001; 2001US-00917265.
:X
)R   04-AUG-2000; 2000US-0223016P.
:X
)A   (WOND/) WONDERLING R S.
)A   (BORO/) BOROUGHS K L.
:X
)I   Wonderling RS,  Boroughs KL;
:X
)R   WPI; 2002-573554/61.
)R   P-PSDB; ABG69303.
:X
)T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
)T   chain and canine IL-12 single chain proteins, useful for treating and
)T   preventing autoimmune diseases, inflammatory diseases and/or graft
)T   rejection in animals.
:X
)S   Claim 1; Page 51-53; 106pp; English.
:X
:C   The present invention discloses new feline interleukin 18 (IL-18), feline
:C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
:C   proteins. A composition comprising a feline IL-18, feline caspase-1,
:C   feline IL-12 single chain or canine IL-12 single chain proteins, a
:C   nucleic acid encoding these proteins, mimetopes of these proteins,
:C   multimeric forms of these proteins, an antibody against these proteins,
:C   or an inhibitor identified by its ability to inhibit the activity of
:C   these proteins, can be used to treat or prevent autoimmune diseases,
:C   allergic reactions, infectious diseases, tumour development, inflammatory
:C   diseases and/or graft rejection in animals. The present nucleic acid
:C   sequence represents a feline interleukin 12 DNA sequence, as described in
:C   the invention
:X
;Q   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:
)red. No.:              3.84e-200       Length:         987
;core:                  206.00          Matches:        306
)ercent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
)uery Match:            67.1%           Indels:         0
)B:                     6               Gaps:           0

US-10-821-670A-27 (1-307) x ABK98944 (1-987)

)y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

)y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

)y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

)y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

)y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

)y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

)y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 16
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
```

```
T   rejection in animals.
X
S   Example 3; Page 54; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a feline interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

lignment Scores:
red. No.:              3.84e-200      Length:        987
core:                  206.00         Matches:       306
ercent Similarity:     99.7%          Conservative:  0
est Local Similarity:  99.7%          Mismatches:    1
uery Match:            67.1%          Indels:        0
B:                     6              Gaps:          0

S-10-821-670A-27 (1-307) x ABK98945 (1-987)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
b        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db        21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 17
ADV34682
ID   ADV34682 standard; cDNA; 987 BP.
XX
AC   ADV34682;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag= a
FT                   /product= "PFeIL-12p40 329 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34683.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 29; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
```

:X
:Q Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.84e-200	Length:	987
Score:	206.00	Matches:	306
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	67.1%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-27 (1-307) x ADV34682 (1-987)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987
```

RESULT 18
ADV34684/c
ID ADV34684 standard; DNA; 987 BP.
XX
AC ADV34684;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 31; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p40 subunit full-length
CC complementary DNA.
XX
SQ Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.84e-200	Length:	987
Score:	206.00	Matches:	306
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	67.1%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-27 (1-307) x ADV34684 (1-987)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742
```

```
y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
b        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b         21 TGGGCATCCGTGTCCTGCAGT 1
```

ESULT 19
AF26082

```
D   AAF26082 standard; DNA; 990 BP.
X
C   AAF26082;
X
T   24-APR-2001  (first entry)
X
E   Feline IL-12p40 encoding DNA SEQ ID 8.
X
W   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
W   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
X
S   Felis sp.
X
N   WO200104280-A2.
X
D   18-JAN-2001.
X
F   08-JUL-2000; 2000WO-DE002262.
X
PR   08-JUL-1999;   99CH-00001258.
X
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
X
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
X
DR   WPI; 2001-147190/15.
X
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
X
PS   Claim 14; Page 36; 37pp; German.
X
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	3.85e-200	Length:	990
Score:	206.00	Matches:	306
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	67.1%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-27 (1-307) x AAF26082 (1-990)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
)b        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

)y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
)b        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

)y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

)y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

)y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

)y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

)y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

)y        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
)b        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 20
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
AC   AAF26085;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 30; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.85e-200      Length:          990
Score:                    206.00         Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              67.1%          Indels:          0
DB:                       4              Gaps:            0

US-10-821-670A-27 (1-307) x AAF26085 (1-990)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
```

```
y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

y       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

y       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

y       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

y       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

y       301 TrpAlaSerValSerCysSer 307
            |||||||||||||||||||||
b       967 TGGGCATCCGTGTCCTGCAGT 987
```

```
ESULT 21
AV56625
D   AAV56625 standard; cDNA; 2193 BP.
X
C   AAV56625;
X
T   23-NOV-1998  (first entry)
X
E   Feline FLAFp40 cDNA.
X
W   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
W   T lymphocyte cell; autoimmune disease; ds.
X
S   Felis catus.
X
H   Key             Location/Qualifiers
T   CDS             64. .1053
T                   /*tag= a
T   sig_peptide     64. .129
T                   /*tag= b
T   mat_peptide     130. .1050
T                   /*tag= c
T                   /product= "FLAFp40"
T                   /note= "feline cytokine"
X
N   WO9746583-A1.
X
D   11-DEC-1997.
X
F   29-MAY-1997;   97WO-JP001824.
X
R   04-JUN-1996;   96JP-00165249.
X
A   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
X
I   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
X
R   WPI; 1998-042118/04.
R   P-PSDB; AAW76173.
X
T   Novel feline cytokine protein - useful for treating feline auto:immune
T   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
X
S   Claim 19; Page 52-54; 94pp; Japanese.
X
```

```
CC   This sequence encodes a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.17e-200       Length:         2193
Score:                  206.00          Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            67.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AAV56625 (1-2193)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
)b        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

)y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

)y        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
)b       1030 TGGGCATCCGTGTCCTGCAGT 1050

(ESULT 22
\AF26076
:D   AAF26076 standard; DNA; 4522 BP.
:X
\C   AAF26076;
:X
)T   24-APR-2001  (first entry)
:X
)E   Feline IL-12p40 encoding DNA SEQ ID 2.
:X
:W   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
:W   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
:X
)S   Felis sp.
:X
)N   WO200104280-A2.
:X
)D   18-JAN-2001.
:X
)F   08-JUL-2000; 2000WO-DE002262.
:X
)R   08-JUL-1999;   99CH-00001258.
:X
)A   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
)A   (UYZU-) UNIV ZUERICH.
:X
)I   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
:X
)R   WPI; 2001-147190/15.
:X
)T   Vaccine for treating or preventing lentivirus infection in cats, contains
)T   nucleic acid sequence encoding viral protein under control of eukaryotic
)T   promoter.
:X
)S   Disclosure; Page 29-31; 37pp; German.
:X
:C   This invention describes a novel vaccine (A) for prevention or treatment
:C   of lentivirus infection in felines which comprises an immunizing nucleic
:C   acid sequence (I) that contains, or comprises, at least part of a gene
:C   encoding a protein (II) of the virus, under control of a eukaryotic
:C   promoter functional in the relevant animal. (II) is especially the
:C   envelope (env) protein. The invention also describes (1) vaccine (A)
:C   containing an immunizing protein, or fragment, from a lentivirus plus at
:C   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
:C   lentivirus protein, or fragment, especially derived from feline immune
:C   deficiency virus (FIV), by expressing the corresponding nucleic acid
:C   sequence in a host cell. The products of the invention have antiviral
:C   activity. The vaccine (A) and related protein-based vaccines, are
:C   particularly used to treat or prevent lentivirus infections in domestic
:C   cats, especially feline immune deficiency virus (FIV). Vaccination with
:C   (A) allows differentiation between vaccinated and infected animals, from
:C   the antibody status. The vaccines may be formulated with an adjuvant
:C   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
:C   immune response, particularly a Th1 response
:X
:Q   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

\lignment Scores:
)red. No.:                1.62e-199       Length:          4522
:core:                    206.00          Matches:         306
)ercent Similarity:       99.7%           Conservative:    0
)est Local Similarity:    99.7%           Mismatches:      1
)uery Match:              67.1%           Indels:          0

DB:                    4              Gaps:          0

US-10-821-670A-27 (1-307) x AAF26076 (1-4522)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db       4013 TGGGCATCCGTGTCCTGCAGT 4033

RESULT 23
AAF26094
ID   AAF26094 standard; DNA; 4522 BP.
XX
AC   AAF26094;
```

```
X
T   24-APR-2001  (first entry)
X
E   Plasmid pMol-fil12p40 DNA SEQ ID 10.
X
W   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
W   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
W   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
X
S   Synthetic.
X
N   WO200104155-A2.
X
D   18-JAN-2001.
X
F   08-JUL-2000; 2000WO-DE002263.
X
R   08-JUL-1999;   99CH-00001259.
X
A   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
A   (UYZU-) UNIV ZUERICH.
A   (REGC ) UNIV CALIFORNIA.
X
I   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
X
R   WPI; 2001-147178/15.
X
T   Recombinant feline interleukin-12, useful as immunostimulant and for
T   treating e.g. viral infections in cats, and related nucleic acid
T   constructs.
X
S   Example 1c; Page 33-35; 35pp; German.
X
C   This invention describes a novel feline interleukin-12 (fIL-12)
C   polypeptide (I) that is expressed, by recombinant gene expression in
C   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
C   of subunits p35 and p40. These proteins are formed so that, in equimolar
C   concentrations and in presence of an immunizing antigen, they can be
C   administered to carnivores, particularly domestic cats. The invention
C   also describes a nucleic acid construct (II) encoding fIL-12 containing
C   sequences at least 95% identical with the p40- and p35-encoding sequences
C   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
C   as immunostimulants for immunization against infectious diseases and/or
C   for treating infections or tumors in felines, especially domestic cats.
C   The products of the invention have immunostimulatory, antiviral and
C   antitumor activity. Nucleic acid constructs that encode (II) are useful
C   as adjuvants for prophylactic immunization against viral diseases and for
C   treating diseases associated with a Th1 defect. IL-12 induces synthesis
C   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
C   is useful for carnivores, and particularly domestic cats in the
C   following: (i) as immunostimulant, for preventative or therapeutic use;
C   and (ii) treating tumors and autoimmune diseases, or diseases associated
C   with a Th1 defect, especially pre-existing infections by feline immune
C   deficiency virus (FIV), feline leukemia virus and corona virus
X
Q   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.62e-199      Length:        4522
core:                  206.00         Matches:       306
ercent Similarity:     99.7%          Conservative:  0
est Local Similarity:  99.7%          Mismatches:    1
uery Match:            67.1%          Indels:        0
B:                     4              Gaps:          0

S-10-821-670A-27 (1-307) x AAF26094 (1-4522)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db      3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db      4013 TGGGCATCCGTGTCCTGCAGT 4033

RESULT 24
ABK98962/c
ID   ABK98962 standard; cDNA; 985 BP.
XX
AC   ABK98962;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
```

```
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 75-76; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.02e-199       Length:          985
Score:                    205.00          Matches:         305
Percent Similarity:       99.7%           Conservative:    0
Best Local Similarity:    99.7%           Mismatches:      1
Query Match:              66.8%           Indels:          0
DB:                       6               Gaps:            0

US-10-821-670A-27 (1-307) x ABK98962 (1-985)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy        301 TrpAlaSerValSerCys 306
              ||||||||||||||||||
Db         19 TGGGCATCCGTGTCCTGC 2

RESULT 25
ABK98961
ID   ABK98961 standard; cDNA; 985 BP.
XX
AC   ABK98961;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69311.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
```

```
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Example 3; Page 73-74; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a feline interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

lignment Scores:
red. No.:               4.02e-199       Length:         985
core:                   205.00          Matches:        305
ercent Similarity:      99.7%           Conservative:   0
est Local Similarity:   99.7%           Mismatches:     1
uery Match:             66.8%           Indels:         0
B:                      6               Gaps:           0

S-10-821-670A-27 (1-307) x ABK98961 (1-985)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
b        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy       301 TrpAlaSerValSerCys 306
             ||||||||||||||||||
Db       967 TGGGCATCCGTGTCCTGC 984

RESULT 26
ADV34707
ID   ADV34707 standard; cDNA; 985 BP.
XX
AC   ADV34707;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-N328 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34708.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40 protein
```

```
:C   encoding cDNA.
:X
:Q   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

\lignment Scores:
>red. No.:              4.02e-199      Length:         985
;core:                  205.00         Matches:        305
>ercent Similarity:     99.7%          Conservative:   0
>est Local Similarity:  99.7%          Mismatches:     1
)uery Match:            66.8%          Indels:         0
)B:                     14             Gaps:           0

)S-10-821-670A-27 (1-307) x ADV34707 (1-985)

)y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

)y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

)y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

)y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

)y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

)y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

)y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

)y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
)b        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

)y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

)y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

)y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

)y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

)y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
```

```
Qy        301 TrpAlaSerValSerCys 306
              ||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGC 984

RESULT 27
ADV34709/c
ID   ADV34709 standard; DNA; 985 BP.
XX
AC   ADV34709;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 57; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40
CC   complementary DNA.
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.02e-199      Length:         985
Score:                  205.00         Matches:        305
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            66.8%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-27 (1-307) x ADV34709 (1-985)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
b        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
b        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

y        301 TrpAlaSerValSerCys 306
             ||||||||||||||||||
b         19 TGGGCATCCGTGTCCTGC 2
```

```
ESULT 28
AD15209
D   AAD15209 standard; DNA; 990 BP.
X
C   AAD15209;
X
T   01-NOV-2001  (first entry)
X
E   Modified human cytokine p40 encoding DNA from clone R16-51.
X
W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
W   p40; mutant; ds.
X
S   Homo sapiens.
S   Synthetic.
X
H   Key             Location/Qualifiers
T   CDS             1. .990
FT                  /*tag=  a
FT                  /product= "Modified p40 protein precursor"
FT   sig_peptide    1. .66
FT                  /*tag=  b
FT   mat_peptide    67. .987
FT                  /*tag=  c
FT                  /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08602.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137-138; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 990 BP; 270 A; 250 C; 254 G; 216 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.88e-43        Length:          990
Score:                    52.00           Matches:         52
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              16.9%           Indels:          0
DB:                       5               Gaps:            0

US-10-821-670A-27 (1-307) x AAD15209 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCTGACCCACCCAAGAACTTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGlu 232
              ||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTAAAGAATTCTCGACACGTGGAG 762

RESULT 29
AAD15206
ID   AAD15206 standard; DNA; 984 BP.
XX
AC   AAD15206;
XX
DT   01-NOV-2001  (first entry)
XX
```

```
)E   Modified human cytokine p40 encoding DNA from clone B1-81.
:X
:W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
:W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
:W   p40; mutant; ds.
:X
)S   Homo sapiens.
)S   Synthetic.
:X
'H   Key             Location/Qualifiers
'T   CDS             1. .984
'T                   /*tag=  a
'T                   /product= "Modified p40 protein precursor"
'T   sig_peptide     1. .66
'T                   /*tag=  b
'T   mat_peptide     67. .981
'T                   /*tag=  c
'T                   /product= "Mature modified p40 protein"
:X
'N   WO200140257-A2.
:X
'D   07-JUN-2001.
:X
'F   30-NOV-2000; 2000WO-US032664.
:X
'R   02-DEC-1999;   99US-0169035P.
'R   28-NOV-2000; 2000US-00725324.
:X
'A   (MAXY-) MAXYGEN INC.
:X
'I   Leong SR,  Punnonen J;
:X
)R   WPI; 2001-502381/55.
)R   P-PSDB; AAE08599.
:X
'T   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
'T   and p35 polypeptides), useful for treating various diseases e.g. diabetic
'T   retinopathy and cancer.
:X
'S   Claim 1; Page 137; 223pp; English.
:X
:C   The invention relates to nucleic acids encoding modified cytokine
:C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
:C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
:C   gamma induction activities. The polypeptides and polynucleotides of the
:C   invention are useful for treating various diseases e.g. bacterial
:C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
:C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
:C   vaccinated host's cell-mediated immunity for protective response to a
:C   pathogen. The present sequence is a modified human p40 protein encoding
:C   DNA
:X
;Q   Sequence 984 BP; 272 A; 254 C; 247 G; 211 T; 0 U; 0 Other;

\lignment Scores:
'red. No.:              8.97e-34      Length:        984
;core:                  43.00         Matches:       43
'ercent Similarity:     100.0%        Conservative:  0
}est Local Similarity:  100.0%        Mismatches:    0
}uery Match:            14.0%         Indels:        0
)B:                     5             Gaps:          0

IS-10-821-670A-27 (1-307) x AAD15206 (1-984)

}y      102 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b      370 AAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGG 429

}y      122 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 141
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b      430 TGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCT 489

}y      142 AspProGln 144
                ||||||||
Db      490 GACCCCCAA 498

RESULT 30
AAD15205
ID   AAD15205 standard; DNA; 984 BP.
XX
AC   AAD15205;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B2-52.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08598.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136-137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 267 A; 246 C; 254 G; 217 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.41e-33      Length:        984
Score:                  42.00         Matches:       42
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            13.7%         Indels:        0
DB:                     5             Gaps:          0
```

```
S-10-821-670A-27 (1-307) x AAD15205 (1-984)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACTTG 726

y       221 GlnLeu 222
            ||||||
b       727 CAGCTG 732

ESULT 31
AD15203
D   AAD15203 standard; DNA; 975 BP.
X
C   AAD15203;
X
T   01-NOV-2001  (first entry)
X
E   Modified human cytokine p40 encoding DNA from clone C2-22.
X
W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
W   p40; mutant; ds.
X
S   Homo sapiens.
S   Synthetic.
X
H   Key             Location/Qualifiers
T   CDS             1. .975
T                   /*tag=  a
T                   /product= "Modified p40 protein precursor"
T   sig_peptide     1. .66
T                   /*tag=  b
T   mat_peptide     67. .972
T                   /*tag=  c
T                   /product= "Mature modified p40 protein"
X
N   WO200140257-A2.
X
D   07-JUN-2001.
X
F   30-NOV-2000; 2000WO-US032664.
X
R   02-DEC-1999;   99US-0169035P.
R   28-NOV-2000; 2000US-00725324.
X
A   (MAXY-) MAXYGEN INC.
X
I   Leong SR,  Punnonen J;
X
R   WPI; 2001-502381/55.
R   P-PSDB; AAE08596.
X
T   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
T   and p35 polypeptides), useful for treating various diseases e.g. diabetic
T   retinopathy and cancer.
X
S   Claim 1; Page 136; 223pp; English.
X
C   The invention relates to nucleic acids encoding modified cytokine
C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
C   gamma induction activities. The polypeptides and polynucleotides of the
C   invention are useful for treating various diseases e.g. bacterial
C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
C   vaccinated host's cell-mediated immunity for protective response to a
C   pathogen. The present sequence is a modified human p40 protein encoding
C   DNA
```

```
XX
SQ   Sequence 975 BP; 269 A; 252 C; 250 G; 204 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.78e-32        Length:         975
Score:                  41.00           Matches:        41
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            13.4%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-27 (1-307) x AAD15203 (1-975)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCA 693

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 234
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694 GACCCACCCAAGAACCTGCAACTGAAGCCATTGAAAAATTCTCGGCATGTGGAGGTCAGC 753

Qy      235 Trp 235
            |||
Db      754 TGG 756

RESULT 32
ABK98959
ID   ABK98959 standard; cDNA; 921 BP.
XX
AC   ABK98959;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-921 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69310.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 71; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
```

```
:C   diseases and/or graft rejection in animals. The present nucleic acid
:C   sequence represents a canine interleukin 12 DNA sequence, as described in
:C   the invention
:X
;Q   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

\lignment Scores:
>red. No.:                1.12e-27       Length:         921
;core:                    37.00          Matches:        37
>ercent Similarity:       100.0%         Conservative:   0
}est Local Similarity:    100.0%         Mismatches:     0
)uery Match:              12.1%          Indels:         0
)B:                       6              Gaps:           0

)S-10-821-670A-27 (1-307) x ABK98959 (1-921)

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
)b        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

!ESULT 33
\BK98960/c
:D   ABK98960 standard; cDNA; 921 BP.
:X
\C   ABK98960;
:X
)T   21-OCT-2002  (first entry)
:X
)E   Canine interleukin-12 nCaIL-12p40-921 complementary strand.
:X
:W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
:W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
:W   tumour development; inflammatory disease; graft rejection; ss.
:X
)S   Canis familiaris.
:X
)N   US2002052030-A1.
:X
)D   02-MAY-2002.
:X
)F   27-JUL-2001; 2001US-00917265.
:X
)R   04-AUG-2000; 2000US-0223016P.
:X
)A   (WOND/) WONDERLING R S.
)A   (BORO/) BOROUGHS K L.
:X
)I   Wonderling RS,  Boroughs KL;
:X
)R   WPI; 2002-573554/61.
:X
)T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
)T   chain and canine IL-12 single chain proteins, useful for treating and
)T   preventing autoimmune diseases, inflammatory diseases and/or graft
)T   rejection in animals.
:X
)S   Disclosure; Page 73; 106pp; English.
:X
:C   The present invention discloses new feline interleukin 18 (IL-18), feline
:C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
:C   proteins. A composition comprising a feline IL-18, feline caspase-1,
:C   feline IL-12 single chain or canine IL-12 single chain proteins, a
:C   nucleic acid encoding these proteins, mimetopes of these proteins,
:C   multimeric forms of these proteins, an antibody against these proteins,
:C   or an inhibitor identified by its ability to inhibit the activity of
:C   these proteins, can be used to treat or prevent autoimmune diseases,
:C   allergic reactions, infectious diseases, tumour development, inflammatory
:C   diseases and/or graft rejection in animals. The present nucleic acid
:C   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.12e-27       Length:         921
Score:                    37.00          Matches:        37
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              12.1%          Indels:         0
DB:                       6              Gaps:           0

US-10-821-670A-27 (1-307) x ABK98960 (1-921)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 34
ADV34706/c
ID   ADV34706 standard; DNA; 921 BP.
XX
AC   ADV34706;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain mature IL-12p40 complementary DNA, nCaIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Disclosure; SEQ ID NO 54; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit reverse
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.12e-27       Length:         921
Score:                    37.00          Matches:        37
```

```
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            12.1%           Indels:        0
B:                     14              Gaps:          0

S-10-821-670A-27 (1-307) x ADV34706 (1-921)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

ESULT 35
DV34704
D   ADV34704 standard; cDNA; 921 BP.
X
C   ADV34704;
X
T   24-FEB-2005  (first entry)
X
E   Canine single chain mature IL-12p40 protein cDNA, nCaIL-12p40 921.
X
W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W   infectious disease; antimicrobial; gene; ss.
X
S   Canis familiaris.
X
H   Key             Location/Qualifiers
T   CDS             1. .921
T                   /*tag=  a
T                   /product= "PCaIL-12P40 307 protein"
T                   /partial
T                   /note= "No start and stop codon"
X
N   US2004248261-A1.
X
D   09-DEC-2004.
X
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2005-020565/02.
R   P-PSDB; ADV34705.
X
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
T   vaccine against infectious diseases in feline animals.
X
S   Example 4; SEQ ID NO 52; 103pp; English.
X
C   The present invention relates to the feline interleukin (IL)-12p35 or p40
C   subunit protein and their encoding nucleic acid molecules and a nucleic
C   acid linker. The invention also provides the feline caspase (casp)-1,
C   feline IL-18 single chain and canine IL-12 single chain proteins and
C   their nucleic acid molecules. The nucleic acid molecule is useful in
C   preparing a vaccine against infectious diseases in feline animals. The
C   present sequence is the canine single chain IL-12p40 subunit protein
C   encoding cDNA.
X
Q   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.12e-27        Length:        921
```

```
Score:                 37.00           Matches:       37
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           12.1%           Indels:        0
DB:                    14              Gaps:          0

US-10-821-670A-27 (1-307) x ADV34704 (1-921)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 36
AAX18177
ID   AAX18177 standard; cDNA; 924 BP.
XX
AC   AAX18177;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74323.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 32; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.12e-27        Length:        924
Score:                 37.00           Matches:       37
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           12.1%           Indels:        0
DB:                    2               Gaps:          0

US-10-821-670A-27 (1-307) x AAX18177 (1-924)
```

```
)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        544 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 603

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
)b        604 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 654

!ESULT 37
\BK98963
:D   ABK98963 standard; cDNA; 987 BP.
:X
\C   ABK98963;
:X
)T   21-OCT-2002  (first entry)
:X
)E   Canine interleukin-12 nCaIL-12p40-987 coding strand.
:X
:W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
:W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
:W   tumour development; inflammatory disease; graft rejection; gene; ss.
:X
)S   Canis familiaris.
:X
)N   US2002052030-A1.
:X
)D   02-MAY-2002.
:X
)F   27-JUL-2001; 2001US-00917265.
:X
)R   04-AUG-2000; 2000US-0223016P.
:X
)A   (WOND/) WONDERLING R S.
)A   (BORO/) BOROUGHS K L.
:X
)I   Wonderling RS,  Boroughs KL;
:X
)R   WPI; 2002-573554/61.
)R   P-PSDB; ABG69312.
:X
)T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
)T   chain and canine IL-12 single chain proteins, useful for treating and
)T   preventing autoimmune diseases, inflammatory diseases and/or graft
)T   rejection in animals.
:X
)S   Claim 1; Page 76-77; 106pp; English.
:X
:C   The present invention discloses new feline interleukin 18 (IL-18), feline
:C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
:C   proteins. A composition comprising a feline IL-18, feline caspase-1,
:C   feline IL-12 single chain or canine IL-12 single chain proteins, a
:C   nucleic acid encoding these proteins, mimetopes of these proteins,
:C   multimeric forms of these proteins, an antibody against these proteins,
:C   or an inhibitor identified by its ability to inhibit the activity of
:C   these proteins, can be used to treat or prevent autoimmune diseases,
:C   allergic reactions, infectious diseases, tumour development, inflammatory
:C   diseases and/or graft rejection in animals. The present nucleic acid
:C   sequence represents a canine interleukin 12 DNA sequence, as described in
:C   the invention
:X
;Q   Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

\lignment Scores:
)red. No.:              1.2e-27       Length:         987
;core:                  37.00         Matches:        37
)ercent Similarity:     100.0%        Conservative:   0
)est Local Similarity:  100.0%        Mismatches:     0
)uery Match:            12.1%         Indels:         0
)B:                     6             Gaps:           0

)S-10-821-670A-27 (1-307) x ABK98963 (1-987)
```

```
Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 38
ABK98964/c
ID   ABK98964 standard; cDNA; 987 BP.
XX
AC   ABK98964;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 78; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.2e-27       Length:         987
Score:                  37.00         Matches:        37
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            12.1%         Indels:         0
DB:                     6             Gaps:           0

US-10-821-670A-27 (1-307) x ABK98964 (1-987)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
b        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

ESULT 39
DV34712/c
D   ADV34712 standard; DNA; 987 BP.
X
C   ADV34712;
X
T   24-FEB-2005  (first entry)
X
E   Canine single chain IL-12p40 complementary DNA, nCaIL-12p40 987.
X
W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
W   infectious disease; antimicrobial; ds.
X
S   Canis familiaris.
X
N   US2004248261-A1.
X
D   09-DEC-2004.
X
F   09-APR-2004; 2004US-00821670.
X
R   04-AUG-2000; 2000US-0223016P.
R   27-JUL-2001; 2001US-00917265.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2005-020565/02.
X
T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
T   p40 subunit protein and a nucleic acid linker, useful in preparing a
T   vaccine against infectious diseases in feline animals.
X
S   Example 4; SEQ ID NO 60; 103pp; English.
X
C   The present invention relates to the feline interleukin (IL)-12p35 or p40
C   subunit protein and their encoding nucleic acid molecules and a nucleic
C   acid linker. The invention also provides the feline caspase (casp)-1,
C   feline IL-18 single chain and canine IL-12 single chain proteins and
C   their nucleic acid molecules. The nucleic acid molecule is useful in
C   preparing a vaccine against infectious diseases in feline animals. The
C   present sequence is the canine single chain IL-12p40 subunit full-length
C   complementary DNA.
X
Q   Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.2e-27        Length:        987
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            12.1%          Indels:        0
B:                     14             Gaps:          0

S-10-821-670A-27 (1-307) x ADV34712 (1-987)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

ESULT 40
```

```
ADV34710
ID   ADV34710 standard; cDNA; 987 BP.
XX
AC   ADV34710;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 full-length cDNA, nCaIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-329 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34711.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 58; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.2e-27        Length:        987
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           12.1%          Indels:        0
DB:                    14             Gaps:          0

US-10-821-670A-27 (1-307) x ADV34710 (1-987)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

```
RESULT 41
AAV13816
ID   AAV13816 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13816;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin-12_P40_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41790.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 8; Page 8; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.2e-27       Length:         990
Score:                  37.00         Matches:        37
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            12.1%         Indels:         0
DB:                     2             Gaps:           0

US-10-821-670A-27 (1-307) x AAV13816 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 42
AAV13817
ID   AAV13817 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13817;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin-12_P40_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41791.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 10; Page 10-11; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.2e-27       Length:         990
Score:                  37.00         Matches:        37
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            12.1%         Indels:         0
DB:                     2             Gaps:           0

US-10-821-670A-27 (1-307) x AAV13817 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 43
AAX03162
ID   AAX03162 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03162;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
```

```
W   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
W   skin disease; viral infection; allergic disease; breast tumour;
W   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
W   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
W   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
W   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
W   dog Parvovirus infection; distemper virus; cat plaque virus infection;
W   feline leukaemia; allergy; pollinosis; ds.
X
S   Canis sp.
X
H   Key             Location/Qualifiers
T   CDS             1. .990
T                   /*tag=  a
T                   /product= "interleukin_12"
X
N   WO9851327-A1.
X
D   19-NOV-1998.
X
F   07-MAY-1998;   98WO-JP002031.
X
R   16-MAY-1997;   97JP-00127690.
X
A   (TORA ) TORAY IND INC.
X
I   Okano F,  Satoh M,  Yamada K;
X
R   WPI; 1999-070100/06.
R   P-PSDB; AAW84373.
X
T   New therapeutic and prophylactic agents - comprise genetically-engineered
T   canine interleukin 12, used to treat, e.g. canine and feline
T   immunological diseases.
X
S   Claim 1; Page 30-32; 45pp; Japanese.
X
C   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
C   IL-12 protein can be used in therapeutic or prophylactic agents. The
C   agents can be used to prevent and treat canine and feline immunological
C   diseases including dog and cat tumours, skin diseases, viral infections
C   and allergic diseases, especially tumours, breast tumour, oesinophilic
C   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
C   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
C   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
C   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
C   and hair loss; infections; dog Parvovirus infection and distemper virus,
C   cat plaque virus infection and feline leukaemia, and allergic diseases,
C   e.g. pollinosis
X
Q   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

lignment Scores:
red. No.:               1.2e-27         Length:         990
core:                   37.00           Matches:        37
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             12.1%           Indels:         0
B:                      2               Gaps:           0

S-10-821-670A-27 (1-307) x AAX03162 (1-990)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 44
AX03152
D   AAX03152 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03152;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84371.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.2e-27         Length:         990
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AAX03152 (1-990)

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
```

```
)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

:ESULT 45
\AX35625
:D   AAX35625 standard; cDNA to mRNA; 990 BP.
:X
\C   AAX35625;
:X
)T   09-JUL-1999  (first entry)
:X
)E   Nucleic acid encoding canine Interleukin-12 (IL-12).
:X
:W   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
:W   tumour; skin disease; infectious disease; allergic disease; ds.
:X
)S   Canis sp.
:X
'H   Key             Location/Qualifiers
'T   CDS             1. .990
'T                   /*tag=  a
:X
'N   JP11106350-A.
:X
'D   20-APR-1999.
:X
'F   15-MAY-1998;   98JP-00133345.
:X
'R   16-MAY-1997;   97JP-00127690.
'R   07-AUG-1997;   97JP-00213755.
:X
'A   (TORA ) TORAY IND INC.
:X
)R   WPI; 1999-308068/26.
)R   P-PSDB; AAY02342.
:X
'T   A prevention and treating agent containing interleukin 12 (CaIL12) - for
'T   prevention and treatment of dog and cat immune diseases.
:X
'S   Claim 1; Page 14-15; 16pp; Japanese.
:X
:C   The present sequence encodes canine interleukin-12 (IL-12). The
:C   specification describes a method for the prevention and treatment of dog
:C   and cat immune diseases. The treatment used an agent comprising dog IL-12
:C   (CaIL12) proteins to form a heterodimer. The agent is useful for
:C   preventing and treating dog and cat immune diseases, including tumours,
:C   skin diseases, infectious diseases and allergic diseases
:X
;Q   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

\lignment Scores:
'red. No.:              1.2e-27        Length:         990
;core:                  37.00          Matches:        37
'ercent Similarity:     100.0%         Conservative:   0
}est Local Similarity:  100.0%         Mismatches:     0
)uery Match:            12.1%          Indels:         0
)B:                     2              Gaps:           0

)S-10-821-670A-27 (1-307) x AAX35625 (1-990)

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

:ESULT 46
\AX35615
:D   AAX35615 standard; cDNA to mRNA; 990 BP.
:X
\C   AAX35615;
:X
)T   09-JUL-1999  (first entry)
:X
)E   Nucleic acid encoding canine Interleukin-12 (IL-12).
:X
:W   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
:W   tumour; skin disease; infectious disease; allergic disease; ds.
:X
)S   Canis sp.
:X
'H   Key             Location/Qualifiers
'T   CDS             1. .990
'T                   /*tag=  a
:X
'N   JP11106350-A.
:X
'D   20-APR-1999.
:X
'F   15-MAY-1998;   98JP-00133345.
:X
'R   16-MAY-1997;   97JP-00127690.
'R   07-AUG-1997;   97JP-00213755.
:X
'A   (TORA ) TORAY IND INC.
:X
)R   WPI; 1999-308068/26.
)R   P-PSDB; AAY02339.
:X
'T   A prevention and treating agent containing interleukin 12 (CaIL12) - for
'T   prevention and treatment of dog and cat immune diseases.
:X
'S   Claim 1; Page 12; 16pp; Japanese.
:X
:C   The present sequence encodes canine interleukin-12 (IL-12). The
:C   specification describes a method for the prevention and treatment of dog
:C   and cat immune diseases. The treatment used an agent comprising dog IL-12
:C   (CaIL12) proteins to form a heterodimer. The agent is useful for
:C   preventing and treating dog and cat immune diseases, including tumours,
:C   skin diseases, infectious diseases and allergic diseases
:X
;Q   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

\lignment Scores:
'red. No.:              1.2e-27        Length:         990
;core:                  37.00          Matches:        37
'ercent Similarity:     100.0%         Conservative:   0
}est Local Similarity:  100.0%         Mismatches:     0
)uery Match:            12.1%          Indels:         0
)B:                     2              Gaps:           0

)S-10-821-670A-27 (1-307) x AAX35615 (1-990)

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

:ESULT 47
\AI64378
:D   AAI64378 standard; DNA; 990 BP.
:X
\C   AAI64378;
:X
)T   23-NOV-2001  (first entry)
:X
)E   Canine coding sequence #1.
:X
:W   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
:X
```

```
S   Canis familiaris.
X
H   Key             Location/Qualifiers
T   CDS             1. .990
T                   /*tag=  a
T                   /product= "Canine protein #1"
T   sig_peptide     1. .66
T                   /*tag=  b
T   mat_peptide     67. .987
T                   /*tag=  c
X
N   JP2001161378-A.
X
D   19-JUN-2001.
X
F   26-SEP-2000; 2000JP-00292946.
X
R   01-OCT-1999;   99JP-00281234.
X
A   (TORA ) TORAY IND INC.
X
R   WPI; 2001-592466/67.
R   P-PSDB; AAG66480.
X
T   Preparation of a highly pure protein, interleukin 12, a protein
T   inhibiting the activity of interleukin 12, and a treating agent and a
T   treating method for immunopathy of mammalian.
X
S   Claim 6; Page 14; 21pp; Japanese.
X
C   The present invention relates to a method for the preparation of a highly
C   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
C   the activity of IL12 is contacted to an ion exchanging carrier and/or a
C   pigment carrier to get IL12 and/or a protein inhibiting the activity of
C   IL12. The protein is used as a preventive agent for dog immunopathy. The
C   present sequence was used in the method of the present invention
X
Q   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.2e-27        Length:        990
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            12.1%          Indels:        0
B:                     4              Gaps:          0

S-10-821-670A-27 (1-307) x AAI64378 (1-990)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 48
AI64388
D   AAI64388 standard; DNA; 990 BP.
X
C   AAI64388;
X
T   23-NOV-2001  (first entry)
X
E   Canine coding sequence #3.
X
W   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
X
S   Canis familiaris.
X
H   Key             Location/Qualifiers
T   CDS             1. .990
FT                  /*tag=  a
FT                  /product= "Canine protein #1"
FT  sig_peptide     1. .66
FT                  /*tag=  b
FT  mat_peptide     67. .987
FT                  /*tag=  c
XX
PN  JP2001161378-A.
XX
PD  19-JUN-2001.
XX
PF  26-SEP-2000; 2000JP-00292946.
XX
PR  01-OCT-1999;   99JP-00281234.
XX
PA  (TORA ) TORAY IND INC.
XX
DR  WPI; 2001-592466/67.
DR  P-PSDB; AAG66482.
XX
PT  Preparation of a highly pure protein, interleukin 12, a protein
PT  inhibiting the activity of interleukin 12, and a treating agent and a
PT  treating method for immunopathy of mammalian.
XX
PS  Claim 6; Page 16-17; 21pp; Japanese.
XX
CC  The present invention relates to a method for the preparation of a highly
CC  pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC  the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC  pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC  IL12. The protein is used as a preventive agent for dog immunopathy. The
CC  present sequence was used in the method of the present invention
XX
SQ  Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.2e-27        Length:        990
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           12.1%          Indels:        0
DB:                    4              Gaps:          0

US-10-821-670A-27 (1-307) x AAI64388 (1-990)

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 49
ADZ25698
ID  ADZ25698 standard; cDNA; 990 BP.
XX
AC  ADZ25698;
XX
DT  16-JUN-2005  (first entry)
XX
DE  Canine interleukin 12 P40 encoding cDNA SEQ ID NO:3.
XX
KW  interleukin-12; antiviral; gene; ss.
XX
OS  Canis sp.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .990
FT                  /*tag=  b
FT                  /product= "interleukin-12 P40"
FT  sig_peptide     1. .66
FT                  /*tag=  a
```

```
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "interleukin-12 P40"
CX
RN   JP2003284585-A.
CX
RD   07-OCT-2003.
CX
RF   28-MAR-2002; 2002JP-00090161.
CX
RR   28-MAR-2002; 2002JP-00090161.
CX
RA   (TORA ) TORAY IND INC.
CX
RR   WPI; 2003-885430/82.
RR   P-PSDB; ADZ25702.
CX
PT   Large scale production of interleukin-12 for pharmaceutical applications,
PT   comprises infecting an insect cell with a recombinant virus containing
PT   gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT   of insect cell.
CX
PS   Example; SEQ ID NO 3; 8pp; Japanese.
CX
CC   The invention related to the large scale production of interleukin-12 (IL
CC   -12), which involves infecting an insect cell with a recombinant virus
CC   containing a gene encoding IL-12, and producing IL-12 by carrying out
CC   spinner culture of insect cell. The method is useful for producing IL-12,
CC   preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC   present sequence encodes canine IL-12 P40, which is used in the
CC   exemplification of the present invention.
CX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.2e-27       Length:          990
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              12.1%         Indels:          0
DB:                       11            Gaps:            0

US-10-821-670A-27 (1-307) x ADZ25698 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 50
ADT04849
ID   ADT04849 standard; DNA; 1015 BP.
XX
AC   ADT04849;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p40 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
PT   Novel gene vector for expression in insect useful for expression of
PT   foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
PS   Claim 4; SEQ ID NO 5; 13pp; Japanese.
XX
CC   The invention relates to a novel gene vector for expression in an insect
CC   comprising at least two promoters, particularly the polyhedrin promoter
CC   and p10 promoter. The vector contains at least two types of foreign
CC   protein expression gene and the gene product of the vector is produced
CC   using a gene recombinant baculovirus, particularly a recombinant silkworm
CC   nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC   silkworm. The vector of the invention may be useful for expression of a
CC   foreign gene, such as canine interleukin 12. Within the vector, two types
CC   of foreign protein expression genes are integrated simultaneously for
CC   their simultaneous expression. The current sequence is that of the canine
CC   interleukin-12 (IL-12) p40 DNA of the invention.
XX
SQ   Sequence 1015 BP; 285 A; 251 C; 254 G; 225 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.23e-27      Length:          1015
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              12.1%         Indels:          0
DB:                       13            Gaps:            0

US-10-821-670A-27 (1-307) x ADT04849 (1-1015)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 51
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69314.
```

```
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Claim 6; Page 83-85; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a canine interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

lignment Scores:
red. No.:               1.81e-27        Length:         1533
core:                   37.00           Matches:        37
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             12.1%           Indels:         0
B:                      6               Gaps:           0

S-10-821-670A-27 (1-307) x ABK98967 (1-1533)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b       601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

ESULT 52
BK98968/c
D   ABK98968 standard; cDNA; 1533 BP.
X
C   ABK98968;
X
T   21-OCT-2002  (first entry)
X
E   Canine interleukin-12 nCaIL-12-1533 complementary strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; ss.
X
S   Canis familiaris.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
X
R   04-AUG-2000; 2000US-0223016P.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2002-573554/61.
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT  chain and canine IL-12 single chain proteins, useful for treating and
PT  preventing autoimmune diseases, inflammatory diseases and/or graft
PT  rejection in animals.
XX
PS  Claim 6; Page 86-87; 106pp; English.
XX
CC  The present invention discloses new feline interleukin 18 (IL-18), feline
CC  caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC  proteins. A composition comprising a feline IL-18, feline caspase-1,
CC  feline IL-12 single chain or canine IL-12 single chain proteins, a
CC  nucleic acid encoding these proteins, mimetopes of these proteins,
CC  multimeric forms of these proteins, an antibody against these proteins,
CC  or an inhibitor identified by its ability to inhibit the activity of
CC  these proteins, can be used to treat or prevent autoimmune diseases,
CC  allergic reactions, infectious diseases, tumour development, inflammatory
CC  diseases and/or graft rejection in animals. The present nucleic acid
CC  sequence represents a canine interleukin 12 DNA sequence, as described in
CC  the invention
XX
SQ  Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.81e-27        Length:         1533
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-27 (1-307) x ABK98968 (1-1533)

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 53
ADV34718/c
ID  ADV34718 standard; DNA; 1533 BP.
XX
AC  ADV34718;
XX
DT  24-FEB-2005  (first entry)
XX
DE  Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW  DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW  infectious disease; antimicrobial; ds.
XX
OS  Canis familiaris.
XX
PN  US2004248261-A1.
XX
PD  09-DEC-2004.
XX
PF  09-APR-2004; 2004US-00821670.
XX
PR  04-AUG-2000; 2000US-0223016P.
PR  27-JUL-2001; 2001US-00917265.
XX
PA  (WOND/) WONDERLING R S.
PA  (BORO/) BOROUGHS K L.
XX
PI  Wonderling RS,  Boroughs KL;
XX
DR  WPI; 2005-020565/02.
XX
PT  New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT  p40 subunit protein and a nucleic acid linker, useful in preparing a
PT  vaccine against infectious diseases in feline animals.
```

```
:X
)S   Example 4; SEQ ID NO 68; 103pp; English.
:X
:C   The present invention relates to the feline interleukin (IL)-12p35 or p40
:C   subunit protein and their encoding nucleic acid molecules and a nucleic
:C   acid linker. The invention also provides the feline caspase (casp)-1,
:C   feline IL-18 single chain and canine IL-12 single chain proteins and
:C   their nucleic acid molecules. The nucleic acid molecule is useful in
:C   preparing a vaccine against infectious diseases in feline animals. The
:C   present sequence is the canine single chain IL-12 complementary DNA.
:X
:Q   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

\lignment Scores:
)red. No.:              1.81e-27        Length:         1533
:core:                  37.00           Matches:        37
)ercent Similarity:     100.0%          Conservative:   0
)est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            12.1%           Indels:         0
)B:                     14              Gaps:           0

)S-10-821-670A-27 (1-307) x ADV34718 (1-1533)

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
)b        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

:ESULT 54
\DV34716
:D   ADV34716 standard; cDNA; 1533 BP.
:X
\C   ADV34716;
:X
)T   24-FEB-2005  (first entry)
:X
)E   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
:X
:W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
:W   infectious disease; antimicrobial; gene; ss.
:X
)S   Canis familiaris.
:X
'H   Key             Location/Qualifiers
'T   CDS             1. .1533
'T                   /*tag=  a
'T                   /product= "PCaIL-12 511 protein"
'T                   /partial
'T                   /note= "No start and stop codon"
:X
)N   US2004248261-A1.
:X
)D   09-DEC-2004.
:X
)F   09-APR-2004; 2004US-00821670.
:X
)R   04-AUG-2000; 2000US-0223016P.
)R   27-JUL-2001; 2001US-00917265.
:X
)A   (WOND/) WONDERLING R S.
)A   (BORO/) BOROUGHS K L.
:X
)I   Wonderling RS,  Boroughs KL;
:X
)R   WPI; 2005-020565/02.
)R   P-PSDB; ADV34717.
:X
)T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
)T   p40 subunit protein and a nucleic acid linker, useful in preparing a
)T   vaccine against infectious diseases in feline animals.
```

```
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.81e-27        Length:         1533
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-27 (1-307) x ADV34716 (1-1533)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 55
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69313.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 79-80; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
```

```
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a canine interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.89e-27      Length:        1599
core:                  37.00         Matches:       37
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            12.1%         Indels:        0
B:                     6             Gaps:          0

S-10-821-670A-27 (1-307) x ABK98965 (1-1599)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 56
BK98966/c
D   ABK98966 standard; cDNA; 1599 BP.
X
C   ABK98966;
X
T   21-OCT-2002  (first entry)
X
E   Canine interleukin-12 nCaIL-12-1599 complementary strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; ss.
X
S   Canis familiaris.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
X
R   04-AUG-2000; 2000US-0223016P.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2002-573554/61.
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Claim 6; Page 82-83; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
CC  multimeric forms of these proteins, an antibody against these proteins,
CC  or an inhibitor identified by its ability to inhibit the activity of
CC  these proteins, can be used to treat or prevent autoimmune diseases,
CC  allergic reactions, infectious diseases, tumour development, inflammatory
CC  diseases and/or graft rejection in animals. The present nucleic acid
CC  sequence represents a canine interleukin 12 DNA sequence, as described in
CC  the invention
XX
SQ  Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.89e-27      Length:        1599
Score:                  37.00         Matches:       37
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            12.1%         Indels:        0
DB:                     6             Gaps:          0

US-10-821-670A-27 (1-307) x ABK98966 (1-1599)

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 57
ADV34715/c
ID  ADV34715 standard; DNA; 1599 BP.
XX
AC  ADV34715;
XX
DT  24-FEB-2005  (first entry)
XX
DE  Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW  DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW  infectious disease; antimicrobial; ds.
XX
OS  Canis familiaris.
XX
PN  US2004248261-A1.
XX
PD  09-DEC-2004.
XX
PF  09-APR-2004; 2004US-00821670.
XX
PR  04-AUG-2000; 2000US-0223016P.
PR  27-JUL-2001; 2001US-00917265.
XX
PA  (WOND/) WONDERLING R S.
PA  (BORO/) BOROUGHS K L.
XX
PI  Wonderling RS,  Boroughs KL;
XX
DR  WPI; 2005-020565/02.
XX
PT  New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT  p40 subunit protein and a nucleic acid linker, useful in preparing a
PT  vaccine against infectious diseases in feline animals.
XX
PS  Example 4; SEQ ID NO 63; 103pp; English.
XX
CC  The present invention relates to the feline interleukin (IL)-12p35 or p40
CC  subunit protein and their encoding nucleic acid molecules and a nucleic
CC  acid linker. The invention also provides the feline caspase (casp)-1,
CC  feline IL-18 single chain and canine IL-12 single chain proteins and
CC  their nucleic acid molecules. The nucleic acid molecule is useful in
CC  preparing a vaccine against infectious diseases in feline animals. The
CC  present sequence is the canine single chain IL-12 complementary DNA.
XX
```

```
;Q   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.89e-27        Length:         1599
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-27 (1-307) x ADV34715 (1-1599)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 58
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX

SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.89e-27        Length:         1599
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       14              Gaps:           0

US-10-821-670A-27 (1-307) x ADV34713 (1-1599)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 59
AAX18176
ID   AAX18176 standard; cDNA; 2154 BP.
XX
AC   AAX18176;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74322.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 30-31; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.5e-27         Length:         2154
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
```

```
uery Match:            12.1%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x AAX18176 (1-2154)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        661 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 720

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        721 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 771

ESULT 60
BK99006/c
D   ABK99006 standard; cDNA; 2267 BP.
X
C   ABK99006;
X
T   21-OCT-2002  (first entry)
X
E   Canine interleukin-12 nCaIL-12p40-2267 complementary strand.
X
W   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
W   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
W   tumour development; inflammatory disease; graft rejection; ss.
X
S   Canis familiaris.
X
N   US2002052030-A1.
X
D   02-MAY-2002.
X
F   27-JUL-2001; 2001US-00917265.
X
R   04-AUG-2000; 2000US-0223016P.
X
A   (WOND/) WONDERLING R S.
A   (BORO/) BOROUGHS K L.
X
I   Wonderling RS,  Boroughs KL;
X
R   WPI; 2002-573554/61.
X
T   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
T   chain and canine IL-12 single chain proteins, useful for treating and
T   preventing autoimmune diseases, inflammatory diseases and/or graft
T   rejection in animals.
X
S   Example 4; Page 99-100; 106pp; English.
X
C   The present invention discloses new feline interleukin 18 (IL-18), feline
C   caspase-1, feline IL-12 single chain and canine IL-12 single chain
C   proteins. A composition comprising a feline IL-18, feline caspase-1,
C   feline IL-12 single chain or canine IL-12 single chain proteins, a
C   nucleic acid encoding these proteins, mimetopes of these proteins,
C   multimeric forms of these proteins, an antibody against these proteins,
C   or an inhibitor identified by its ability to inhibit the activity of
C   these proteins, can be used to treat or prevent autoimmune diseases,
C   allergic reactions, infectious diseases, tumour development, inflammatory
C   diseases and/or graft rejection in animals. The present nucleic acid
C   sequence represents a canine interleukin 12 DNA sequence, as described in
C   the invention
X
Q   Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

lignment Scores:
red. No.:              2.62e-27       Length:        2267
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            12.1%          Indels:        0
B:                     6              Gaps:          0
```

US-10-821-670A-27 (1-307) x ABK99006 (1-2267)

```
Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

RESULT 61
ABK99005
ID   ABK99005 standard; cDNA; 2267 BP.
XX
AC   ABK99005;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-2267 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69317.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 97-98; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             2.62e-27       Length:        2267
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           12.1%          Indels:        0
DB:                    6              Gaps:          0
```

```
)S-10-821-670A-27 (1-307) x ABK99005 (1-2267)

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
)b        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

{ESULT 62
\DV34757
:D   ADV34757 standard; cDNA; 2267 BP.
:X
\C   ADV34757;
:X
)T   24-FEB-2005  (first entry)
:X
)E   Canine single chain IL-12p40 protein cDNA, nCaIL-12p40 2267.
:X
:W   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
:W   infectious disease; antimicrobial; gene; ss.
:X
)S   Canis familiaris.
:X
'H   Key             Location/Qualifiers
'T   CDS             154. .1143
'T                   /*tag=  a
'T                   /product= "PCaIL-12p40 329 protein"
:X
)N   US2004248261-A1.
:X
)D   09-DEC-2004.
:X
)F   09-APR-2004; 2004US-00821670.
:X
)R   04-AUG-2000; 2000US-0223016P.
)R   27-JUL-2001; 2001US-00917265.
:X
)A   (WOND/) WONDERLING R S.
)A   (BORO/) BOROUGHS K L.
:X
)I   Wonderling RS,  Boroughs KL;
:X
)R   WPI; 2005-020565/02.
)R   P-PSDB; ADV34758.
:X
)T   New nucleic acid molecule comprising a sequence encoding a feline p35 or
)T   p40 subunit protein and a nucleic acid linker, useful in preparing a
)T   vaccine against infectious diseases in feline animals.
:X
)S   Example 4; SEQ ID NO 107; 103pp; English.
:X
:C   The present invention relates to the feline interleukin (IL)-12p35 or p40
:C   subunit protein and their encoding nucleic acid molecules and a nucleic
:C   acid linker. The invention also provides the feline caspase (casp)-1,
:C   feline IL-18 single chain and canine IL-12 single chain proteins and
:C   their nucleic acid molecules. The nucleic acid molecule is useful in
:C   preparing a vaccine against infectious diseases in feline animals. The
:C   present sequence is the canine single chain IL-12p40 subunit protein
:C   encoding cDNA.
:X
:Q   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

\lignment Scores:
'red. No.:              2.62e-27        Length:         2267
:core:                  37.00           Matches:        37
'ercent Similarity:     100.0%          Conservative:   0
}est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            12.1%           Indels:         0
)B:                     14              Gaps:           0

)S-10-821-670A-27 (1-307) x ADV34757 (1-2267)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 63
ADV34759/c
ID   ADV34759 standard; DNA; 2267 BP.
XX
AC   ADV34759;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 complementary DNA, nCaIL-12p35 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 109; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.62e-27        Length:         2267
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-27 (1-307) x ADV34759 (1-2267)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
b       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

ESULT 64
AQ04701
D   AAQ04701 standard; DNA; 906 BP.
X
C   AAQ04701;
X
T   25-MAR-2003  (revised)
T   11-OCT-1990  (first entry)
X
E   Sequence encoding natural killer cell stimulatory factor (NKSF).
X
W   Natural killer cell stimulatory factor; NKSF; cancer; leukopaenia;
W   anaemia; radiation; bone marrow transplantation; ds.
X
S   Homo sapiens.
X
N   WO9005147-A.
X
D   17-MAY-1990.
X
F   10-NOV-1988;   88US-00269945.
X
R   10-NOV-1988;   88US-00269945.
R   07-FEB-1989;   89US-00307817.
X
A   (GEMY ) GENETICS INST INC.
A   (WIST-) WISTAR INST.
X
I   Trinchieri G,  Perussia B,  Kobayashi M,  Clark SC,  Wong GG;
X
R   WPI; 1990-178800/23.
R   P-PSDB; AAR05171.
X
T   New natural killer cell stimulatory factor - useful for treating cancer
T   and e.g. leukopenia, bacterial and viral infections, anaemia and B or T
T   cell deficiencies.
X
S   Claim 16; Page 60; 69pp; English.
X
C   Natural killer cell stimulatory factor (NKSF) is useful in treating
C   cancer and other disease states which respond to NK cell activity. Such
C   states may arise from immune or haematopoietic-cell deficiency following
C   a bone marrow translpantation, exposure to radiation and disease.
C   (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
C   correct PA field.)
X
Q   Sequence 906 BP; 244 A; 220 C; 238 G; 204 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.21e-25      Length:        906
core:                  35.00         Matches:       35
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            11.4%         Indels:        0
B:                     2             Gaps:          0

S-10-821-670A-27 (1-307) x AAQ04701 (1-906)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

ESULT 65
AD15208
D   AAD15208 standard; DNA; 975 BP.
X
C   AAD15208;
X
T   01-NOV-2001  (first entry)
X
E   Modified human cytokine p40 encoding DNA from clone A16-94.
X
W   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
W   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
W   p40; mutant; ds.
X
S   Homo sapiens.
S   Synthetic.
X
H   Key             Location/Qualifiers
T   CDS             1. .975
T                   /*tag=  a
T                   /product= "Modified p40 protein precursor"
T   sig_peptide     1. .66
T                   /*tag=  b
T   mat_peptide     67. .972
T                   /*tag=  c
T                   /product= "Mature modified p40 protein"
X
N   WO200140257-A2.
X
D   07-JUN-2001.
X
F   30-NOV-2000; 2000WO-US032664.
X
R   02-DEC-1999;   99US-0169035P.
R   28-NOV-2000; 2000US-00725324.
X
A   (MAXY-) MAXYGEN INC.
X
I   Leong SR,  Punnonen J;
X
R   WPI; 2001-502381/55.
R   P-PSDB; AAE08601.
X
T   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
T   and p35 polypeptides), useful for treating various diseases e.g. diabetic
T   retinopathy and cancer.
X
S   Claim 1; Page 137; 223pp; English.
X
C   The invention relates to nucleic acids encoding modified cytokine
C   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
C   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
C   gamma induction activities. The polypeptides and polynucleotides of the
C   invention are useful for treating various diseases e.g. bacterial
C   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
C   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
C   vaccinated host's cell-mediated immunity for protective response to a
C   pathogen. The present sequence is a modified human p40 protein encoding
C   DNA
X
SQ  Sequence 975 BP; 261 A; 250 C; 255 G; 209 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.3e-25       Length:        975
Score:                  35.00         Matches:       35
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            11.4%         Indels:        0
DB:                     5             Gaps:          0

US-10-821-670A-27 (1-307) x AAD15208 (1-975)

Qy      106 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      382 TTTCTAAAGTGTGAGGCAAAGAATTACTCCGGACGTTTCACCTGCTGGTGGCTGACGGCA 441

Qy      126 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
            |||||||||||||||||||||||||||||||||||||||||||||
```

```
)b        442 ATCAGTACTGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

(ESULT 66
\AQ12149
:D   AAQ12149 standard; DNA; 979 BP.
:X
\C   AAQ12149;
:X
)T   10-SEP-1991  (first entry)
:X
)E   Cytotoxic lymphocyte maturation factor (40 kD subunit) gene.
:X
:W   Cytotoxic lymphocyte maturation factor; CLMF; probe; antitumour;
:W   monoclonal antibodies; T cell; ss.
:X
)S   Homo sapiens.
:X
?H   Key             Location/Qualifiers
?T   CDS             41. .979
?T                   /*tag=  a
?T                   /product= "CLMF"
?T   sig_peptide     41. .106
?T                   /*tag=  b
?T                   /note= "hydrophobic signal peptide"
?T   mat_peptide     107. .979
?T                   /*tag=  c
:X
)N   EP433827-A.
:X
)D   26-JUN-1991.
:X
)F   09-DEC-1990;   90EP-00123670.
:X
)R   22-DEC-1989;   89US-00455708.
)R   09-MAY-1990;   90US-00520935.
)R   27-AUG-1990;   90US-00572284.
:X
)A   (HOFF ) HOFFMANN-LA ROCHE AG.
:X
)I   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YCE;
)I   Podlaski FJ,  Stern AS;
:X
)R   WPI; 1991-186715/26.
)R   P-PSDB; AAR12493.
:X
)T   New cytotoxic lymphocyte maturation factor - used as antitumour agent and
)T   monoclonal antibodies used in transplantation to block proliferation and
)T   activation of cytotoxic T cells.
:X
)S   Disclosure; Fig 25 (a-c); 90pp; English.
:X
:C   The natural CLMF protein is a 75 kD heterodimer comprising two
:C   polypeptide subunits, a 40 kD and a 35 kD subunit (AAQ12150). The
:C   subunits are bonded together via one or more disulfide bonds. The CLMF
:C   can interact with IL-2 to synergistically induce the cytolytic activity
:C   of Lymphokine Activated Killer (LAK) cells. It is also capable of
:C   stimulating T-cell growth. It can be used for the prepn. of LAK- and T-
:C   cell activator and antitumour compsns. and for stimulating Natural Killer
:C   (NK) cells
:X
)Q   Sequence 979 BP; 261 A; 245 C; 257 G; 216 T; 0 U; 0 Other;

\lignment Scores:
)red. No.:              1.31e-25        Length:         979
)core:                  35.00           Matches:        35
)ercent Similarity:     100.0%          Conservative:   0
)est Local Similarity:  100.0%          Mismatches:     0
}uery Match:            11.4%           Indels:         0
)B:                     2               Gaps:           0

)S-10-821-670A-27 (1-307) x AAQ12149 (1-979)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
                  |||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 67
ADG39430
ID   ADG39430 standard; DNA; 984 BP.
XX
AC   ADG39430;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CLMF 40 kDa subunit DNA.
XX
KW   human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67. .984
FT                   /*tag=  a
FT                   /partial
FT                   /product= "CLMF 40 kDa subunit"
FT                   /note= "No start or stop codon given"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39429.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Claim 17; Page 28-29; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 984 BP; 263 A; 243 C; 258 G; 220 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.31e-25        Length:         984
```

```
core:                   35.00          Matches:       35
ercent Similarity:      100.0%         Conservative:  0
est Local Similarity:   100.0%         Mismatches:    0
uery Match:             11.4%          Indels:        0
B:                      12             Gaps:          0

S-10-821-670A-27 (1-307) x ADG39430 (1-984)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 68
AQ97484
D   AAQ97484 standard; cDNA; 987 BP.
X
C   AAQ97484;
X
T   25-MAR-2003  (revised)
T   22-DEC-1995  (first entry)
X
E   Human interleukin-12 40 kD subunit.
X
W   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
W   natural killer cell; graft vs. host disease; ss.
X
S   Homo sapiens.
X
H   Key             Location/Qualifiers
T   CDS             1. .987
T                   /*tag=  a
X
N   WO9519786-A1.
X
D   27-JUL-1995.
X
F   20-JAN-1995;   95WO-US000879.
X
R   21-JAN-1994;   94US-00186529.
X
A   (GEMY ) GENETICS INST INC.
A   (GEHO ) GEN HOSPITAL CORP.
X
I   Wolf SF,  Sykes M;
X
R   WPI; 1995-269273/35.
R   P-PSDB; AAR79186.
X
T   Control of graft versus host disease using interleukin 12 - partic.
T   admin. at the time of bone marrow transplant.
X
S   Disclosure; Page 21-22; 32pp; English.
X
C   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
C   12 is a heterodimeric cytokine which was originally identified as a
C   factor which induces gamma-interferon from T cells and natural killer
C   cells as set forth in PCT/US91/06332, published April 2 1992, and
C   incorporated by reference. EP 433827, published June 26 1991, disclosed
C   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
C   is defined as a heterodimeric glycoprotein comprised of two covalently
C   linked subunits having mol. wts of about 40 kD and 35 kD. The two
C   subunits may be disulfide-bonded. IL-12 is administered to prevent or
C   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
C   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
C   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
C   correct PN field.)
X
Q   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.32e-25       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-27 (1-307) x AAQ97484 (1-987)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 69
AAV07273
ID  AAV07273 standard; cDNA; 987 BP.
XX
AC  AAV07273;
XX
DT  25-SEP-1998  (first entry)
XX
DE  Human Interleukin-12 p40 gene.
XX
KW  IL-12 subunit; expression construct; treatment; asthma;
KW  microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .987
FT                  /*tag=  a
FT                  /product= "IL-12 p40"
XX
PN  WO9817689-A2.
XX
PD  30-APR-1998.
XX
PF  10-OCT-1997;   97WO-US018779.
XX
PR  18-OCT-1996;   96US-0028676P.
XX
PA  (GENE-) GENEMEDICINE INC.
XX
PI  Nordstrom J,  Freimark B,  Deshpande D;
XX
DR  WPI; 1998-261428/23.
DR  P-PSDB; AAW51311.
XX
PT  Constructs for expression of interleukin-12 sub-units - are used for
PT  delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT  infections and certain cancers.
XX
PS  Claim 1; Page 34; 80pp; English.
XX
CC  The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
CC  appropriate expression construct engineered into a plasmid. The plasmids
CC  can provide for efficient expression of IL-12 subunits. The products can
CC  be used for the treatment of asthma, microbial and viral infections and
CC  certain cancers
XX
SQ  Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.32e-25       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
```

```
)B:                    2             Gaps:          0

)S-10-821-670A-27 (1-307) x AAV07273 (1-987)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
)b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

:ESULT 70
\AV07217
:D   AAV07217 standard; DNA; 987 BP.
:X
\C   AAV07217;
:X
)T   12-AUG-1998  (first entry)
:X
)E   DNA encoding human interleukin-12 40kDa subunit.
:X
:W   Interleukin-12; IL-12; graft-versus-host disease;
:W   GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
:X
)S   Homo sapiens.
:X
'H   Key             Location/Qualifiers
'T   CDS             1. .987
'T                   /*tag=  a
'T                   /product= "Interleukin-12_40kDa_subunit"
:X
'N   US5756085-A.
:X
'D   26-MAY-1998.
:X
'F   30-APR-1996;   96US-00640386.
:X
'R   21-JAN-1994;   94US-00186529.
:X
'A   (GEMY ) GENETICS INST INC.
'A   (GEHO ) GEN HOSPITAL CORP.
:X
'I   Sykes M,  Wolf SF;
:X
)E   WPI; 1998-321459/28.
)E   P-PSDB; AAW51221.
:X
'T   Therapy of graft-versus-host disease - by administration of interleukin-
'T   12 to maintain and/or promote graft-versus-leukaemia effects.
:X
'S   Disclosure; Col 17-20; 20pp; English.
:X
:C   The invention relates to a method for the treatment or prevention of
:C   graft-versus-host disease (GVHD) which comprises the administration of
:C   interleukin-12 (IL-12) at the time of bone-marrow transplantation to
:C   maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
:C   0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
:C   the bone marrow transplant. IL-12 is administered daily until there is an
:C   improvement in the condition. Administration is oral, cutaneous,
:C   subcutaneous, intravenous or by inhalation preferably subcutaneous, or
:C   intravenous. The present sequence encodes the human interleukin-12 40kDa
:C   subunit
:X
:Q   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

\lignment Scores:
'red. No.:              1.32e-25      Length:         987
:core:                  35.00         Matches:        35
'ercent Similarity:     100.0%        Conservative:   0
'est Local Similarity:  100.0%        Mismatches:     0
)uery Match:            11.4%         Indels:         0
)B:                     2             Gaps:           0
```

```
US-10-821-670A-27 (1-307) x AAV07217 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 71
AAZ40406
ID   AAZ40406 standard; DNA; 987 BP.
XX
AC   AAZ40406;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p40 subunit semi-optimised coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9947678-A2.
XX
PD   23-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005394.
XX
PR   19-MAR-1998;   98US-0078654P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR   WPI; 1999-562116/47.
DR   P-PSDB; AAY42487.
XX
PT   New plasmids containing an interferon-alpha coding sequence, used for the
PT   treatment of a mammalian condition or disease, particularly cancer.
XX
PS   Claim 11; Page 43-45; 137pp; English.
XX
CC   This sequence represents a semi-optimised coding region for the human
CC   interleukin 12 p40 subunit. The invention relates to a novel plasmid
CC   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC   untranslated region (UTR). The plasmids can be used for treating a
CC   mammalian condition or disease, particularly cancer
XX
SQ   Sequence 987 BP; 216 A; 330 C; 296 G; 145 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.32e-25      Length:         987
Score:                  35.00         Matches:        35
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            11.4%         Indels:         0
DB:                     2             Gaps:           0

US-10-821-670A-27 (1-307) x AAZ40406 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750
```

```
ESULT 72
AZ40404
D   AAZ40404 standard; DNA; 987 BP.
X
C   AAZ40404;
X
T   15-FEB-2000  (first entry)
X
E   Human interleukin 12 p40 subunit wild type coding sequence.
X
W   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
W   promoter; growth hormone; untranslated region; UTR; mammal; disease;
W   cancer; ss.
X
S   Homo sapiens.
X
N   WO9947678-A2.
X
D   23-SEP-1999.
X
F   12-MAR-1999;   99WO-US005394.
X
R   19-MAR-1998;   98US-0078654P.
X
A   (GENE-) GENEMEDICINE INC.
X
I   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
X
R   WPI; 1999-562116/47.
R   P-PSDB; AAY42487.
X
T   New plasmids containing an interferon-alpha coding sequence, used for the
T   treatment of a mammalian condition or disease, particularly cancer.
X
S   Claim 11; Page 43-45; 137pp; English.
X
C   This sequence represents the wild type coding region for the human
C   interleukin 12 p40 subunit. The invention relates to a novel plasmid
C   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
C   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
C   untranslated region (UTR). The plasmids can be used for treating a
C   mammalian condition or disease, particularly cancer
X
Q   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.32e-25       Length:        987
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x AAZ40404 (1-987)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 73
AZ40405
D   AAZ40405 standard; DNA; 987 BP.
X
C   AAZ40405;
X
T   15-FEB-2000  (first entry)
X
E   Human interleukin 12 p40 subunit optimised coding sequence.
XX
KW  Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW  promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW  cancer; ss.
XX
OS  Homo sapiens.
XX
PN  WO9947678-A2.
XX
PD  23-SEP-1999.
XX
PF  12-MAR-1999;   99WO-US005394.
XX
PR  19-MAR-1998;   98US-0078654P.
XX
PA  (GENE-) GENEMEDICINE INC.
XX
PI  Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR  WPI; 1999-562116/47.
DR  P-PSDB; AAY42487.
XX
PT  New plasmids containing an interferon-alpha coding sequence, used for the
PT  treatment of a mammalian condition or disease, particularly cancer.
XX
PS  Claim 11; Page 43-45; 137pp; English.
XX
CC  This sequence represents an optimised coding region for the human
CC  interleukin 12 p40 subunit. The invention relates to a novel plasmid
CC  comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC  an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC  untranslated region (UTR). The plasmids can be used for treating a
CC  mammalian condition or disease, particularly cancer
XX
SQ  Sequence 987 BP; 220 A; 324 C; 318 G; 125 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.32e-25       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-27 (1-307) x AAZ40405 (1-987)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 74
AAD15210
ID  AAD15210 standard; DNA; 987 BP.
XX
AC  AAD15210;
XX
DT  01-NOV-2001  (first entry)
XX
DE  Human cytokine p40 DNA.
XX
KW  Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW  diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW  p40; ds.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  CDS             1. .987
FT                  /*tag=  a
```

```
FT                   /product= "p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .984
FT                   /*tag=  c
FT                   /product= "Mature p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08603.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 5; Page 142; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is human p40 protein encoding DNA
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.32e-25       Length:          987
Score:                    35.00          Matches:         35
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              11.4%          Indels:          0
DB:                       5              Gaps:            0

US-10-821-670A-27 (1-307) x AAD15210 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 75
ADF77278
ID   ADF77278 standard; DNA; 987 BP.
XX
AC   ADF77278;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p40 subunit optimised DNA #2.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; Page 14-15; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 987 BP; 216 A; 331 C; 294 G; 145 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:                1.32e-25       Length:          987
Score:                    35.00          Matches:         35
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              11.4%          Indels:          0
DB:                       12             Gaps:            0

US-10-821-670A-27 (1-307) x ADF77278 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

RESULT 76
ADF77263
ID   ADF77263 standard; DNA; 987 BP.
XX
AC   ADF77263;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p40 subunit optimised DNA #4.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
```

```
X
A   (NORD/) NORDSTROM J L.
A   (PERI/) PERICLE F.
A   (ROLL/) ROLLAND A.
A   (RALS/) RALSTON R O.
X
I   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
X
R   WPI; 2004-020834/02.
X
T   A mammalian interferon alpha expression plasmid is useful in gene therapy
T   to deliver interferon alpha to cells to modulate tumor activity in the
T   treatment of cancer.
X
S   Disclosure; SEQ ID NO 32; 65pp; English.
X
C   The invention relates to a mammalian interferon alpha expression plasmid,
C   comprising a promoter and a synthetic 5' intron transcriptionally linked
C   with an interferon alpha coding sequence and a 3' untranslated region.
C   The mammalian interferon alpha expression plasmid is useful for treating
C   tumour growth. The present sequence is used in the exemplification of the
C   present invention.
X
Q   Sequence 987 BP; 272 A; 138 C; 164 G; 413 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.32e-25      Length:        987
core:                  35.00         Matches:       35
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            11.4%         Indels:        0
B:                     12            Gaps:          0

S-10-821-670A-27 (1-307) x ADF77263 (1-987)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CATAAATTAAAATATGAAAATTATACTTCTTCTTTTTTTATTCGTGATATTATTAAACCT 705

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
b        706 GATCCTCCTAAAAATTTACAATTAAAACCTTTAAAAAATTCTCGT 750

ESULT 77
DF77277
D   ADF77277 standard; DNA; 987 BP.
X
C   ADF77277;
X
T   26-FEB-2004  (first entry)
X
E   Human IL-12 p40 subunit optimised DNA #1.
X
W   ds; human; interferon alpha expression plasmid; tumour; IL-12.
X
S   Synthetic.
S   Homo sapiens.
X
N   US2003181405-A1.
X
D   25-SEP-2003.
X
F   29-APR-2002; 2002US-00136837.
X
R   12-MAR-1999;   99US-00268135.
X
A   (NORD/) NORDSTROM J L.
A   (PERI/) PERICLE F.
A   (ROLL/) ROLLAND A.
A   (RALS/) RALSTON R O.
X
I   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
X
```

```
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; Page 14-15; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 987 BP; 220 A; 325 C; 317 G; 125 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.32e-25      Length:        987
Score:                  35.00         Matches:       35
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            11.4%         Indels:        0
DB:                     12            Gaps:          0

US-10-821-670A-27 (1-307) x ADF77277 (1-987)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 78
ADF77276
ID   ADF77276 standard; DNA; 987 BP.
XX
AC   ADF77276;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p40 subunit DNA.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; Page 14-15; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
```

:C comprising a promoter and a synthetic 5' intron transcriptionally linked
:C with an interferon alpha coding sequence and a 3' untranslated region.
:C The mammalian interferon alpha expression plasmid is useful for treating
:C tumour growth. The present sequence is used in the exemplification of the
:C present invention.
:X
;Q Sequence 987 BP; 264 A; 243 C; 258 G; 221 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	1.32e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.4%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-27 (1-307) x ADF77276 (1-987)

```
Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 79
ADO07653
ID ADO07653 standard; DNA; 987 BP.
XX
AC ADO07653;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human interleukin-12 40kDa coding sequence.
XX
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS Homo sapiens.
XX
PN WO2004035799-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011252.
XX
PR 11-OCT-2002; 2002DE-01048141.
XX
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI Waehler R, Schnieders F;
XX
DR WPI; 2004-357221/33.
XX
PT Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
PS Claim 4; Fig 19; 129pp; German.
XX
CC The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a human interleukin-12 coding sequence used in the
CC exemplification of the invention.
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.32e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.4%	Indels:	0
DB:	12	Gaps:	0

US-10-821-670A-27 (1-307) x ADO07653 (1-987)

```
Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750
```

RESULT 80
ADS00006
ID ADS00006 standard; DNA; 987 BP.
XX
AC ADS00006;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human interleukin-23 (IL-23) p40 subunit DNA.
XX
KW tumour; interleukin-23; IL-23; cytostatic; immunostimulant; cancer;
KW p40 subunit; ds; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a
FT /product= "Human interleukin-23 (IL-23) p40 subunit
FT protein"
XX
PN JP2004262797-A.
XX
PD 24-SEP-2004.
XX
PF 28-FEB-2003; 2003JP-00052999.
XX
PR 28-FEB-2003; 2003JP-00052999.
XX
PA (CHIB-) CHIBA PREFECTURE.
XX
DR WPI; 2004-665614/65.
DR P-PSDB; ADS00010.
XX
PT Novel anti-tumor agent comprising interleukin-23 gene, or cell transduced
PT with interleukin-23 gene, as active ingredient, useful for activating
PT anti-tumor immune response and treating tumor.
XX
PS Disclosure; SEQ ID NO 2; 23pp; Japanese.
XX
CC The invention relates to a novel anti-tumour agent comprising an
CC interleukin-23 (IL-23) gene, or a cell transduced with an IL-23 gene, as
CC an active ingredient. The molecules of the invention demonstrate
CC cytostatic and immunostimulant activities and may be useful within an
CC anti-tumour agent which activates an anti-tumour immune response. The
CC agent is safe when used in cancer treatment, may be combined with other
CC treatments and induces tumour-specific acquired immunity. The current
CC sequence is that of the human interleukin-23 (IL-23) p40 subunit DNA of
CC the invention.
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.32e-25	Length:	987
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0

```
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            11.4%         Indels:        0
B:                     13            Gaps:          0

S-10-821-670A-27 (1-307) x ADS00006 (1-987)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 81
DV42753
D   ADV42753 standard; cDNA; 987 BP.
X
C   ADV42753;
X
T   10-MAR-2005  (first entry)
X
E   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 381.
X
W   microarray; psychoneuroendocrinimmune; chronic fatigue;
W   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
W   cancer; neoplasm; infection; expressed sequence tag; ss.
X
S   Homo sapiens.
X
N   WO2004108899-A2.
X
D   16-DEC-2004.
X
F   04-JUN-2004; 2004WO-US017686.
X
R   04-JUN-2003; 2003US-0475915P.
X
A   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
X
I   Nicholson A,  Vernon SD;
X
R   WPI; 2005-031682/03.
X
T   New microarray comprising probes for genes involved in
T   psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
T   condition associated with PNI activity, e.g., inflammatory or infectious
T   diseases.
X
S   Claim 1; SEQ ID NO 381; 254pp; English.
X
C   The invention relates to a new microarray which comprises probes for
C   genes involved in psychoneuroendocrinimmune (PNI) activity. The
C   microarray is useful in diagnosing a condition associated with PNI
C   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
C   cancer and infection. The present sequence represents a
C   psychoneuroendocrinimmune gene expressed sequence tag. Note the
C   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
C   SEQ ID NO 1829 are provided.
X
Q   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.32e-25      Length:        987
core:                  35.00         Matches:       35
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            11.4%         Indels:        0
B:                     14            Gaps:          0

S-10-821-670A-27 (1-307) x ADV42753 (1-987)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 82
ADW97242
ID   ADW97242 standard; DNA; 987 BP.
XX
AC   ADW97242;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human p40 gene that inhibits IL-23 immune response Seq 1a.
XX
KW   immune inhibition; transplant rejection; immune disorder;
KW   autoimmune disease; allergy; immunosuppressive; antiallergic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "P40 protein"
XX
PN   JP2005060313-A.
XX
PD   10-MAR-2005.
XX
PF   13-AUG-2003; 2003JP-00292937.
XX
PR   13-AUG-2003; 2003JP-00292937.
XX
PA   (CHIB-) CHIBA PREFECTURE.
XX
DR   WPI; 2005-200132/21.
DR   P-PSDB; ADW97244.
XX
PT   Pharmaceutical formulation for inhibiting immune response generated by
PT   interleukin-23 (IL-23) and treating e.g. autoimmune diseases, comprises
PT   p40 molecules or gene encoding p40 molecules.
XX
PS   Claim 3; SEQ ID NO 1; 12pp; Japanese.
XX
CC   This invention relates to a novel pharmaceutical formulation used for
CC   inhibiting the immune response generated by interleukin-23 (IL-23).
CC   Specifically, it refers to a formulation comprising the p40 protein or
CC   the gene encoding this protein thereof. The present invention describes
CC   the p40 gene contained in the form of a viral or non-viral vector that is
CC   capable of expressing and secreting the p40 protein. This vector can be
CC   introduced into a cell such that it can in turn inhibit the immune
CC   response generated by the production of IL-23. Accordingly, this method
CC   is useful for suppressing organ transplant rejection or treating
CC   immunological disorders associated with abnormal immune response with
CC   regard to IL-23. Furthermore, it can be used to treat autoimmune diseases
CC   and allergy. As such, compositions exhibit immunosuppressive and
CC   antiallergic activities. This polynucleotide sequence is the human p40
CC   gene of the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.32e-25      Length:        987
Score:                 35.00         Matches:       35
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           11.4%         Indels:        0
DB:                    14            Gaps:          0

US-10-821-670A-27 (1-307) x ADW97242 (1-987)
```

```
Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 83
AEB48822
ID   AEB48822 standard; cDNA to mRNA; 987 BP.
XX
AC   AEB48822;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human interleukin-12 p40 domain coding sequence.
XX
KW   Interleukin-12; cytokine; lymphokine; cancer; tumor; glioblastoma;
KW   neoplasm; neurological disease; cytostatic; therapy; immunoconjugate;
KW   fusion protein; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  b
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .984
FT                   /*tag=  c
FT                   /product= "Mature interleukin-12 p40 subunit"
XX
PN   WO2005066348-A2.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-GB000007.
XX
PR   05-JAN-2004; 2004US-0534307P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
PA   (ANTI-) ANTISOMA PLC.
XX
PI   Gillies S,  Lo K,  Lan Y,  Verma R;
XX
DR   WPI; 2005-512669/52.
XX
PT   Novel compound comprising target specific portion having monoclonal
PT   antibody having specificity for oncofetal fibronectin and effector
PT   portion having interleukin-12, useful for treating cancer e.g.
PT   glioblastoma.
XX
PS   Claim 36; SEQ ID NO 10; 83pp; English.
XX
CC   The invention provides a compound comprising a target specific portion
CC   and an effector portion, in which the target specific portion comprises
CC   or consists of a monoclonal antibody having specificity for oncofetal
CC   fibronectin, or its fragment or variant which retains the antigen binding
CC   specificity of the parent monoclonal antibody, and the effector portion
CC   comprises or consists of interleukin-12, or its functional fragment or
CC   variant. The monoclonal antibody binds to a region of oncofetal
CC   fibronectin other than the extra-domain B region. Preferably, the
CC   compound comprises a target specific portion that is capable of binding
CC   to an amino acid sequence present in fibronectin expressed in both fetal
CC   and normal adult tissue, especially the repeat 7 domain of fibronectin,
CC   and is preferably specific for human oncofetal fibronectin. The
CC   monoclonal antibody is preferably a BC1 antibody. The invention also
CC   provides nucleic acids encoding the compounds of the invention and
CC   methods of their use in the production of these compounds, as well as
CC   methods of using the compounds in medicine, especially for the treatment
CC   of cancer in a patient, where the patient is a mammal, preferably a
CC   human, and the patient has a solid tumor. The cancer is a glioblastoma
CC   (claimed) or ovarian, gastric, colorectal or pancreatic cancer. The
CC   present sequence is the coding sequence of the p40 domain of human
CC   interleukin-12. In a claimed compound, the effector portion consists of a
CC   single chain interleukin-12 comprising or consisting of an interleukin-12
CC   p40 domain conjugated to the interleukin-12 and p35 domain AEB48815 via a
CC   disulfide bond. A further claimed compound comprises the p40 sequence
CC   linked by disulfide bond to a fusion protein AEB48818 comprising the BC1
CC   heavy chain fused to human interleukin-12 p35.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.32e-25      Length:          987
Score:                    35.00         Matches:         35
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              11.4%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-27 (1-307) x AEB48822 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 84
AAD18585
ID   AAD18585 standard; DNA; 1007 BP.
XX
AC   AAD18585;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human interleukin-12 (IL-12) p40 subunit DNA.
XX
KW   Human; interleukin-12; IL-12; p40 subunit; cytostatic; virucide; AIDS;
KW   Acquired Immune Deficiency Syndrome; immunisation; hepatitis; malaria;
KW   tuberculosis; vaccine; gene therapy; cancer; influenza; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .993
FT                   /*tag=  a
FT                   /product= "Human IL-12p40 subunit protein"
XX
PN   WO200168802-A2.
XX
PD   20-SEP-2001.
XX
PF   15-MAR-2001; 2001WO-KR000408.
XX
PR   15-MAR-2000; 2000KR-00013133.
PR   13-MAR-2001; 2001KR-00012987.
XX
PA   (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
PA   (PROG-) PROGEN CO LTD.
XX
PI   Sung YC,  Lee SH,  Ha SJ,  Song MK,  Chang J;
XX
DR   WPI; 2001-596904/67.
DR   P-PSDB; AAE11198.
XX
PT   Novel human or mouse interleukin (IL)-12p40 subunit mutant genes, that
PT   inhibit secretion of IL-12p40, but normally secrete IL-12p70, useful as
PT   adjuvant for DNA vaccination and gene therapy to AIDS, cancer, malaria.
XX
PS   Claim 1; Page 89-90; 103pp; English.
XX
```

```
C   The invention relates to mutant interleukin (IL)-12p40 subunit genes
C   which produces highly active human or mouse IL-12p40 sequence. IL-12p40
C   DNA is useful for DNA immunisation or gene therapy for treating diseases
C   such as cancer, AIDS, hepatitis C, hepatitis B or influenza, malaria or
C   tuberculosis, as an therapeutic or prophylactic adjuvant. IL-12p40 DNA
C   induces immune response by increasing the hydrolysis activity of
C   cytotoxic T lymphocytes when IL-12p40 subunit gene is injected with the
C   DNA vaccine, or increasing secretion of interferon (IFN)-gamma from T
C   helper cells or CD8+ T cells when IL-12p40 subunit gene is injected with
C   DNA vaccine. IL-12p40 DNA is useful in gene therapy and as a DNA vaccine.
C   The present sequence is a DNA encoding human Interleukin (IL)-12p40
C   subunit protein
X
Q   Sequence 1007 BP; 270 A; 247 C; 265 G; 225 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.34e-25      Length:        1007
core:                  35.00         Matches:       35
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            11.4%         Indels:        0
B:                     5             Gaps:          0

S-10-821-670A-27 (1-307) x AAD18585 (1-1007)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756

ESULT 85
AQ67879
D   AAQ67879 standard; DNA; 1018 BP.
X
C   AAQ67879;
X
T   25-MAR-2003  (revised)
T   23-MAR-1995  (first entry)
X
E   EPV 42 kD promoter/Human IL-12 p40 subunit expression cassette.
X
W   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
W   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
W   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
W   polymerase chain reaction; poxvirus; pSD542; immunological response;
W   pathogen; human; interferon; IFN; ss.
X
S   Synthetic.
X
H   Key             Location/Qualifiers
T   promoter        1. .31
T                   /*tag= a
T                   /note= "EPV 42 kD promoter"
T   CDS             32. .1018
T                   /*tag= b
T                   /product= "Human IL-12 p40"
X
N   WO9416716-A1.
X
D   04-AUG-1994.
X
F   21-JAN-1994;   94WO-US000888.
X
R   21-JAN-1993;   93US-00007115.
R   19-JAN-1994;   94US-00184009.
X
A   (VIRO-) VIROGENETICS CORP.
X
I   Paoletti E,  Tartaglia J,  Cox WI;
X
DR  WPI; 1994-263767/32.
XX
PT  Attenuated recombinant virus used for cancer therapy - comprises DNA
PT  encoding cytokine and/or tumour associated antigen.
XX
PS  Example 27; Fig 33; 232pp; English.
XX
CC  The sequences given in AAQ67879-80 are expression cassettes which contain
CC  the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC  control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC  promoter, respectively. These sequences were used in the construction of
CC  an ALVAC-based recombinant virus containing the genes for the two
CC  subunits of human IL-12. The p40 subunit was amplified using primers
CC  JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC  42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC  using primers JP186 and JP201 and placed under the control of the
CC  vaccinia E3L promoter using primers JP218 and JP220. The expression
CC  cassette was isolated and ligated with pBSSK+ generating plasmid
CC  PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC  assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC  cassettes are orientated head-to-head relative to each other. The
CC  combination casette containing the poxvirus promoted genes for both IL-12
CC  subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC  plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC  and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC  contains both the human IL-12 genes in the C6 locus. The resulting virus
CC  may be used in a composition for inducing an antigenic or immunological
CC  response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC  to correct PN field.)
XX
SQ  Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.36e-25      Length:        1018
Score:                  35.00         Matches:       35
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            11.4%         Indels:        0
DB:                     2             Gaps:          0

US-10-821-670A-27 (1-307) x AAQ67879 (1-1018)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 86
AAZ08510
ID  AAZ08510 standard; DNA; 1018 BP.
XX
AC  AAZ08510;
XX
DT  19-OCT-1999  (first entry)
XX
DE  EPV 42 kDa/human IL-12 P40 expression cassette.
XX
KW  Attenuated recombinant virus; cytokine; tumour associated antigen;
KW  NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW  cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW  interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW  carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW  immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS  Synthetic.
OS  pox virus.
OS  Homo sapiens.
OS  Unidentified.
XX
PN  US5942235-A.
```

```
:X
)D   24-AUG-1999.
:X
)F   02-JUN-1995;   95US-00458356.
:X
)R   24-DEC-1981;   81US-00334456.
)R   08-DEC-1982;   82US-00446824.
)R   19-JUN-1984;   84US-00622135.
)R   27-AUG-1987;   87US-00090209.
)R   28-AUG-1987;   87US-00090711.
)R   20-OCT-1987;   87US-00110335.
)R   25-APR-1988;   88US-00186054.
)R   23-AUG-1988;   88US-00234390.
)R   14-JUN-1990;   90US-00537882.
)R   14-JUN-1990;   90US-00537890.
)R   16-DEC-1991;   91US-00805567.
)R   03-MAR-1992;   92US-00847977.
)R   06-MAR-1992;   92US-00847951.
)R   04-MAY-1992;   92US-00881995.
)R   22-JUL-1992;   92US-00918278.
)R   20-JAN-1993;   93US-00007115.
)R   19-JAN-1994;   94US-00184009.
)R   14-APR-1994;   94US-00228926.
)R   13-SEP-1994;   94US-00306259.
:X
)A   (HEAL-) HEALTH RES INC.
:X
)I   Paoletti E;
:X
)R   WPI; 1999-493494/41.
:X
)T   Recombinant poxviruses comprising exogenous DNA encoding antigenic
)T   determinants useful in immunotherapy to immunize against cancers and
)T   other diseases such as influenza, Newcastle Disease and rabies.
:X
)S   Example 27; Fig 33; 163pp; English.
:X
:C   The present invention describes a recombinant poxvirus (I), comprising
:C   exogenous DNA encoding an antigenic determinant of a pathogen which is
:C   then expressed in vivo in infected host cells after administration to a
:C   patient and therefore induces an immunological response. (I) may be used
:C   to vaccinate patients against a wide range of diseases and disorders
:C   depending on the type of antigen encoded by the exogenous DNA. (I) may be
:C   used to vaccinate against diseases such as rabies, influenza and
:C   Newcastle Disease. It is particularly useful for immunising against
:C   cancers. The poxvirus (I) also provides a means of manipulating
:C   lymphocytes and tumour cells for use in cell-based immunotherapeutic
:C   modalities for cancer. (I) also have enhanced safety compared to
:C   unattenuated viruses (attenuation reduces the virulence of the viruses)
:C   and known recombinant poxvirus vaccines. This increased level of safety
:C   reduces the possibility of a 'runaway' infection in the host and reduces
:C   the chance of transmission from vaccinated to unvaccinated individuals
:C   and contamination of the environment. The present sequence represents a
:C   EPV 42 kDa/human IL-12 P40 expression cassette used in the
:C   exemplification of the present invention
:X
)Q   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

)lignment Scores:
)red. No.:              1.36e-25        Length:         1018
)core:                  35.00           Matches:        35
)ercent Similarity:     100.0%          Conservative:   0
)est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            11.4%           Indels:         0
)B:                     2               Gaps:           0

)S-10-821-670A-27 (1-307) x AAZ08510 (1-1018)

)y      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b      677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

)y      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
```

```
            ||||||||||||||||||||||||||||||||||||||||||||
Db      737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 87
ADR21886
ID   ADR21886 standard; DNA; 1018 BP.
XX
AC   ADR21886;
XX
DT   04-NOV-2004  (first entry)
XX
DE   EPV 42kDa/human IL-12 expression cassette.
XX
KW   Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW   attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW   cancer therapy; ds; human; IL-12; EPV 42kDa; expression cassette.
XX
OS   Heliothis armigera entomopoxvirus.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6780407-B1.
XX
PD   24-AUG-2004.
XX
PF   15-SEP-2000; 2000US-00663667.
XX
PR   08-MAR-1989;   89US-00320471.
PR   14-FEB-1990;   90US-00478179.
PR   07-JAN-1991;   91US-00638080.
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   30-AUG-1995;   95US-00521016.
XX
PA   (AVET ) AVENTIS PASTEUR.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 2004-601998/58.
XX
PT   New recombinant poxvirus which is an attenuated avipox Virus that
PT   expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT   exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
PS   Example 27; SEQ ID NO 194; 181pp; English.
XX
CC   The invention describes a recombinant poxvirus containing exogenous DNA
CC   in a nonessential region of the poxvirus, where the poxvirus is an
CC   attenuated avipox Virus that expresses an exogenous DNA encoding
CC   carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC   described are: a composition comprising a poxvirus above in admixture
CC   with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC   vivo comprising administering to a mammal the composition above.
CC   Disclosed are: making recombinant poxvirus defined above; recombinant
CC   poxvirus vaccine having an increased level of safety compared to known
CC   recombinant poxvirus vaccines; and a modified vector for expressing a
CC   gene product in a host. The recombinant poxvirus is useful for providing
CC   a recombinant poxvirus vaccine having an increased level of safety
CC   compared to known recombinant poxvirus vaccines. The recombinant poxvirus
CC   is useful for cancer therapy. This sequence represents a human IL-12
CC   expression cassette used in the creation of NYVAC rescue virus and
CC   canarypox virus vector ALVAC comprising the human IL-12 gene.
XX
SQ   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.36e-25        Length:         1018
Score:                  35.00           Matches:        35
```

```
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            11.4%           Indels:        0
B:                     13              Gaps:          0

S-10-821-670A-27 (1-307) x ADR21886 (1-1018)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

ESULT 88
DP88402
D   ADP88402 standard; cDNA; 1029 BP.
X
C   ADP88402;
X
T   09-SEP-2004  (first entry)
X
E   Human interleukin-12 beta chain coding sequence.
X
W   antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
W   antibacterial; protozoacide; gene therapy; expression vector;
W   interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
W   human.
X
S   Homo sapiens.
X
N   WO2004052929-A2.
X
D   24-JUN-2004.
X
F   08-DEC-2003; 2003WO-IB006404.
X
R   06-DEC-2002; 2002GB-00028465.
X
A   (UYBE-) UNIV QUEENS BELFAST.
X
I   Vandenbroeck K,  Alloza I;
X
R   WPI; 2004-487887/46.
X
T   New expression vector comprising DNA encoding a subunit of a dimeric form
T   of interleukin under transcriptional control of an ecdysone-inducible
T   promoter, useful in preparing a composition for treating e.g.,
T   inflammatory disease.
X
S   Disclosure; Page 86-87; 87pp; English.
X
C   The present invention relates to an expression vector comprising DNA
C   encoding a subunit of a dimeric form of interleukin under transcriptional
C   control of an ecdysone-inducible promoter. The expression vector is
C   useful in preparing a composition for treating a disease having a
C   pathogenesis which includes endogenous production of cytokine IL-12, IL-
C   23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
C   induced inflammation, epithelial airway inflammation such as asthma,
C   allergic disease, or autoimmune disease such as multiple sclerosis or
C   inflammatory bowel disease. The present sequence is the coding sequence
C   of the human interleukin-12 beta chain used in the exemplification of the
C   invention.
X
Q   Sequence 1029 BP; 275 A; 261 C; 267 G; 226 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.37e-25        Length:        1029
core:                  35.00           Matches:       35
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            11.4%           Indels:        0
DB:                    12              Gaps:          0

US-10-821-670A-27 (1-307) x ADP88402 (1-1029)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 720

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db       721 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 765

RESULT 89
AAF76880
ID   AAF76880 standard; DNA; 1389 BP.
XX
AC   AAF76880;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human p40-IL-2 coding sequence.
XX
KW   Human; p40-IL-2; interleukin-2; IL-2; antiviral; antibacterial;
KW   antifungal; cytostatic; antiparasitic; vaccine; gene therapy;
KW   fusion protein; protein complex; cytokine; immunoglobulin; cancer;
KW   infection; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200110912-A1.
XX
PD   15-FEB-2001.
XX
PF   09-AUG-2000; 2000WO-US021715.
XX
PR   09-AUG-1999;   99US-0147924P.
XX
PA   (LEXI-) LEXIGEN PHARM CORP.
XX
PI   Gillies SD,  Lo KM;
XX
DR   WPI; 2001-191523/19.
XX
PT   Novel multifunctional fusion protein or protein complexes useful for
PT   treating cancer and viral infections, comprise two different cytokine
PT   molecules and a targeting group.
XX
PS   Example 1; Page 75-76; 90pp; English.
XX
CC   The present sequence is given in a specification relating to
CC   multifunctional fusion proteins and protein complexes comprising at least
CC   two different cytokine molecules and a targeting group such as an
CC   immunoglobulin. The fusion proteins and protein complexes are useful for
CC   treating cancers, and bacterial, viral, fungal and parasitic infections.
CC   They are also useful in gene therapy and as vaccines to prevent or treat
CC   various diseases
XX
SQ   Sequence 1389 BP; 413 A; 325 C; 327 G; 324 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.82e-25        Length:        1389
Score:                 35.00           Matches:       35
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           11.4%           Indels:        0
DB:                    4               Gaps:          0

US-10-821-670A-27 (1-307) x AAF76880 (1-1389)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705
```

```
Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 90
AAT77849
ID   AAT77849 standard; DNA; 1397 BP.
XX
AC   AAT77849;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790255-A2.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104656.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YE;
PI   Podlanski FJ,  Stern AS;
XX
DR   WPI; 1997-404698/38.
DR   P-PSDB; AAW24235.
XX
PT   Antibodies to cytotoxic lymphocyte maturation factor protein - useful as
PT   affinity ligands, assay reagents and medicaments.
XX
PS   Disclosure; Fig 25; 80pp; English.
XX
CC   The present DNA sequence encodes the 40 kDa subunit of cytotoxic
CC   lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC   a 75 kDa heterodimer, where the 2 subunits (see AAT77850 for the 35 kDa
CC   subunit) are bonded together via one or more disulphide bonds. CLMF
CC   protein is produced by a human B lyphoblastoid cell line. CLMF
CC   synergistically induces, in the presence of interleukin-2, the cytolytic
CC   activity of lymphokine activated killer cells. CLMF is also capable of
CC   stimulating T-cell growth. A novel antibody directed against an epitope
CC   of CLMF protein (see AAW24237 for epitope) is capable of neutralising
CC   and/or inhibiting CLMF bioactivity. This antibody may be used as an
CC   affinity ligand for purifying the CLMF protein. The antibody can also be
CC   used as an assay reagent for detecting the CLMF protein, and as a
CC   medicament for selectively blocking the proliferation and activation of
CC   cytotoxic T cells, e.g. in transplantation. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.83e-25        Length:         1397
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AAT77849 (1-1397)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 91
AAT97969
ID   AAT97969 standard; DNA; 1397 BP.
XX
AC   AAT97969;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790308-A1.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104682.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YE;
PI   Podlanski FJ,  Stern AS;
XX
DR   WPI; 1997-404733/38.
DR   P-PSDB; AAW36939.
XX
PT   Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT   producing protein and as antitumour agent.
XX
PS   Disclosure; Fig 25; 83pp; English.
XX
CC   The present DNA sequence encodes a 40 kDa subunit of cytotoxic lymphocyte
CC   maturation factor (CLMF) protein. The natural CLMF protein is a 75 kDa
CC   heterodimer, where the 2 subunits (see AAT97970 for the 35 kDa subunit)
CC   are bonded together via one or more disulphide bonds. CLMF protein is
CC   produced by a human B lyphoblastoid cell line. CLMF synergistically
CC   induces, in the presence of interleukin-2, the cytolytic activity of
CC   lymphokine activated killer cells. CLMF is also capable of stimulating T-
CC   cell growth. The subunits may be used for preparing the CLMF protein and
CC   for preparing medicants for antitumour therapy. (Updated on 25-MAR-2003
CC   to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;
```

```
lignment Scores:
red. No.:               1.83e-25        Length:         1397
core:                   35.00           Matches:        35
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             11.4%           Indels:         0
B:                      2               Gaps:           0

S-10-821-670A-27 (1-307) x AAT97969 (1-1397)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

ESULT 92
AV00401
D   AAV00401 standard; DNA; 1397 BP.
X
C   AAV00401;
X
T   25-MAR-2003  (revised)
T   18-MAR-1998  (first entry)
X
E   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
X
W   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
W   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
W   CLMF bioactivity inhibition; affinity ligand; transplantation;
W   cytotoxic T cell proliferation; ss.
X
S   Homo sapiens.
X
H   Key             Location/Qualifiers
T   CDS             41. .1027
T                   /*tag=  a
X
N   EP790309-A1.
X
D   20-AUG-1997.
X
F   09-DEC-1990;   97EP-00104860.
X
R   22-DEC-1989;   89US-00455708.
R   09-MAY-1990;   90US-00520935.
R   27-AUG-1990;   90US-00572284.
R   09-DEC-1990;   90EP-00123670.
X
A   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
X
I   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes J,  Pan YE;
I   Podlanski FJ,  Stern AS,  Witte H;
X
R   WPI; 1997-404734/38.
R   P-PSDB; AAW36941.
X
T   Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
T   producing CLMF protein and as an antitumour agent.
X
S   Disclosure; Fig 25; 83pp; English.
X
C   The present DNA sequence encodes a novel 40 kDa subunit of cytotoxic
C   lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
C   a 75 kDa heterodimer, where the 2 subunits (see AAV00402 for the 35 kDa
C   subunit) are bonded together via one or more disulphide bonds. CLMF
C   protein is produced by a human B lyphoblastoid cell line. CLMF
C   synergistically induces, in the presence of interleukin-2, the cytolytic
C   activity of lymphokine activated killer cells. CLMF is also capable of
C   stimulating T-cell growth. The subunits may be used for preparing the
C   CLMF protein and for preparing medicants for antitumour therapy. (Updated
```

```
CC   on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC   PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.83e-25        Length:         1397
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AAV00401 (1-1397)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 93
AAV37767
ID   AAV37767 standard; cDNA; 1397 BP.
XX
AC   AAV37767;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Cytotoxic lymphocyte maturation factor 40 kD subunit encoding cDNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize;
KW   interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying;
KW   proliferation; cytotoxic T cell; transplantation; antibody; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
FT                   /product= "CLMF 40 kD subunit"
XX
PN   US5780597-A.
XX
PD   14-JUL-1998.
XX
PF   02-JUN-1995;   95US-00460061.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Podlaski FJ,  Stern AS,  Gately MK,  Pan YE,  Hulmes JD;
PI   Chizzonite RA,  Gubler UA;
XX
DR   WPI; 1998-413150/35.
DR   P-PSDB; AAW58725.
XX
PT   New antibodies to cytotoxic lymphocyte maturation factor - useful for
PT   detecting, purifying, and/or blocking proliferation and activation of
PT   cytotoxic T cells, such as in transplantation(s).
XX
PS   Example 10; Fig 25; 71pp; English.
XX
CC   An isolated antibody has been developed which binds specifically to
CC   cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF
CC   induced proliferation by more than 50% in a CLMF dependent T cell growth
```

```
:C   assay and/or inhibits binding of at least 60% of the factor to
:C   phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL)
:C   blasts as determined in a CLMF receptor binding assay. CLMF is a
:C   heterodimeric protein having a molecular weight band of 75 kD, determined
:C   by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE)
:C   under non-reducing and/or reducing conditions, providing a first subunit
:C   having a molecular weight band of 40 kD and a second subunit having a
:C   molecular weight of 35 kD. The present sequence encodes the CLMF 40 kD
:C   subunit, from an example of the present invention. The antibody can be
:C   used for the purification and/or detection of CLMF. It is also used in
:C   therapeutic treatments which require selective blocking of proliferation
:C   and activation of cytotoxic T cells (CTLs) such as in transplantation
:X
:Q   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.83e-25      Length:         1397
Score:                    35.00         Matches:        35
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              11.4%         Indels:         0
DB:                       2             Gaps:           0

US-10-821-670A-27 (1-307) x AAV37767 (1-1397)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 94
ADG39387
ID   ADG39387 standard; DNA; 1397 BP.
XX
AC   ADG39387;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human cytotoxic lymphocyte maturation factor, CLMF, 40 kDa subunit DNA.
XX
KW   ds; gene; human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
FT                   /product= "CLMF 40 kDa subunit"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39388.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Disclosure; Fig 25; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.83e-25      Length:         1397
Score:                    35.00         Matches:        35
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              11.4%         Indels:         0
DB:                       12            Gaps:           0

US-10-821-670A-27 (1-307) x ADG39387 (1-1397)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 95
ADO03758
ID   ADO03758 standard; cDNA; 1397 BP.
XX
AC   ADO03758;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human CLMF 40kDa subunit cDNA.
XX
KW   pharmaceutical composition; T cell growth factor assay; cytokine;
KW   cytokine lymphocyte maturation factor; CLMF; interleukin-12; IL-12;
KW   NC-37 B lymphoblastoid cell; T-cell growth stimulator; human; gene; ss;
KW   40 kDa subunit.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  b
FT                   /product= "CLMF 40 kDa subunit"
FT                   /note= "Cytotoxic Lymphocyte Maturation Factor"
FT   sig_peptide     41. .106
FT                   /*tag=  a
FT   mat_peptide     107. .1024
FT                   /*tag=  c
FT                   /note= "Mature CLMF 40 kDa subunit"
XX
PN   US6683046-B1.
XX
PD   27-JAN-2004.
XX
PF   02-JUN-1995;   95US-00459151.
```

```
X
R   22-DEC-1989;   89US-00455708.
R   09-MAY-1990;   90US-00520935.
R   27-AUG-1990;   90US-00572284.
R   24-MAR-1992;   92US-00857023.
R   02-MAR-1994;   94US-00205011.
X
A   (HOFF ) HOFFMANN LA ROCHE INC.
X
I   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
I   Chizzonite RA,  Pan YE;
X
R   WPI; 2004-118577/12.
R   P-PSDB; ADO03759, ADO03795.
X
T   Pharmaceutical composition useful for activating T cell growth factors in
T   assays comprises heterodimeric protein comprising first and second
T   subunits and carrier.
X
S   Disclosure; Fig 25; 72pp; English.
X
C   The invention describes a pharmaceutical composition active in a T cell
C   growth factor assay. The pharmaceutical composition comprises a
C   heterodimeric protein having a molecular weight of 75 kDa as determined
C   by Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)
C   under non-reducing conditions, and under reducing conditions, providing a
C   first subunit having a molecular weight of 40 kDa as determined by (SDS-
C   PAGE), and having a fully defined sequence of 306 amino acids as given in
C   the specification, and second subunit having a molecular weight of 35 kDa
C   as determined by (SDS-PAGE). Also described are: a novel cytokine protein
C   called Cytokine lymphocyte maturation factor (CLMF) or interleukin-12 (IL
C   -12) synthesised by mammalian cells, particularly human NC-37 B
C   lymphoblastoid cells, and capable of stimulating T-cell growth; and
C   monoclonal antibodies directed against (CLMF). (I) is useful as a
C   pharmaceutical composition which is active in a T cell growth factor
C   assay. This sequence encodes human cytotoxic lymphocyte maturation factor
C   (CLMF) 40 kDa subunit.
X
Q   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

lignment Scores:
red. No.:              1.83e-25      Length:          1397
core:                  35.00         Matches:         35
ercent Similarity:     100.0%        Conservative:    0
est Local Similarity:  100.0%        Mismatches:      0
uery Match:            11.4%         Indels:          0
B:                     12            Gaps:            0

S-10-821-670A-27 (1-307) x ADO03758 (1-1397)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

ESULT 96
AZ40021
D   AAZ40021 standard; DNA; 1399 BP.
X
C   AAZ40021;
X
T   14-FEB-2000  (first entry)
X
E   Human p40 coding sequence.
X
W   Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
W   IL-12 p40 subunit; gene therapy; tumour; leukaemia; ss.
X
S   Homo sapiens.
X
PN  US5994104-A.
XX
PD  30-NOV-1999.
XX
PF  08-NOV-1996;   96US-00751767.
XX
PR  08-NOV-1996;   96US-00751767.
XX
PA  (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI  Anderson RJ,  Prentice HG,  Macdonald ID;
XX
DR  WPI; 2000-038261/03.
DR  P-PSDB; AAY54919.
XX
PT  Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT  for treating leukemia and other cancers.
XX
PS  Example; Fig 9; 73pp; English.
XX
CC  This sequence encodes the human p40 protein sequence. The invention
CC  relates to an isolated nucleic acid construct (I) comprising a region
CC  encoding an interleukin-12 (IL-12) fusion protein (comprising an IL-12
CC  p35 subunit, an IL-12 p40 subunit and a linker peptide (joining the
CC  subunits)) and a region encoding a B7 protein. (I) may be used to produce
CC  IL-12 fusion proteins according to standard recombinant DNA
CC  methodologies. The fusion proteins may be produced either in vitro in a
CC  fermentation culture or in vivo as part of a gene therapy protocol (in
CC  this case (I) is used to transform a patients cells, which then secrete
CC  the functional polypeptide to supplement the patients own production of
CC  IL-12 or to rectify mutations which lead to the expression of inactive
CC  polypeptides). The fusion proteins produced in this way may be used to
CC  treat any disease which responds to IL-12 such as tumours (both solid and
CC  dispersed of the kidney, breast, colon, ovarian and cervical tumours and
CC  melanomas) and in particular, tumours of the blood such as leukaemia.
CC  Alternatively, the polypeptides may be used as antigens in the production
CC  of antibodies to IL-12 and to assay for agonists and antagonists of its
CC  activity. The antibodies and antagonists may be used to inhibit the
CC  activity of IL-12. (I) may also be used diagnostically as a probe which
CC  hybridizes to sequences encoding IL-12 and the antibodies may be used to
CC  detect the presence of IL-12 polypeptides in samples. They may be used
CC  diagnostically to quantitate the expression of the polypeptide by
CC  patients and hence which subjects may be in need of restorative therapy
XX
SQ  Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             1.83e-25      Length:          1399
Score:                 35.00         Matches:         35
Percent Similarity:    100.0%        Conservative:    0
Best Local Similarity: 100.0%        Mismatches:      0
Query Match:           11.4%         Indels:          0
DB:                    3             Gaps:            0

US-10-821-670A-27 (1-307) x AAZ40021 (1-1399)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 97
ADY86632
ID  ADY86632 standard; DNA; 1399 BP.
XX
AC  ADY86632;
XX
DT  02-JUN-2005  (first entry)
XX
DE  Human interleukin-12 40 kDa (IL-12 p40) subunit gene.
```

```
:X
:W   Gene expression; screening; multiple sclerosis; neuroprotective;
:W   immune disorder; neurological disease; DNA microarray; gene; ds;
:W   interleukin-12; lymphokine; cytokine.
:X
)S   Homo sapiens.
:X
)N   US2005064483-A1.
:X
)D   24-MAR-2005.
:X
)F   30-AUG-2004; 2004US-00929182.
:X
)R   28-AUG-2003; 2003US-0498731P.
:X
)A   (BAYU ) BAYLOR COLLEGE MEDICINE.
:X
)I   Zang JZ,  Hong J;
:X
)R   WPI; 2005-252668/26.
)R   GENBANK; M65272.
:X
)T   Monitoring multiple sclerosis patient taking beta-interferon or
)T   glatiramer acetate to predict treatment response by determining
)T   expression profile of inflammatory nucleic acids using RNA of patient and
)T   comparing to control.
:X
)S   Claim 1; SEQ ID NO 22; 73pp; English.
:X
:C   The present invention relates to gene expression profiling technology to
:C   quantatively measure the expression profiles of genes selected based on
:C   their role in inflammation and their susceptibility to regulation by
:C   current multiple sclerosis (MS) treatment agents by isolating RNA from
:C   peripheral blood mononuclear cells (PBMC) of patient. The invention is
:C   particularly useful for monitoring a multiple sclerosis patient taking
:C   interferon-beta (IFN-beta) or glatiramer acetate (GA) in order to predict
:C   treatment response. The present sequence is human interleukin-12 40 kDa
:C   (IL-12 p40) subunit gene. This gene is used to illustrate the evaluation
:C   of PBMC responses to in Vitro treatment with IFN-beta or GA agents by
:C   gene expression profiling technology.
:X
)Q   Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

\lignment Scores:
)red. No.:              1.83e-25      Length:        1399
)core:                  35.00         Matches:       35
)ercent Similarity:     100.0%        Conservative:  0
)est Local Similarity:  100.0%        Mismatches:    0
)uery Match:            11.4%         Indels:        0
)B:                     14            Gaps:          0

)S-10-821-670A-27 (1-307) x ADY86632 (1-1399)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
)b        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

:ESULT 98
\AA92406
:D   AAA92406 standard; cDNA; 2300 BP.
:X
\C   AAA92406;
:X
)T   15-JAN-2001  (first entry)
:X
)E   Human interleukin 2 encoding p35 and p40 proteins.
:X
:W   Human; interleukin 2; IL-2; p35; p40; immune response; tumour;
:W   infectious disease; bacteria; virus; parasite; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             19. .678
FT                   /*tag=  a
FT                   /product= "p35"
FT   CDS             1304. .2290
FT                   /*tag=  b
FT                   /product= "p40"
XX
PN   CN1258740-A.
XX
PD   05-JUL-2000.
XX
PF   31-DEC-1998;   98CN-00126748.
XX
PR   31-DEC-1998;   98CN-00126748.
XX
PA   (HUAC-) HUACHEN BIOLOGICAL TECHNOLOGY INST SHANG.
XX
PI   Cao X,  Zhang W,  Ju D;
XX
DR   WPI; 2000-558956/52.
DR   P-PSDB; AAB23795, AAB23796.
XX
PT   Recombinant adenovirus expressing human interleukin-12 and its
PT   preparation and use.
XX
PS   Example 3; Fig 4; 27pp; Chinese.
XX
CC   The present invention describes a recombinant adenovirus and its
CC   preparation and use, as well as medicine composite containing the
CC   recombinant adenovirus. The recombinant adenovirus is used clinically,
CC   has the advantages of low cost, easy use and high efficiency and is
CC   especially suitable for immune treatment of tumour and infectious
CC   diseases caused by bacteria, virus and parasite. The present sequence
CC   represents human interleukin 2 (IL-2) cDNA which encodes the p35 and p40
CC   proteins, which is used in an example from the present invention
XX
SQ   Sequence 2300 BP; 598 A; 591 C; 571 G; 540 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.93e-25      Length:        2300
Score:                  35.00         Matches:       35
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            11.4%         Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-27 (1-307) x AAA92406 (1-2300)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1949 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 2008

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db       2009 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 2053

RESULT 99
AEE03207
ID   AEE03207 standard; DNA; 2336 BP.
XX
AC   AEE03207;
XX
DT   26-JAN-2006  (first entry)
XX
DE   Human interleukin-12 DNA, SEQ ID 13.
XX
KW   Cytostatic; gene therapy; tumor; immune stimulation; cancer; vector; ds.
XX
OS   Homo sapiens.
```

```
X
N   WO2005112541-A2.
X
D   01-DEC-2005.
X
F   18-MAY-2005; 2005WO-ES000277.
X
R   20-MAY-2004; 2004ES-00001219.
X
A   (PROY-) PROYECTO BIOMEDICINA CIMA SL.
X
I   Qian C,  Guan M,  Smerdou Picazo C,  Prieto Valtuena J;
X
R   WPI; 2005-812033/82.
X
T   Hybrid adenoviral gene expression vector for treating cancer, comprises
T   adenovirus liberation system, alpha virus derived vector and specific
T   tumoral promoter.
X
S   Disclosure; SEQ ID NO 13; 149pp; Spanish.
X
C   The invention relates to a novel adenovirus/alphavirus hybrid vector used
C   in the expression of therapeutic genes in tumor cells. The vector
C   comprises: a first chain of adenoviral origin containing a first inverted
C   terminal repeated sequence and a signal sequence for packing the
C   adenovirus; a first non-coding filler sequence; a sequence corresponding
C   to a specific tissue promoter; an alpha virus-derived cDNA chain, the
C   sequence of which is in part complementary to an alpha viral RNA,
C   comprising at least one sequence coding for at least one exogenous gene
C   of interest, a polyadenylation sequence and a second adenoviral ITR
C   sequence. The invention further includes pharmaceutical compositions
C   containing the vector. The novel vector is used to transfer genetic
C   material to a cell, preferably a tumoral cell, especially one which
C   expresses an alfa fetoprotein (AFP). The vector is used to prepare drugs
C   for treating tumors. The vector or pharmaceutical compositions containing
C   them can be used to induce an immune response against foreign antigens.
C   This gene therapy method can be used to treat cancer. This polynucleotide
C   represents a human interleukin-12 DNA sequence used in the construction
C   of a novel vector of the invention.
X
Q   Sequence 2336 BP; 612 A; 602 C; 577 G; 545 T; 0 U; 0 Other;

lignment Scores:
red. No.:               2.97e-25        Length:         2336
core:                   35.00           Matches:        35
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             11.4%           Indels:         0
B:                      14              Gaps:           0

S-10-821-670A-27 (1-307) x AEE03207 (1-2336)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1964 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 2023

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
b       2024 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 2068

ESULT 100
CF57534
D   ACF57534 standard; DNA; 2347 BP.
X
C   ACF57534;
X
T   22-APR-2004  (first entry)
X
E   Human IL12B DNA SEQ ID NO: 35.
X
W   Protein targeting; angiogenesis inhibitor; fusion gene; cancer; gene; ds;
W   antiangiogenic; cytostatic; ophthalmological; antiarthritic;
W   antirheumatic; antiinflammatory; dermatological; immunosuppressive;
KW  antipsoriatic; antidiabetic; neuroprotective; vasotropic; anorectic.
XX
OS  Homo sapiens.
XX
PN  WO2003093303-A1.
XX
PD  13-NOV-2003.
XX
PF  06-MAY-2003; 2003WO-US014243.
XX
PR  06-MAY-2002; 2002US-0380063P.
XX
PA  (TEXA ) UNIV TEXAS SYSTEM.
XX
PI  Hung M,  Lan K,  Ou-Yang F,  Liu J,  Lan K;
XX
DR  WPI; 2004-053038/05.
XX
PT  New polypeptide comprising an antiangiogenesis polypeptide region linked
PT  to a therapeutic protein or a diagnostic protein, useful for diagnosing
PT  or treating angiogenesis-dependent diseases e.g. cancer, lupus or
PT  restenosis.
XX
PS  Disclosure; Page 111-112; 0pp; English.
XX
CC  The present invention relates to a polypeptide comprising an
CC  antiangiogenesis polypeptide region linked to a therapeutic protein or
CC  polypeptide region, or a diagnostic protein or polypeptide region. The
CC  polypeptide comprising an antiangiogenesis polypeptide region or the
CC  nucleic acid encoding the polypeptide comprising the antiangiogenesis
CC  polypeptide is useful for diagnosing or treating angiogenesis-dependent
CC  diseases or cancer. Angiogenesis-dependent diseases include age-related
CC  macular degeneration, artherosclerosis, angiofibroma, neovascular
CC  glaucoma, arteriovenous malformations, nonunion fractures, arthritis,
CC  rheumatoid arthritis, lupus, connective tissue disorders, Osler-Weber
CC  syndrome, psoriasis, corneal graft neovascularisation, pyogenic
CC  granuloma, delayed wound healing, retrolental fibroplasia, diabetic
CC  retinopathy, scleroderma, granulations, haemangioma, trachoma,
CC  haemophilic joints, vascular adhesions, hypertrophic scars, multiple
CC  sclerosis, restenosis or obesity. The present sequence is a coding
CC  sequence shown in the exemplification of the invention
XX
SQ  Sequence 2347 BP; 695 A; 486 C; 543 G; 623 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.98e-25        Length:         2347
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     12              Gaps:           0

US-10-821-670A-27 (1-307) x ACF57534 (1-2347)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
Db       748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792


Search completed: June 10, 2006, 02:28:11
Job time : 784.84 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

M protein - nucleic search, using frame_plus_p2n model

un on: June 10, 2006, 01:35:52 ; Search time 4253.81 Seconds
(without alignments)
6053.601 Million cell updates/sec

itle: US-10-821-670A-27
erfect score: 307
equence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

coring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

earched: 48236798 seqs, 27959665780 residues

ord size: 1

otal number of hits satisfying chosen parameters: 96471816

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Listing first 200 summaries

ommand line parameters:
MODEL=frame+_p2n.model -DEV=xlp
Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110453_27580/app_query.fasta_1
DB=EST -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rst -MINMATCH=0.1 -LOOPCL=0
LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL
OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
USER=US10821670_@CGN_1_1_22222_@runat_07062006_110453_27580 -NCPU=6 -ICPU=3
NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

atabase : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
c 1	35	11.4	725	5	CD559454	CD559454 AGENCOURT
c 2	35	11.4	736	5	CD559453	CD559453 AGENCOURT
c 3	35	11.4	762	5	CD559451	CD559451 AGENCOURT
c 4	35	11.4	766	5	CD559449	CD559449 AGENCOURT
c 5	35	11.4	772	5	CD559450	CD559450 AGENCOURT
c 6	35	11.4	785	5	CD559448	CD559448 AGENCOURT
7	31	10.1	700	12	CE093997	CE093997 tigr-gss-
8	24	7.8	735	5	CD559605	CD559605 AGENCOURT
c 9	23	7.5	754	5	CD559452	CD559452 AGENCOURT
10	20	6.5	252	10	DV799576	DV799576 est_t_tru
11	20	6.5	724	5	CD559603	CD559603 AGENCOURT
12	20	6.5	745	5	CD559602	CD559602 AGENCOURT
13	20	6.5	747	5	CD559607	CD559607 AGENCOURT
14	20	6.5	756	5	CK130264	CK130264 AGENCOURT
15	20	6.5	772	5	CD559604	CD559604 AGENCOURT
16	20	6.5	1042	5	CD559606	CD559606 AGENCOURT
17	18	5.9	704	13	CZ422673	CZ422673 1018376 R
18	17	5.5	1839	6	AK162981	AK162981 Mus muscu
19	17	5.5	2908	6	AK155593	AK155593 Mus muscu
c 20	16	5.2	581	11	AQ394113	AQ394113 CITBI-E1-
21	13	4.2	346	4	BY164658	BY164658 BY164658
22	13	4.2	355	4	BY221814	BY221814 BY221814
23	13	4.2	375	4	BY222535	BY222535 BY222535
24	13	4.2	387	4	BY167742	BY167742 BY167742
25	13	4.2	417	8	CO949904	CO949904 UMC-pd12c
26	13	4.2	423	4	BY218447	BY218447 BY218447
27	13	4.2	432	4	BY154173	BY154173 BY154173
28	13	4.2	475	7	BF704417	BF704417 MI-P-E6-a
c 29	13	4.2	569	11	AZ853726	AZ853726 2M0157M01
30	13	4.2	649	5	CJ134671	CJ134671 CJ134671
31	13	4.2	666	4	BY749553	BY749553 BY749553
c 32	13	4.2	668	14	AG079702	AG079702 Pan trogl
33	12	3.9	535	11	AZ441303	AZ441303 1M0232M24
c 34	10	3.3	385	1	AA879565	AA879565 vx37c03.r
c 35	10	3.3	414	13	CW885638	CW885638 RPCI42_10
c 36	9	2.9	115	14	ATH521069	AJ521069 Arabidops
37	9	2.9	263	3	BQ356685	BQ356685 PM0-HT033
38	9	2.9	353	4	BY024612	BY024612 BY024612
39	9	2.9	354	4	BY024263	BY024263 BY024263
40	9	2.9	355	4	BY013557	BY013557 BY013557
41	9	2.9	361	10	W00972	W00972 za55d07.r1
42	9	2.9	382	4	BY204279	BY204279 BY204279
43	9	2.9	409	4	BY183786	BY183786 BY183786
c 44	9	2.9	415	11	AQ305003	AQ305003 HS_2012_A
c 45	9	2.9	423	7	AW382621	AW382621 PM0-HT033
c 46	9	2.9	435	7	BE153120	BE153120 PM0-HT033
c 47	9	2.9	442	5	CI330861	CI330861 CI330861
c 48	9	2.9	442	7	BE677126	BE677126 7d80f03.x
c 49	9	2.9	463	1	AU143811	AU143811 AU143811
c 50	9	2.9	477	1	AI754066	AI754066 cr19c06.x
51	9	2.9	479	1	AI683279	AI683279 tw50a03.x
52	9	2.9	479	4	CA699592	CA699592 wlk8.pk00
c 53	9	2.9	494	2	BI325004	BI325004 ic21a08.x
54	9	2.9	500	11	AQ300559	AQ300559 HS_3175_B
c 55	9	2.9	504	2	BM090808	BM090808 ig15e03.x
56	9	2.9	507	7	AW367597	AW367597 MR0-HT016
c 57	9	2.9	510	1	AI554405	AI554405 tq11a12.x
c 58	9	2.9	516	1	AV706519	AV706519 AV706519
c 59	9	2.9	546	9	DA098991	DA098991 DA098991
c 60	9	2.9	553	9	DB284546	DB284546 DB284546
c 61	9	2.9	561	9	DA102042	DA102042 DA102042
62	9	2.9	563	13	CW054731	CW054731 104_295_1
63	9	2.9	566	9	DB349096	DB349096 DB349096
64	9	2.9	572	3	BM907722	BM907722 AGENCOURT
c 65	9	2.9	593	5	CK818181	CK818181 ic21a08.y
c 66	9	2.9	624	13	CW136151	CW136151 104_521_1
67	9	2.9	628	8	CN207623	CN207623 Tor8042 G
68	9	2.9	638	13	CW136150	CW136150 104_521_1
69	9	2.9	645	13	CL344654	CL344654 RPCI44_27
c 70	9	2.9	648	10	DT874689	DT874689 AGENCOURT
c 71	9	2.9	649	13	CW374083	CW374083 fsbb001f0
72	9	2.9	650	2	BG696339	BG696339 602658709
73	9	2.9	657	13	CL344592	CL344592 RPCI44_27
c 74	9	2.9	661	3	BU773963	BU773963 SJEGBC03
75	9	2.9	677	7	AW956339	AW956339 EST368409
76	9	2.9	683	10	DR724059	DR724059 AGENCOURT
77	9	2.9	688	4	CA413781	CA413781 UI-H-EZ0-

78	9	2.9	692	13	CW470377	CW470377 fsbb001f2
79	9	2.9	697	7	BE387304	BE387304 601275594
80	9	2.9	700	3	BQ009739	BQ009739 UI-H-ED0-
81	9	2.9	707	8	CN279085	CN279085 170004247
82	9	2.9	722	8	CN412356	CN412356 170005325
83	9	2.9	757	3	BU633670	BU633670 UI-H-FL1-
84	9	2.9	763	3	BP446084	BP446084 BP446084
85	9	2.9	780	3	BU375548	BU375548 603807808
86	9	2.9	796	11	BZ056171	BZ056171 llb95f10.
87	9	2.9	798	11	BZ020584	BZ020584 oeg90c01.
88	9	2.9	798	14	CT202661	CT202661 Sus scrof
89	9	2.9	802	9	DN518405	DN518405 1259097 M
90	9	2.9	819	9	DN521145	DN521145 1263973 M
91	9	2.9	841	2	BG582789	BG582789 EST484535
92	9	2.9	864	8	CR551254	CR551254 CR551254
93	9	2.9	894	2	BI258748	BI258748 602970329
94	9	2.9	895	2	BI088766	BI088766 602851556
95	9	2.9	913	5	CF409178	CF409178 CH3#059_B
96	9	2.9	923	9	DN565372	DN565372 90930534
97	9	2.9	937	9	DN786150	DN786150 94044776
98	9	2.9	943	13	DU365640	DU365640 109831307
99	9	2.9	960	2	BG035474	BG035474 602325507
100	9	2.9	986	2	BG027599	BG027599 602294475
101	9	2.9	1037	1	AL539211	AL539211 AL539211
102	9	2.9	1315	14	AG430040	AG430040 Mus muscu
103	9	2.9	1340	14	AG448476	AG448476 Mus muscu
104	9	2.9	1447	10	DV783213	DV783213 HW_LIVER_
105	9	2.9	2562	6	CR592197	CR592197 full-leng
106	8	2.6	88	1	AA727638	AA727638 vv02c12.r
107	8	2.6	113	4	C00679	C00679 HUMGS000823
108	8	2.6	113	11	AQ282443	AQ282443 RPCI11-79
109	8	2.6	117	7	AW478729	AW478729 21097 MAR
110	8	2.6	123	7	BE721839	BE721839 189673 MA
111	8	2.6	141	1	AU260162	AU260162 AU260162
112	8	2.6	142	7	BE812604	BE812604 RC3-AN004
113	8	2.6	168	11	B28469	B28469 F25I18TR IG
114	8	2.6	168	12	CE024998	CE024998 tigr-gss-
115	8	2.6	195	2	BG953233	BG953233 CM4-CT063
116	8	2.6	201	7	BE843494	BE843494 CM3-TN006
117	8	2.6	202	1	AI450727	AI450727 ms78g05.x
118	8	2.6	209	4	CD087249	CD087249 MC1-0036T
119	8	2.6	215	1	AA863462	AA863462 oh43c02.s
120	8	2.6	215	12	BZ949925	BZ949925 CH240_38B
121	8	2.6	221	2	BF950279	BF950279 CM3-NN021
122	8	2.6	223	13	CZ024046	CZ024046 CH240_184
123	8	2.6	232	2	BF767515	BF767515 CM4-CN009
124	8	2.6	235	1	AI639761	AI639761 ms78g05.y
125	8	2.6	235	1	AA174908	AA174908 ms78g05.r
126	8	2.6	235	3	BP888606	BP888606 BP888606
127	8	2.6	238	7	AW893763	AW893763 RC4-NN002
128	8	2.6	240	5	CK886537	CK886537 SGP166980
129	8	2.6	242	2	BJ656057	BJ656057 BJ656057
130	8	2.6	242	7	BE204318	BE204318 EST396994
131	8	2.6	243	14	TA90A03P	AL465275 T. brucei
132	8	2.6	244	12	CE767861	CE767861 tigr-gss-
133	8	2.6	250	12	CE820902	CE820902 tigr-gss-
134	8	2.6	252	1	AI152063	AI152063 ud19c07.r
135	8	2.6	252	5	CD240364	CD240364 AREL5P2LH
136	8	2.6	258	4	BW840228	BW840228 BW840228
137	8	2.6	259	1	AI077000	AI077000 BSBmMFSZ1
138	8	2.6	264	8	CN801148	CN801148 DI8P00356
139	8	2.6	270	9	CX357606	CX357606 ssalrgb51
140	8	2.6	272	7	AW660342	AW660342 98331 MAR
141	8	2.6	275	10	DW181457	DW181457 SGP307413
142	8	2.6	276	7	AW383445	AW383445 PM0-HT034
143	8	2.6	277	8	CN635347	CN635347 114G02_54
144	8	2.6	279	10	DY126470	DY126470 001017BEM
145	8	2.6	285	14	FR0014280	AL005523 F.rubripe
146	8	2.6	290	7	BF053671	BF053671 EST438901
147	8	2.6	293	7	BF283817	BF283817 EST448408
148	8	2.6	296	1	AA459674	AA459674 zx49c07.s
149	8	2.6	296	7	BB231764	BB231764 BB231764
150	8	2.6	297	2	BM002849	BM002849 1031107A0
c 151	8	2.6	298	1	AV144660	AV144660 AV144660
c 152	8	2.6	300	1	AA766328	AA766328 oa31b01.s
c 153	8	2.6	301	2	BI504009	BI504009 BB170026B
c 154	8	2.6	301	2	BI508512	BI508512 BB170008B
c 155	8	2.6	302	10	DY126242	DY126242 000910BEM
156	8	2.6	303	1	AJ670502	AJ670502 AJ670502
c 157	8	2.6	309	8	CX215577	CX215577 MNS25532
c 158	8	2.6	320	7	BB830723	BB830723 BB830723
c 159	8	2.6	324	11	AQ981401	AQ981401 RPCI-23-3
160	8	2.6	327	7	AW613780	AW613780 hh81b08.x
161	8	2.6	337	8	CO884451	CO884451 BovGen_12
c 162	8	2.6	338	3	BQ374466	BQ374466 RC0-TT000
163	8	2.6	340	3	BQ081130	BQ081130 san20b06.
164	8	2.6	342	12	CC507444	CC507444 CH240_349
165	8	2.6	346	1	AA894731	AA894731 oj28d02.s
c 166	8	2.6	346	7	AW388577	AW388577 MR2-ST012
c 167	8	2.6	346	8	CN999170	CN999170 UMC-bend_
168	8	2.6	347	4	BX638688	BX638688 BX638688
169	8	2.6	351	1	AA970176	AA970176 op60g06.s
170	8	2.6	351	1	AL385304	AL385304 MtBC27F11
c 171	8	2.6	353	7	BF515693	BF515693 UI-H-BW1-
c 172	8	2.6	355	11	BH257866	BH257866 CH230-283
c 173	8	2.6	355	13	CZ241047	CZ241047 AIAA-aah1
174	8	2.6	357	12	BZ934589	BZ934589 CH240_90J
c 175	8	2.6	361	7	BE109169	BE109169 UI-R-BS1-
c 176	8	2.6	374	4	BW924716	BW924716 BW924716
177	8	2.6	377	2	BM409394	BM409394 EST583721
c 178	8	2.6	379	7	AW122097	AW122097 UI-M-BH2.
179	8	2.6	382	3	BP638893	BP638893 BP638893
180	8	2.6	384	9	DR284868	DR284868 3727058 C
181	8	2.6	385	7	AW046046	AW046046 UI-M-BH1-
c 182	8	2.6	385	7	AW062446	AW062446 MR0-CT006
c 183	8	2.6	387	3	BP611161	BP611161 BP611161
c 184	8	2.6	387	10	DY091092	DY091092 000125BLI
c 185	8	2.6	388	1	AA780837	AA780837 ac67h04.s
c 186	8	2.6	388	3	BP637645	BP637645 BP637645
c 187	8	2.6	390	1	AV589562	AV589562 AV589562
c 188	8	2.6	390	11	AZ467249	AZ467249 1M0278F01
189	8	2.6	392	1	AA494381	AA494381 ne28f09.s
190	8	2.6	392	3	BP614488	BP614488 BP614488
191	8	2.6	392	3	BP848008	BP848008 BP848008
c 192	8	2.6	392	4	BY635513	BY635513 BY635513
193	8	2.6	396	3	BQ033771	BQ033771 UI-1-CF0-
194	8	2.6	396	11	AQ445059	AQ445059 GSSTc0710
195	8	2.6	397	1	AI476432	AI476432 tm21g10.x
196	8	2.6	397	2	BI421353	BI421353 EST532019
c 197	8	2.6	397	11	AZ020373	AZ020373 RPCI-23-3
198	8	2.6	399	3	BP795048	BP795048 BP795048
199	8	2.6	400	1	AA480179	AA480179 ne30d09.s
200	8	2.6	400	7	AV811170	AV811170 AV811170

ALIGNMENTS

RESULT 1
CD559454/c

```
LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
```

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 11
High quality sequence start: 13
High quality sequence stop: 573.

'EATURES Location/Qualifiers
source 1. .725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971868"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

)RIGIN

Alignment Scores:

;ed. No.:	4.71e-24	Length:	725
;core:	35.00	Matches:	35
)ercent Similarity:	100.0%	Conservative:	0
)est Local Similarity:	100.0%	Mismatches:	0
)uery Match:	11.4%	Indels:	0
)B:	5	Gaps:	0

)S-10-821-670A-27 (1-307) x CD559454 (1-725)

)y 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b 441 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 382

)y 215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
|||||||||||||||||||||||||||||||||||||||||||||
)b 381 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 337

)ESULT 2
)D559453/c
)OCUS CD559453 736 bp mRNA linear EST 19-NOV-2003
)EFINITION AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
)CCESSION CD559453
)ERSION CD559453.2 GI:38453475
)EYWORDS EST.
)OURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 736)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585521.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 683.
FEATURES Location/Qualifiers
source 1. .736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	4.77e-24	Length:	736
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.4%	Indels:	0
DB:	5	Gaps:	0

US-10-821-670A-27 (1-307) x CD559453 (1-736)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 416 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 357

Qy 215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
|||||||||||||||||||||||||||||||||||||||||||||
Db 356 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 312

RESULT 3
CD559451/c
LOCUS CD559451 762 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CD559451
VERSION CD559451.2 GI:38453471
KEYWORDS EST.

```
:URCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 762)
 AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
 TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL    Unpublished (1999)
:MMENT      On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 38
            High quality sequence stop: 761.
EATURES             Location/Qualifiers
     source         1. .762
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971871"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
RIGIN

lignment Scores:
red. No.:              4.92e-24       Length:        762
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
st Local Similarity:   100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     5              Gaps:          0

S-10-821-670A-27 (1-307) x CD559451 (1-762)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c       437 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 378

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
c       377 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 333

:SULT 4
:559449/c
```

```
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES            Location/Qualifiers
     source         1. .766
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971873"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.94e-24       Length:        766
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-27 (1-307) x CD559449 (1-766)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      429 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 370

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
```

```
                  ||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 325

RESULT 5
CD559450/c
LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 2
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
     source          1. .772
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.98e-24        Length:         772
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-27 (1-307) x CD559450 (1-772)
```

```
Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 381

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
                |||||||||||||||||||||||||||||||||||||||||||||
Db        380 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 336

RESULT 6
CD559448/c
LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              5.05e-24        Length:         785
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
```

```
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            11.4%         Indels:        0
B:                     5             Gaps:          0

S-10-821-670A-27 (1-307) x CD559448 (1-785)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        431 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 372

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
c        371 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 327

ESULT 7
093997
OCUS       CE093997                700 bp    DNA     linear   GSS 24-SEP-2003
EFINITION  tigr-gss-dog-17000359883851 Dog Library Canis familiaris genomic,
           genomic survey sequence.
CCESSION   CE093997
ERSION     CE093997.1  GI:35160844
EYWORDS    GSS.
OURCE      Canis familiaris (dog)
 ORGANISM  Canis familiaris
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
           Canis.
EFERENCE   1  (bases 1 to 700)
 AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
           Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
           Venter,J.C.
 TITLE     The dog genome: survey sequencing and comparative analysis
 JOURNAL   Science 301 (5641), 1898-1903 (2003)
  PUBMED   14512627
OMMENT     Contact: Kirkness EF
           The Institute for Genomic Research
           Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
           Rockville, MD 20850, USA
           Tel: 301-838-0200
           Fax: 301-838-0208
           Email: ekirknes@tigr.org
           Class: shotgun.
EATURES              Location/Qualifiers
    source           1. .700
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
IGIN

 ignment Scores:
ed. No.:               4.49e-20      Length:        700
core:                  31.00         Matches:       31
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            10.1%         Indels:        0
B:                     12            Gaps:          0

S-10-821-670A-27 (1-307) x CE093997 (1-700)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
c        430 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 489

y        201 AsnTyrThrSerSerPhePheIleArgAspIle 211
            |||||||||||||||||||||||||||||||||
c        490 AACTACACCAGCAGCTTCTTCATCAGAGACATC 522

ESULT 8
559605
```

```
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:               4.54e-13      Length:        735
Score:                   24.00         Matches:       24
Percent Similarity:      100.0%        Conservative:  0
Best Local Similarity:   100.0%        Mismatches:    0
Query Match:             7.8%          Indels:        0
DB:                      5             Gaps:          0

US-10-821-670A-27 (1-307) x CD559605 (1-735)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       662 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 721

Qy       215 AspProProLys 218
```

```
                ||||||||||||
)b        722 GACCCACCCAAG 733

:ESULT 9
:D559452/c
:OCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
)EFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
:CCESSION   CD559452
:ERSION     CD559452.2  GI:38453473
:EYWORDS    EST.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
:OMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
'EATURES              Location/Qualifiers
     source           1. .754
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971870"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
)RIGIN

\lignment Scores:
':ed. No.:              4.62e-12        Length:         754
;core:                  23.00           Matches:        23
)ercent Similarity:     100.0%          Conservative:   0
)est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            7.5%            Indels:         0
)B:                     5               Gaps:           0

)S-10-821-670A-27 (1-307) x CD559452 (1-754)

Qy        206 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TTTTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 344

Qy        226 LysAsnSer 228
              ||||||||
Db        343 AAGAATTCT 335

RESULT 10
DV799576
LOCUS       DV799576                252 bp    mRNA    linear   EST 23-NOV-2005
DEFINITION  est_t_truncatus2262 HML_TuTr_IL-2_PBL Tursiops truncatus cDNA, mRNA
            sequence.
ACCESSION   DV799576
VERSION     DV799576.1  GI:82652485
KEYWORDS    EST.
SOURCE      Tursiops truncatus (bottlenosed dolphin)
  ORGANISM  Tursiops truncatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
            Odontoceti; Delphinidae; Tursiops.
REFERENCE   1  (bases 1 to 252)
  AUTHORS   Mancia,A., Gefroh,H.A., Lundqvist,M.L., Romano,T.A., Almeida,J.S.,
            Chen,Y., McKillen,D.J., Trent,H.F., Wu,S. and Warr,G.W.
  TITLE     Construction and validation of T. truncatus immunospecific cDNA
            microarray at marinegenomics.org
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Annalaura Mancia
            Hollings Marine Lab
            Medical University of South Carolina
            Hollings Marine Lab, 331 Ft. Johnson Rd., Charleston, SC 29412, USA
            Tel: (843) 762 8962
            Fax: (843) 762 8737
            Email: mancia@musc.edu.
FEATURES              Location/Qualifiers
     source           1. .252
                      /organism="Tursiops truncatus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9739"
                      /tissue_type="PBL"
                      /cell_type="PBL"
                      /clone_lib="HML_TuTr_IL-2_PBL"
                      /note="Vector: pCR2.1TOPO; Site_1: GAATTC"
ORIGIN

Alignment Scores:
Pred. No.:              1.75e-09        Length:         252
Score:                  20.00           Matches:        20
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.5%            Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-27 (1-307) x DV799576 (1-252)

Qy        172 CysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValVal 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 TGTCAGGAGGGCAGCGCCTGCCCAGCCGCCGAGGAGAGCCTGCCCATTGAGGTCGTGGTG 202

RESULT 11
CD559603
LOCUS       CD559603                724 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559603
VERSION     CD559603.2  GI:38558932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```

```
:FERENCE   1  (bases 1 to 724)
 AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
 TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL   Unpublished (1999)
:MMENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 04
           High quality sequence stop: 525.
EATURES              Location/Qualifiers
     source          1. .724
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
:IGIN

lignment Scores:
red. No.:              4.4e-09        Length:        724
core:                  20.00          Matches:       20
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            6.5%           Indels:        0
B:                     5              Gaps:          0

S-10-821-670A-27 (1-307) x CD559603 (1-724)

y          41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
o         200 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 259

ESULT 12
D559602
:CUS       CD559602                745 bp    mRNA    linear   EST 26-NOV-2003
:FINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
           IMAGE:6971874 5', mRNA sequence.
:CCESSION  CD559602
ERSION     CD559602.2  GI:38558930
EYWORDS    EST.
:URCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE  1  (bases 1 to 745)
  AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
COMMENT    On Jun 10, 2003 this sequence version replaced gi:31585670.
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 05
           High quality sequence start: 2
           High quality sequence stop: 644.
FEATURES             Location/Qualifiers
     source          1. .745
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:             4.51e-09       Length:        745
Score:                 20.00          Matches:       20
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           6.5%           Indels:        0
DB:                    5              Gaps:          0

US-10-821-670A-27 (1-307) x CD559602 (1-745)

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 251

RESULT 13
CD559607
LOCUS      CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
           IMAGE:6971868 5', mRNA sequence.
ACCESSION  CD559607
VERSION    CD559607.2  GI:38558941
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
```

```
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
EFERENCE   1  (bases 1 to 747)
 AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
 TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL   Unpublished (1999)
OMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: g  column: 11
           High quality sequence start: 14
           High quality sequence stop: 671.
EATURES              Location/Qualifiers
     source          1. .747
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971868"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
RIGIN

lignment Scores:
red. No.:               4.52e-09       Length:        747
core:                   20.00          Matches:       20
ercent Similarity:      100.0%         Conservative:  0
est Local Similarity:   100.0%         Mismatches:    0
uery Match:             6.5%           Indels:        0
B:                      5              Gaps:          0

S-10-821-670A-27 (1-307) x CD559607 (1-747)

y          41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         215 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 274

ESULT 14
K130264
OCUS       CK130264                 756 bp    mRNA    linear   EST 02-DEC-2003
EFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
           IMAGE:6971871 5', mRNA sequence.
CCESSION   CK130264
ERSION     CK130264.1  GI:38622200
EYWORDS    EST.
```

```
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE  1  (bases 1 to 756)
  AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 02
           High quality sequence start: 5
           High quality sequence stop: 731.
FEATURES             Location/Qualifiers
     source          1. .756
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971871"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.57e-09       Length:        756
Score:                  20.00          Matches:       20
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            6.5%           Indels:        0
DB:                     5              Gaps:          0

US-10-821-670A-27 (1-307) x CK130264 (1-756)

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 279

RESULT 15
CD559604
LOCUS      CD559604                 772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
           IMAGE:6971872 5', mRNA sequence.
ACCESSION  CD559604
VERSION    CD559604.2  GI:38558934
```

```
EYWORDS     EST.
OURCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 772)
 AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
 TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL    Unpublished (1999)
OMMENT      On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 13
            High quality sequence stop: 750.
EATURES             Location/Qualifiers
     source         1. .772
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971872"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
RIGIN

lignment Scores:
ed. No.:              4.65e-09      Length:         772
core:                 20.00         Matches:        20
ercent Similarity:    100.0%        Conservative:   0
st Local Similarity:  100.0%        Mismatches:     0
ery Match:            6.5%          Indels:         0
:                     5             Gaps:           0

-10-821-670A-27 (1-307) x CD559604 (1-772)

Y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          224 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 283

ESULT 16
D559606
CUS         CD559606               1042 bp    mRNA    linear   EST 11-JUN-2003
EFINITION   AGENCOURT_14497125 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
```

```
ACCESSION   CD559606
VERSION     CD559606.1  GI:31585674
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1042)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 386.
FEATURES            Location/Qualifiers
     source         1. .1042
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:6971869"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              6.04e-09      Length:         1042
Score:                  20.00         Matches:        20
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            6.5%          Indels:         0
DB:                     5             Gaps:           0

US-10-821-670A-27 (1-307) x CD559606 (1-1042)

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 249

RESULT 17
CZ422673
LOCUS       CZ422673                704 bp    DNA     linear   GSS 06-APR-2005
DEFINITION  1018376 RP42 Bos taurus genomic clone RP42-49A21, genomic survey
            sequence.
```

```
ACCESSION   CZ422673
VERSION     CZ422673.1  GI:62309882
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   Sonstegard,T.S., Van Tassell,C.P., Capuco,A.V., de Jong,P.,
            Matukumalli,L.K., Shade,L.S., Bosak,S., Rubenfield,M. and
            Gasbarre,L.C.
  TITLE     Bovine BAC End Sequences from Library RPCI-42
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Tad S. Sonstegard
            Bovine Functional Genomics Laboratory
            Animal and Natural Resources Institute
            Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
            Tel: 3015048416
            Fax: 3015048414
            Email: tads@anri.barc.usda.gov
            Clones are derived from the bovine BAC library RPCI-42
            (http://bacpac.chori.org/mbovine42.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering_information.htm). This work
            was undertaken as part of the International Bovine BAC Mapping
            Consortium (IBBMC) by USDA-ARS-BFGL.
            Plate: 49  row: A  column: 21
            Seq primer: TAATACGACTCACTATAGGG
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .704
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="RP42-49A21"
                     /sex="male"
                     /cell_type="Blood"
                     /clone_lib="RP42"
                     /note="Vector: pBACe3.6; Site_1: MboI; Site_2: MboI;
                     RPCI-42 Bovine BAC library (Male Holstein) produced by
                     Pieter de Jong"
ORIGIN

Alignment Scores:
Seq. No.:               4.25e-07        Length:         704
Score:                  18.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.9%            Indels:         0
DB:                     13              Gaps:           0

RS-10-821-670A-27 (1-307) x CZ422673 (1-704)

QY        235 TrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPhe 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 TGGGAGTACCCTGACACGTGGAGCACCCCGCATTCCTACTTCTCCCTGACGTTT 57

RESULT 18
AK162981
LOCUS       AK162981               1839 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A430014H12 product:interleukin 12b, full insert
            sequence.
ACCESSION   AK162981
VERSION     AK162981.1  GI:74188061
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  PUBMED    11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  PUBMED    11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
```

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
EFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
EFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
EFERENCE 8 (bases 1 to 1839)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
source 1. .1839
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A430014H12"
/db_xref="taxon:10090"
/clone="A430014H12"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
CDS 58. .1065
/note="unnamed protein product; interleukin 12b (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%, match=1816)
putative"
/codon_start=1
/protein_id="BAE37146.1"
/db_xref="GI:74188062"
/translation="MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGE
TVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHL
LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
S"
ORIGIN

Alignment Scores:

Pred. No.:	9.8e-06	Length:	1839
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.5%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-27 (1-307) x AK162981 (1-1839)

```
Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 777
```

RESULT 19
AK155593
LOCUS AK155593 2908 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730005O03 product:interleukin 12b, full insert sequence.
ACCESSION AK155593
VERSION AK155593.1 GI:74212721
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 2908)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,

URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
OMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

```
EATURES             Location/Qualifiers
    source          1. .2908
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="FANTOM_DB:F730005O03"
                    /db_xref="taxon:10090"
                    /clone="F730005O03"
                    /cell_type="B6-derived CD11 +ve dendritic cells"
                    /clone_lib="RIKEN full-length enriched mouse cDNA library"
    misc_feature    1. .2908
                    /note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence:
                    BLASTN, 99%, match=1807)
                    putative"
RIGIN

lignment Scores:
red. No.:               1.46e-05        Length:         2908
core:                   17.00           Matches:        17
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             5.5%            Indels:         0
B:                      6               Gaps:           0

-10-821-670A-27 (1-307) x AK155593 (1-2908)

Y        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
c       1131 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1181

ESULT 20
Q394113/c
OCUS        AQ394113                581 bp    DNA     linear   GSS 06-MAR-1999
EFINITION   CITBI-E1-2542F7.TF CITBI-E1 Homo sapiens genomic clone 2542F7,
            genomic survey sequence.
CCESSION    AQ394113
ERSION      AQ394113.1  GI:4365136
EYWORDS     GSS.
OURCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 581)
 AUTHORS    Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
 TITLE      Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
 JOURNAL    Unpublished (1997)
OMMENT      Other_GSSs: CITBI-E1-2542F7.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES            Location/Qualifiers
     source         1. .581
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /clone="2542F7"
                    /sex="male"
                    /cell_type="sperm"
                    /clone_lib="CITBI-E1"
                    /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                    CalTech Human BAC Library D"
ORIGIN

Alignment Scores:
Pred. No.:              3.56e-05        Length:         581
Score:                  16.00           Matches:        16
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.2%            Indels:         0
DB:                     11              Gaps:           0

US-10-821-670A-27 (1-307) x AQ394113 (1-581)

Qy        213 LysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 AAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCG 1

RESULT 21
BY164658
LOCUS       BY164658                346 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY164658 RIKEN full-length enriched, bone marrow macrophage Mus
            musculus cDNA clone I830052P21 5', mRNA sequence.
ACCESSION   BY164658
VERSION     BY164658.1  GI:26301304
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
```

JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .346
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I830052P21"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"

ORIGIN

Alignment Scores:

Pred. No.:	0.0223	Length:	346
Score:	13.00	Matches:	13
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.2%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-27 (1-307) x BY164658 (1-346)

Qy 30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
||||||||||||||||||||||||||||||||||||||||||||
Db 211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

RESULT 22
BY221814
LOCUS BY221814 355 bp mRNA linear EST 10-DEC-2002
DEFINITION BY221814 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830223O08 5', mRNA sequence.
ACCESSION BY221814
VERSION BY221814.1 GI:26402917
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 355)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
EATURES             Location/Qualifiers
    source          1. .355
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="NOD"
                    /db_xref="taxon:10090"
                    /clone="F830223O08"
                    /tissue_type="activated spleen"
                    /clone_lib="RIKEN full-length enriched, activated spleen"
RIGIN

lignment Scores:
red. No.:               0.0229          Length:         355
core:                   13.00           Matches:        13
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             4.2%            Indels:         0
B:                      4               Gaps:           0

S-10-821-670A-27 (1-307) x BY221814 (1-355)

y          30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
              ||||||||||||||||||||||||||||||||||||||||
o         210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248

ESULT 23
Y222535
OCUS        BY222535                 375 bp    mRNA    linear   EST 10-DEC-2002
EFINITION   BY222535 RIKEN full-length enriched, activated spleen Mus musculus
            cDNA clone F830228K06 5', mRNA sequence.
CCESSION    BY222535
ERSION      BY222535.1  GI:26403638
EYWORDS     EST.
OURCE       Mus musculus (house mouse)
 ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
EFERENCE    1  (bases 1 to 375)
 AUTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
 TITLE      Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
 JOURNAL    Nature 420, 563-573 (2002)
  PUBMED    12466851
OMMENT      Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES            Location/Qualifiers
     source         1. .375
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="NOD"
                    /db_xref="taxon:10090"
                    /clone="F830228K06"
                    /tissue_type="activated spleen"
                    /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

Alignment Scores:
Pred. No.:              0.024           Length:         375
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.2%            Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-27 (1-307) x BY222535 (1-375)

Qy          30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
               ||||||||||||||||||||||||||||||||||||||||
Db         210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248

RESULT 24
BY167742
LOCUS       BY167742                 387 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY167742 RIKEN full-length enriched, bone marrow macrophage Mus
            musculus cDNA clone I830068I17 5', mRNA sequence.
ACCESSION   BY167742
VERSION     BY167742.1  GI:26304388
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 387)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
```

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .387
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I830068I17"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"

ORIGIN

Alignment Scores:

Pred. No.:	0.0246	Length:	387
Score:	13.00	Matches:	13
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.2%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-27 (1-307) x BY167742 (1-387)

```
Qy         30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
              ||||||||||||||||||||||||||||||||||||||||
Db        211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249
```

RESULT 25
CO949904
LOCUS CO949904 417 bp mRNA linear EST 09-SEP-2004
DEFINITION UMC-pd12cl-003-b07 Day 12 Corpus Luteum pd12cl Sus scrofa cDNA 3', mRNA sequence.
ACCESSION CO949904
VERSION CO949904.1 GI:51326849
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 417)
AUTHORS Jiang,H., Whitworth,K.M., Bivens,N.J., Ries,J.E., Woods,R.J., Forrester,L.J., Springer,G.K., Mathialagan,N., Agca,C., Prather,R.S. and Lucy,M.C.
TITLE Large-scale Generation and Analysis of Expressed Sequence Tags from Porcine Ovary
JOURNAL Unpublished (2004)
COMMENT Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: porcine@rnet.missouri.edu
POLYA=No.

FEATURES Location/Qualifiers
source 1. .417
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/dev_stage="Day 12 Corpus Luteum"
/clone_lib="pd12cl"
/note="Vector: T3T7PAC; Funding: A grant from the Monsanto Company to the University of Missouri. Genetic Source: Ovarian tissue (whole ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea; Day 12 corpora lutea and Day 12 follicles. More information regarding the methods can be found at:
http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996;

Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mg of poly(A)+ RNA will be annealed at 37 degrees Celsius with 10mg of NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs was ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pSPORT1 vector (Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. 2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
TAG_TISSUE=Day 12 Corpus Luteum
TAG_SEQ=Not found"

RIGIN

lignment Scores:

ted. No.:	0.0263	Length:	417
core:	13.00	Matches:	13
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	4.2%	Indels:	0
:	8	Gaps:	0

S-10-821-670A-27 (1-307) x CO949904 (1-417)

Y 30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
||||||||||||||||||||||||||||||||||||||||||

Db 198 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 236

RESULT 26
BY218447
LOCUS BY218447 423 bp mRNA linear EST 10-DEC-2002
DEFINITION BY218447 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830107N16 5', mRNA sequence.
ACCESSION BY218447
VERSION BY218447.1 GI:26399344
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
'EATURES             Location/Qualifiers
     source          1. .423
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="NOD"
                     /db_xref="taxon:10090"
                     /clone="F830107N16"
                     /tissue_type="activated spleen"
                     /clone_lib="RIKEN full-length enriched, activated spleen"
)RIGIN

.lignment Scores:
'ed. No.:                0.0266          Length:         423
core:                    13.00           Matches:        13
'ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
)uery Match:             4.2%            Indels:         0
)B:                      4               Gaps:           0

'S-10-821-670A-27 (1-307) x BY218447 (1-423)

)y          30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
               ||||||||||||||||||||||||||||||||||||||||
)b         210 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 248

'ESULT 27
'Y154173
)OCUS        BY154173                 432 bp    mRNA    linear   EST 10-DEC-2002
)EFINITION   BY154173 RIKEN full-length enriched, bone marrow macrophage Mus
             musculus cDNA clone G530005B20 5', mRNA sequence.
.'CCESSION   BY154173
'ERSION      BY154173.1  GI:26290747
:EYWORDS     EST.
:OURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
             Sciurognathi; Muroidea; Muridae; Murinae; Mus.
'EFERENCE    1  (bases 1 to 432)
  AUTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
             Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
             Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
             Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
             Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
             Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
             Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
             Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
             Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
             Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
             Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
             Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
             Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
             Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
             Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
             Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
             Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
             Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
             Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
             Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
             Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
             Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
             Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
             Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
             Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
             Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
             Rogers,J., Birney,E. and Hayashizaki,Y.
    TITLE    Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
  JOURNAL    Nature 420, 563-573 (2002)
   PUBMED    12466851
COMMENT      Contact: Yoshihide Hayashizaki
             Laboratory for Genome Exploration Research Group, RIKEN Genomic
             Sciences Center(GSC), Yokohama Institute
             The Institute of Physical and Chemical Research (RIKEN)
             1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
             Tel: 81-45-503-9222
             Fax: 81-45-503-9216
             Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
             Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
             Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
             Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
             Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
             Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
             Hayashizaki,Y. Direct Submission
              Computational Analysis of Full-Length Mouse cDNAs Compared with
             Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
              Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new
             genes. Genome Res. 10 (10), 1617-1630 (2000)
              RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer. Genome Res.
             10 (11), 1757-1771 (2000)
              Computer-based methods for the mouse full-length cDNA
             encyclopedia: real-time sequence clustering for construction of a
             nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
              cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
              Tissues were provided by David A. Hume ( Depts. of Biochemistry
             and Microbiology/Parasitology Institute for Molecular Bioscience
             University of Queensland Brisbane,Q 4072 Australia ) whose
             assistance we gratefully acknowledge.
              Please visit our web site (http://genome.gsc.riken.go.jp) for
             further details.
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G530005B20"
                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched, bone marrow
                     macrophage"
ORIGIN

Alignment Scores:
Pred. No.:               0.0271          Length:         432
Score:                   13.00           Matches:        13
Percent Similarity:      100.0%          Conservative:   0
Best Local Similarity:   100.0%          Mismatches:     0
Query Match:             4.2%            Indels:         0
DB:                      4               Gaps:           0

US-10-821-670A-27 (1-307) x BY154173 (1-432)

Qy          30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
               ||||||||||||||||||||||||||||||||||||||||
Db         211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

RESULT 28
BF704417
LOCUS        BF704417                 475 bp    mRNA    linear   EST 22-DEC-2000
```

```
EFINITION  MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
           MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
CCESSION   BF704417
ERSION     BF704417.1  GI:11989825
EYWORDS    EST.
URCE       Sus scrofa (pig)
 ORGANISM  Sus scrofa
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
           Sus.
EFERENCE   1  (bases 1 to 475)
 AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE     Normalization and subtraction: two approaches to facilitate gene
           discovery
 JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  PUBMED   8889548
OMMENT     Contact: Tuggle CK
           Molecular Genetics Laboratory, Department of Animal Science
           Iowa State University
           201 Kildee Hall, Ames, IA 50011-3150, USA
           Tel: 5152944252
           Fax: 5152942401
           Email: cktuggle@iastate.edu
           Oligo-dT track not found, Not I site shown in beginning of sequence
           is likely internal to the message. cDNA Library Preparation: RJ
           Woods, JA Green, RS Prather S142 Animal Science Research Center,
           Department of Animal Science, University of Missouri-Columbia,
           65211 Clone distribution: clones will be available through Research
           Genetics (www.resgen.com)
           Seq primer: M13 Forward
           POLYA=No.
EATURES              Location/Qualifiers
     source          1. .475
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-E6-acc-g-09-1-UM"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="MI-P-E6"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: EcoRI;
                     The MI-P-E6 library is derived from fetus at gestational
                     day 20.  For a detailed description of the  library from
                     which this clone was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/.
                     TAG_SEQ=None found"
RIGIN

lignment Scores:
red. No.:              0.0295          Length:         475
core:                  13.00           Matches:        13
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            4.2%            Indels:         0
B:                     7               Gaps:           0

S-10-821-670A-27 (1-307) x BF704417 (1-475)

y          30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
              ||||||||||||||||||||||||||||||||||||||||
o         199 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 237

ESULT 29
Z853726/c
OCUS       AZ853726                569 bp    DNA     linear   GSS 21-FEB-2001
EFINITION  2M0157M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
           clone UUGC2M0157M01 F, genomic survey sequence.
CCESSION   AZ853726
ERSION     AZ853726.1  GI:13042136
EYWORDS    GSS.
OURCE      Mus musculus (house mouse)
 ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
EFERENCE   1  (bases 1 to 569)
 AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
           Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
           Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
           Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
 JOURNAL   Unpublished (2000)
OMMENT     Contact: Robert B. Weiss
           University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000   Std Error: 0.00
           Plate: 0157  row: M  column: 01
           Seq primer: CGTTGTAAAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 569.
EATURES              Location/Qualifiers
     source          1. .569
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157M01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Alignment Scores:
Pred. No.:             0.0345          Length:         569
Score:                 13.00           Matches:        13
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           4.2%            Indels:         0
DB:                    11              Gaps:           0

US-10-821-670A-27 (1-307) x AZ853726 (1-569)

Qy         30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
              ||||||||||||||||||||||||||||||||||||||||
Db        217 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 179

RESULT 30
CJ134671
LOCUS      CJ134671                649 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION CJ134671 RIKEN full-length enriched mouse cDNA library, C57BL/6J
           bone marrow macrophage Mus musculus cDNA clone G530135F14 5', mRNA
```

```
            sequence.
ACCESSION   CJ134671
VERSION     CJ134671.1  GI:76234999
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
    PUBMED  16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by David A. Hume (
            Depts. of Biochemistry and Microbiology/Parasitology Institute for
            Molecular Bioscience University of Queensland Brisbane,Q 4072
            Australia ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES                Location/Qualifiers
     source             1. .649
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="G530135F14"
                        /tissue_type="bone marrow"
                        /cell_type="macrophage"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library,
                        C57BL/6J bone marrow macrophage"
ORIGIN

Alignment Scores:
Pred. No.:              0.0387          Length:         649
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.2%            Indels:         0
DB:                     5               Gaps:           0

US-10-821-670A-27 (1-307) x CJ134671 (1-649)

Qy          30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
               ||||||||||||||||||||||||||||||||||||||||
Db         211 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 249

RESULT 31
BY749553
LOCUS       BY749553                  666 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY749553 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730005O03 5', mRNA sequence.
ACCESSION   BY749553
VERSION     BY749553.1  GI:27179008
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
    PUBMED  12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES                Location/Qualifiers
     source             1. .666
                        /organism="Mus musculus"
```

```
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F730005O03"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
RIGIN

lignment Scores:
red. No.:                0.0396          Length:         666
core:                    13.00           Matches:        13
ercent Similarity:       100.0%          Conservative:   0
est Local Similarity:    100.0%          Mismatches:     0
uery Match:              4.2%            Indels:         0
B:                       4               Gaps:           0

S-10-821-670A-27 (1-307) x BY749553 (1-666)

Y          30 ThrProGluGluAspAspIleThrTrpThrSerAspGln 42
              ||||||||||||||||||||||||||||||||||||||||
b         611 ACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAG 649

ESULT 32
3079702/c
CUS       AG079702                668 bp    DNA     linear   GSS 03-NOV-2001
EFINITION Pan troglodytes DNA, clone: PTB-075I07.R, genomic survey sequence.
CCESSION  AG079702
ERSION    AG079702.1  GI:16631504
EYWORDS   GSS.
OURCE     Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Pan.
EFERENCE  1
 AUTHORS  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE    BAC end sequences of Library PTB
 JOURNAL  Unpublished
EFERENCE  2  (bases 1 to 668)
 AUTHORS  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
          Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE    Direct Submission
 JOURNAL  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
          Tel:81-45-503-9111, Fax:81-45-503-9170)
OMMENT    Clones are derived from the chimpanzee BAC library PTB This BAC end
          was generated during the R&D process and may have higher chance of
          clone tracking errors.
           PRIMERS
               Sequencing: M13Rev
           LIBRARY
               Vector    : pKS145
               R.Site 1  : SacI
               R.Site 2  : SacI.
EATURES             Location/Qualifiers
    source          1. .668
                    /organism="Pan troglodytes"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9598"
                    /clone="PTB-075I07.R"
                    /sex="male"
                    /cell_type="lymphoblast"
                    /clone_lib="PTB Chimpanzee Male BAC Library"
RIGIN

lignment Scores:
red. No.:                0.0397          Length:         668
core:                    13.00           Matches:        13
ercent Similarity:       100.0%          Conservative:   0
```

```
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.2%            Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-27 (1-307) x AG079702 (1-668)

Qy        112 LysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThr 124
              ||||||||||||||||||||||||||||||||||||||||
Db        506 AAGAATTATTCAGGACGTTTCACCTGCTGGTGGCTGACG 468

RESULT 33
AZ441303
LOCUS       AZ441303                535 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0232M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0232M24 R, genomic survey sequence.
ACCESSION   AZ441303
VERSION     AZ441303.1  GI:10565316
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 535.
FEATURES            Location/Qualifiers
     source         1. .535
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0232M24"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
```

```
)RIGIN

.lignment Scores:
'red. No.:                0.326          Length:         535
;core:                    12.00          Matches:        12
'ercent Similarity:       100.0%         Conservative:   0
lest Local Similarity:    100.0%         Mismatches:     0
)uery Match:              3.9%           Indels:         0
)B:                       11             Gaps:           0

IS-10-821-670A-27 (1-307) x AZ441303 (1-535)

)y         62 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGlu 73
              ||||||||||||||||||||||||||||||||||||
)b        249 GATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAG 284

'ESULT 34
.A879565/c
.OCUS       AA879565                 385 bp    mRNA    linear   EST 26-MAR-1998
)EFINITION  vx37c03.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone
            IMAGE:1277380 5' similar to TR:Q24331 Q24331 TUMOROUS IMAGINAL
            DISCS. ;, mRNA sequence.
.CCESSION   AA879565
'ERSION     AA879565.1  GI:2990270
:EYWORDS    EST.
:OURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
:EFERENCE   1  (bases 1 to 385)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
:OMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:669180
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 292.
'EATURES             Location/Qualifiers
     source          1. .385
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6 x CBA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1277380"
                     /sex="female"
                     /tissue_type="lung"
                     /dev_stage="6-8 month old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="Stratagene mouse lung 937302"
                     /note="Organ: lung; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. 6-8 month old female lung and 1.5 year old male
                     lung were source of mRNA. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
)RIGIN

.lignment Scores:
'red. No.:                24.2           Length:         385
;core:                    10.00          Matches:        10
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              3.3%           Indels:         0
DB:                       1              Gaps:           0

US-10-821-670A-27 (1-307) x AA879565 (1-385)

Qy          72 GlyGluValLeuSerHisSerPheLeuLeu 81
               ||||||||||||||||||||||||||||||
Db         346 GGAGAAGTGTTGTCACATAGTTTTCTGTTG 317

RESULT 35
CW885638/c
LOCUS       CW885638                 414 bp    DNA     linear   GSS 08-DEC-2004
DEFINITION  RPCI42_102G16.TV RPCI-42 Bos taurus genomic clone RPCI42_102G16,
            genomic survey sequence.
ACCESSION   CW885638
VERSION     CW885638.1  GI:56424578
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Larkin,D.M., Donthu,K., LeDuc,R., Ryan,K., Liu,L., de Jong,P.J. and
            Lewin,H.A.
  TITLE     End sequencing of Holstein BAC library RPCI-42
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Harris Lewin
            Department of Animal Sciences
            University of Illinois at Urbana Champaign
            1201 W. Gregory Dr., Urbana, IL 61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Clones are derived from the bovine BAC library RPCI-42
            (http://bacpac.chori.org/mbovine42.htm). For BAC library
            availability, please contact Pieter de Jong
            (pdejong@mail.cho.org).Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/ordering_information.htm).
            Funding was provided in part by grant no. AG2004-34480-14417 from
            USDA-CSREES (Livestock Genome Sequencing Initiative) and
            AG58-5438-2-313 from USDA-ARS
            Plate: 102  row: G  column: 16
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="RPCI42_102G16"
                     /sex="male"
                     /cell_type="blood"
                     /clone_lib="RPCI-42"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI-42 Bovine BAC library (Male) produced by Pieter de
                     Jong"
ORIGIN

Alignment Scores:
Pred. No.:                25.8           Length:         414
Score:                    10.00          Matches:        10
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              3.3%           Indels:         0
DB:                       13             Gaps:           0

US-10-821-670A-27 (1-307) x CW885638 (1-414)

Qy         213 LysProAspProProLysAsnLeuGlnLeu 222
```

```
                    ||||||||||||||||||||||||||||||
o         30 AAACCAGACCCACCCAAGAACCTGCAACTG 1

ESULT 36
TH521069/c
OCUS       ATH521069               115 bp    DNA     linear   GSS 08-FEB-2006
EFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
           052B02, genomic survey sequence.
CCESSION   AJ521069
ERSION     AJ521069.1  GI:26789305
EYWORDS    GSS; left border; T-DNA flanking sequence.
OURCE      Arabidopsis thaliana (thale cress)
 ORGANISM  Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
EFERENCE   1
 AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
           Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
           Lepiniec,L., Caboche,M. and Lecharny,A.
 TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
           of pre-insertion sites
 JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  PUBMED   12446565
EFERENCE   2  (bases 1 to 115)
 AUTHORS   Balzergue,S.
 TITLE     Direct Submission
 JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
           Gaston Cremieux, 91057 Evry cedex, FRANCE
OMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
           plants from INRA (Versailles). The DNA fragment(s) resulting from
           the PCR were directly sequenced from the left or the right border
           to determine the genomic sequence flanking the insertion. T-DNA
           derived sequences were removed. Information to order the
           corresponding mutant line and a link to a database providing a
           graphical display of the insertion site are available at
           http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
           been generated in the framework of the French plant genomics
           program 'Genoplante' (http://www.genoplante.com and
           http://genoplante-info.infobiogen.fr).
EATURES              Location/Qualifiers
     source          1. .115
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="052B02"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Wassilewskija"
     misc_feature    1. .115
                     /note="T-DNA flanking sequence
                     left border"
RIGIN

lignment Scores:
red. No.:              83.8           Length:        115
core:                  9.00           Matches:       9
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            2.9%           Indels:        0
B:                     14             Gaps:          0

S-10-821-670A-27 (1-307) x ATH521069 (1-115)

y        217 ProLysAsnLeuGlnLeuLysProLeu 225
             |||||||||||||||||||||||||||
o         59 CCCAAAAATTTACAATTAAAACCCTTA 33

ESULT 37
Q356685
OCUS       BQ356685               263 bp    mRNA    linear   EST 20-MAY-2002
EFINITION  PM0-HT0335-050400-007-G05 HT0335 Homo sapiens cDNA, mRNA sequence.
CCESSION   BQ356685
VERSION    BQ356685.1  GI:21021850
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE  1  (bases 1 to 263)
  AUTHORS  Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
           Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
           Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
           Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
           O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
           Simpson,A.J.
  TITLE    Shotgun sequencing of the human transcriptome with ORF expressed
           sequence tags
  JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED  10737800
COMMENT    Contact: Simpson A.J.G.
           Laboratory of Cancer Genetics
           Ludwig Institute for Cancer Research
           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           Project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-HT0335-
           050400-007-G05&t3=2000-04-05&t4=1)
           Seq primer: puc 18 forward
           High quality sequence start: 31
           High quality sequence stop: 69.
FEATURES             Location/Qualifiers
     source          1. .263
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0335"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:             173            Length:        263
Score:                 9.00           Matches:       9
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           2.9%           Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-27 (1-307) x BQ356685 (1-263)

Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||
Db         160 TTTTTACTGATTCACAAAAAGGAAGAC 186

RESULT 38
BY024612
LOCUS      BY024612               353 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION BY024612 RIKEN full-length enriched, mammary gland RCB-0527
           Jyg-MC(B) cDNA Mus musculus cDNA clone G930023O12 5', mRNA
           sequence.
ACCESSION  BY024612
VERSION    BY024612.1  GI:26130055
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
EFERENCE 1 (bases 1 to 353)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
OMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
EATURES Location/Qualifiers
source 1. .353
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="G930023O12"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
/clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
ORIGIN

Alignment Scores:

Pred. No.:	223	Length:	353
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.9%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-27 (1-307) x BY024612 (1-353)

```
Qy        243 ThrProHisSerTyrPheSerLeuThr 251
              |||||||||||||||||||||||||
Db         83 ACCCCTCATTCCTACTTCTCCCTCACC 109
```

RESULT 39
BY024263
LOCUS BY024263 354 bp mRNA linear EST 06-DEC-2002
DEFINITION BY024263 RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA Mus musculus cDNA clone G930022C19 5', mRNA sequence.
ACCESSION BY024263
VERSION BY024263.1 GI:26129706
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 354)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222

```
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
EATURES             Location/Qualifiers
    source          1. .354
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="G930022C19"
                    /tissue_type="mammary gland"
                    /cell_line="RCB-0527 Jyg-MC(B)"
                    /clone_lib="RIKEN full-length enriched, mammary gland
                    RCB-0527 Jyg-MC(B) cDNA"
RIGIN

lignment Scores:
red. No.:              224            Length:        354
core:                  9.00           Matches:       9
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            2.9%           Indels:        0
B:                     4              Gaps:          0

S-10-821-670A-27 (1-307) x BY024263 (1-354)

y        243 ThrProHisSerTyrPheSerLeuThr 251
             |||||||||||||||||||||||||||
b         83 ACCCCTCATTCCTACTTCTCCCTCACC 109

ESULT 40
Y013557
OCUS        BY013557                355 bp    mRNA    linear   EST 06-DEC-2002
EFINITION   BY013557 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus
            musculus cDNA clone G730040C02 5', mRNA sequence.
CCESSION    BY013557
ERSION      BY013557.1  GI:26073806
EYWORDS     EST.
OURCE       Mus musculus (house mouse)
 ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
EFERENCE    1  (bases 1 to 355)
 AUTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES            Location/Qualifiers
    source          1. .355
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="G730040C02"
                    /tissue_type="lung"
                    /cell_line="RCB-0558 LLC"
                    /clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
                    cDNA"
ORIGIN

Alignment Scores:
Pred. No.:              224            Length:        355
Score:                  9.00           Matches:       9
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
```

```
)uery Match:            2.9%          Indels:        0
)B:                     4             Gaps:          0

)S-10-821-670A-27 (1-307) x BY013557 (1-355)

)y        243 ThrProHisSerTyrPheSerLeuThr 251
              |||||||||||||||||||||||||
)b         82 ACCCCTCATTCCTACTTCTCCCTCACC 108

:ESULT 41
/00972
)OCUS       W00972                 361 bp    mRNA    linear   EST 18-APR-1996
)EFINITION  za55d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:296461 5' similar to contains element L1 repetitive element
            ;, mRNA sequence.
)CCESSION   W00972
'ERSION     W00972.1  GI:1272951
:EYWORDS    EST.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 361)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
:OMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 217.
'EATURES             Location/Qualifiers
     source          1. .361
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1241382"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:296461"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
)RIGIN

.lignment Scores:
'red. No.:              228           Length:        361
;core:                  9.00          Matches:       9
'ercent Similarity:     100.0%        Conservative:  0
)est Local Similarity:  100.0%        Mismatches:    0
)uery Match:            2.9%          Indels:        0
)B:                     10            Gaps:          0

)S-10-821-670A-27 (1-307) x W00972 (1-361)

Qy         79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||
Db        118 TTTTTACTGATTCACAAAAAGGAAGAC 144

RESULT 42
BY204279
LOCUS       BY204279                382 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY204279 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730212J07 5', mRNA sequence.
ACCESSION   BY204279
VERSION     BY204279.1  GI:26384080
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 382)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
```

```
          nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
           cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
           Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
          Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
          Trust/MRC building Addenbrookes Hospital Cambridge) whose
          assistance we gratefully acknowledge.
           Please visit our web site (http://genome.gsc.riken.go.jp) for
          further details.
EATURES             Location/Qualifiers
    source          1. .382
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="F730212J07"
                    /cell_type="B6-derived CD11 +ve dendritic cells"
                    /clone_lib="RIKEN full-length enriched, B6-derived CD11
                    +ve dendritic cells"
RIGIN

lignment Scores:
red. No.:              239           Length:        382
core:                  9.00          Matches:       9
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            2.9%          Indels:        0
B:                     4             Gaps:          0

S-10-821-670A-27 (1-307) x BY204279 (1-382)

y        243 ThrProHisSerTyrPheSerLeuThr 251
             |||||||||||||||||||||||||||
b         76 ACCCCTCATTCCTACTTCTCCCTCACC 102

ESULT 43
Y183786
OCUS        BY183786                409 bp    mRNA    linear   EST 10-DEC-2002
EFINITION   BY183786 RIKEN full-length enriched, NOD-derived CD11c +ve
            dendritic cells Mus musculus cDNA clone F630110G11 5', mRNA
            sequence.
CCESSION    BY183786
ERSION      BY183786.1  GI:26320432
EYWORDS     EST.
OURCE       Mus musculus (house mouse)
 ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
EFERENCE    1  (bases 1 to 409)
 AUTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES            Location/Qualifiers
     source         1. .409
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="NOD"
                    /db_xref="taxon:10090"
                    /clone="F630110G11"
                    /cell_type="NOD-derived CD11c +ve dendritic cells"
                    /clone_lib="RIKEN full-length enriched, NOD-derived CD11c
                    +ve dendritic cells"
ORIGIN

Alignment Scores:
Pred. No.:              254           Length:        409
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.9%          Indels:        0
DB:                     4             Gaps:          0

US-10-821-670A-27 (1-307) x BY183786 (1-409)

Qy         243 ThrProHisSerTyrPheSerLeuThr 251
               |||||||||||||||||||||||||||
Db          82 ACCCCTCATTCCTACTTCTCCCTCACC 108
```

```
:ESULT 44
\Q305003/c
\OCUS       AQ305003                 415 bp    DNA     linear   GSS 16-DEC-1998
)EFINITION  HS_2012_A1_E07_T7 CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2012 Col=13 Row=I, genomic survey
            sequence.
\CCESSION   AQ305003
'ERSION     AQ305003.1  GI:4024789
:EYWORDS    GSS.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 415)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
    PUBMED  10449764
:OMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 2012  row: I  column: 13
            Class: BAC ends
            High quality sequence stop: 415.
'EATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=2012 Col=13 Row=I"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
)RIGIN

\lignment Scores:
'red. No.:                257            Length:         415
:core:                    9.00           Matches:        9
'ercent Similarity:       100.0%         Conservative:   0
'est Local Similarity:    100.0%         Mismatches:     0
)uery Match:              2.9%           Indels:         0
)B:                       11             Gaps:           0

'S-10-821-670A-27 (1-307) x AQ305003 (1-415)

)y          87 AspGlyIleTrpSerThrAspIleLeu 95
               |||||||||||||||||||||||||||
)b         249 GACGGTATTTGGTCAACCGATATTCTT 223

:ESULT 45
\W382621/c
\OCUS       AW382621                 423 bp    mRNA    linear   EST 04-FEB-2000
)EFINITION  PM0-HT0335-171199-002-f07 HT0335 Homo sapiens cDNA, mRNA sequence.
\CCESSION   AW382621
'ERSION     AW382621.1  GI:6887280
:EYWORDS    EST.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 423)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
:OMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-HT0335-
            171199-002-f07&t3=1999-11-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 151.
'EATURES             Location/Qualifiers
     source          1. .423
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0335"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
)RIGIN

\lignment Scores:
'red. No.:                262            Length:         423
:core:                    9.00           Matches:        9
'ercent Similarity:       100.0%         Conservative:   0
'est Local Similarity:    100.0%         Mismatches:     0
)uery Match:              2.9%           Indels:         0
)B:                       7              Gaps:           0

'S-10-821-670A-27 (1-307) x AW382621 (1-423)

)y          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
)b         271 TTTTTACTGATTCACAAAAAGGAAGAC 245

:ESULT 46
\E153120/c
\OCUS       BE153120                 435 bp    mRNA    linear   EST 21-JUN-2000
)EFINITION  PM0-HT0335-060300-006-h01 HT0335 Homo sapiens cDNA, mRNA sequence.
\CCESSION   BE153120
'ERSION     BE153120.1  GI:8615841
:EYWORDS    EST.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 435)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
    PUBMED  10737800
:OMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
```

```
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM0-HT0335-060
          300-006-h01&t3=2000-03-06&t4=1)
          Seq primer: puc 18 forward
          High quality sequence start: 6
          High quality sequence stop: 435.
EATURES             Location/Qualifiers
    source          1. .435
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /dev_stage="Adult"
                    /clone_lib="HT0335"
                    /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                    Site_2: SmaI; A mini-library was made by cloning products
                    derived from  ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 -  Ludwig Institute for Cancer Research)
                    profiles into  the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
RIGIN

lignment Scores:
red. No.:              268          Length:        435
core:                  9.00         Matches:       9
ercent Similarity:     100.0%       Conservative:  0
est Local Similarity:  100.0%       Mismatches:    0
uery Match:            2.9%         Indels:        0
B:                     7            Gaps:          0

S-10-821-670A-27 (1-307) x BE153120 (1-435)

y          79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||
b         283 TTTTTACTGATTCACAAAAAGGAAGAC 257

ESULT 47
I330861/c
OCUS        CI330861                442 bp    mRNA    linear   EST 07-FEB-2006
EFINITION   CI330861 Oryza sativa (japonica cultivar-group) shoot Oryza sativa
            (japonica cultivar-group) cDNA clone J01B3122J01M3 3', mRNA
            sequence.
CCESSION    CI330861
ERSION      CI330861.1  GI:86865330
EYWORDS     EST.
OURCE       Oryza sativa (japonica cultivar-group)
 ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
EFERENCE    1  (bases 1 to 442)
 AUTHORS    Kikuchi,S.
 TITLE      Collection and mapping of over 30,000 transcription units by the
            rice full- length cDNA project from japonica rice
 JOURNAL    Unpublished (2006)
OMMENT      Contact: Shoshi Kikuchi
            Department of Molecular Genetics, Head of Laboratory of Gene
            Expression
            National Institute of Agrobiological Sciences
            2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
            Tel: 81-29-838-7007
            Fax: 81-29-838-7007
            Email: skikuchi@nias.affrc.go.jp
            This EST clone is one of 780k ESTs of Rice full length cDNA Project
            URL:http://cdna01.dna.affrc.go.jp/cDNA/
            NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
            Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
            Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
            Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
            Yamamoto,M. and Nakahama,Y.
            FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
            Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
            Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
            Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
            Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
            Yoshimura,A., Matsubara,K. and Murakami,K.
            Genome Exploration Research Group in Riken Genomic Sciences Center
            and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
            Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
            Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
            Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
            Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
            Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
            Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
            Yasunishi,A. and Hayashizaki,Y.
FEATURES             Location/Qualifiers
     source          1. .442
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="J01B3122J01M3"
                     /tissue_type="shoot"
                     /clone_lib="Oryza sativa (japonica cultivar-group) shoot"
ORIGIN

Alignment Scores:
Pred. No.:              272          Length:        442
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.9%         Indels:        0
DB:                     5            Gaps:          0

US-10-821-670A-27 (1-307) x CI330861 (1-442)

Qy         262 ArgGluLysLysAspArgLeuSerVal 270
               |||||||||||||||||||||||||||
Db         166 AGAGAAAAGAAGGATCGCCTGTCAGTG 140

RESULT 48
BE677126/c
LOCUS       BE677126                442 bp    mRNA    linear   EST 08-SEP-2000
DEFINITION  7d80f03.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone
            IMAGE:3279293 3' similar to contains Alu repetitive
            element;contains element MER14 repetitive element ;, mRNA sequence.
ACCESSION   BE677126
VERSION     BE677126.1  GI:10037667
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lupski
             cDNA Library Preparation: Lupski Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
```

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 410.

'EATURES Location/Qualifiers
source 1. .442
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3279293"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

)RIGIN

Alignment Scores:

'red. No.:	272	Length:	442
core:	9.00	Matches:	9
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.9%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-27 (1-307) x BE677126 (1-442)

)y 79 PheLeuLeuIleHisLysLysGluAsp 87
||||||||||||||||||||||||||
)b 405 TTTTTACTGATTCACAAAAAGGAAGAC 379

ESULT 49
U143811/c
OCUS AU143811 463 bp mRNA linear EST 05-AUG-2002
)EFINITION AU143811 HEMBA1 Homo sapiens cDNA clone HEMBA1000076 3', mRNA sequence.
CCESSION AU143811
'ERSION AU143811.1 GI:11005332
EYWORDS EST.
OURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
EFERENCE 1 (bases 1 to 463)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
OMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES Location/Qualifiers
source 1. .463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1000076"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBA1"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.:	283	Length:	463
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.9%	Indels:	0
DB:	1	Gaps:	0

US-10-821-670A-27 (1-307) x AU143811 (1-463)

Qy 79 PheLeuLeuIleHisLysLysGluAsp 87
||||||||||||||||||||||||||
Db 400 TTTTTACTGATTCACAAAAAGGAAGAC 374

RESULT 50
AI754066/c
LOCUS AI754066 477 bp mRNA linear EST 20-JUN-2002
DEFINITION cr19c06.x1 Human bone marrow stromal cells Homo sapiens cDNA clone HBMSC_cr19c06 3', mRNA sequence.
ACCESSION AI754066
VERSION AI754066.1 GI:5132330
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 477)
AUTHORS Jia,L., Young,M.F., Powell,J., Yang,L., Ho,N.C., Hotchkiss,R., Robey,P.G. and Francomano,C.A.
TITLE Gene expression profile of human bone marrow stromal cells: high-throughput expressed sequence tag sequencing analysis
JOURNAL Genomics 79 (1), 7-17 (2002)
PUBMED 11827452
COMMENT Contact: Libin Jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).
Plate: 19 row: c column: 06
Seq primer: -21M13 forward primer (ABI).

FEATURES Location/Qualifiers
source 1. .477
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HBMSC_cr19c06"
/sex="mixed"
/tissue_type="bone marrow stroma"
/dev_stage="mixed"
/lab_host="XL1-Blue MRF'/SOLR"
/clone_lib="Human bone marrow stromal cells"

/note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI; mRNA made from human bone marrow stroma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected for average insert size >0.5 kb. Library constructed by Dr. Marian Young and Dr. Pamela Gehron Robey (NIDCR). Library supplied by Dr. Libin Jia (NHGRI)"

RIGIN

lignment Scores:

red. No.:	291	Length:	477
core:	9.00	Matches:	9
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.9%	Indels:	0
B:	1	Gaps:	0

S-10-821-670A-27 (1-307) x AI754066 (1-477)

```
y         79 PheLeuLeuIleHisLysLysGluAsp 87
             |||||||||||||||||||||||||||
o        418 TTTTTACTGATTCACAAAAAGGAAGAC 392
```

ESULT 51
I683279
OCUS AI683279 479 bp mRNA linear EST 26-MAY-1999
EFINITION tw50a03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2263084 3', mRNA sequence.
CCESSION AI683279
ERSION AI683279.1 GI:4893461
EYWORDS EST.
OURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
EFERENCE 1 (bases 1 to 479)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
OMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 415.
EATURES Location/Qualifiers
source 1. .479
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2263084"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

RIGIN

lignment Scores:

red. No.:	292	Length:	479
core:	9.00	Matches:	9
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.9%	Indels:	0
DB:	1	Gaps:	0

US-10-821-670A-27 (1-307) x AI683279 (1-479)

```
Qy         79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||
Db        451 TTTTTACTGATTCACAAAAAGGAAGAC 477
```

RESULT 52
CA699592
LOCUS CA699592 479 bp mRNA linear EST 26-NOV-2002
DEFINITION wlk8.pk0021.d7 wlk8 Triticum aestivum cDNA clone wlk8.pk0021.d7 5' end, mRNA sequence.
ACCESSION CA699592
VERSION CA699592.1 GI:25421385
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 479)
AUTHORS Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
TITLE DuPont Wheat cDNA Sequence
JOURNAL Unpublished (2002)
COMMENT Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
FEATURES Location/Qualifiers
source 1. .479
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Stephens"
/db_xref="taxon:4565"
/clone="wlk8.pk0021.d7"
/tissue_type="leaf"
/clone_lib="wlk8"
/note="Vector: pGEM-7; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum L.) seedlings 8 hr after treatment with 6-iodo-3-propyl-2-propyloxy-4(3H)-quinazolinone"
ORIGIN

Alignment Scores:

Pred. No.:	292	Length:	479
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.9%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-27 (1-307) x CA699592 (1-479)

```
Qy        217 ProLysAsnLeuGlnLeuLysProLeu 225
              |||||||||||||||||||||||||
Db        394 CCCAAGAATCTTCAACTCAAGCCGTTA 420
```

RESULT 53
BI325004/c
LOCUS BI325004 494 bp mRNA linear EST 30-JUL-2001
DEFINITION ic21a08.x2 HR85 islet Homo sapiens cDNA 3', mRNA sequence.
ACCESSION BI325004
VERSION BI325004.1 GI:15004190
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 494)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
:OMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Seq primer: -40UP from Gibco
            High quality sequence stop: 455.
'EATURES             Location/Qualifiers
     source          1. .494
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
)RIGIN

\lignment Scores:
'red. No.:                 300             Length:         494
;core:                     9.00            Matches:        9
'ercent Similarity:        100.0%          Conservative:   0
)est Local Similarity:     100.0%          Mismatches:     0
)uery Match:               2.9%            Indels:         0
)B:                        2               Gaps:           0

!S-10-821-670A-27 (1-307) x BI325004 (1-494)

)y          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
)b         400 TTTTTACTGATTCACAAAAAGGAAGAC 374

!ESULT 54
\Q300559
\OCUS       AQ300559                500 bp    DNA     linear   GSS 16-DEC-1998
)EFINITION  HS_3175_B1_B09_T7 CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3175 Col=17 Row=D, genomic survey
            sequence.
\CCESSION   AQ300559
'ERSION     AQ300559.1  GI:4020236
:EYWORDS    GSS.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 500)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3175  row: D  column: 17
            Class: BAC ends
            High quality sequence stop: 500.
FEATURES             Location/Qualifiers
     source          1. .500
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=3175 Col=17 Row=D"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

Alignment Scores:
Pred. No.:                 303             Length:         500
Score:                     9.00            Matches:        9
Percent Similarity:        100.0%          Conservative:   0
Best Local Similarity:     100.0%          Mismatches:     0
Query Match:               2.9%            Indels:         0
DB:                        11              Gaps:           0

US-10-821-670A-27 (1-307) x AQ300559 (1-500)

Qy          72 GlyGluValLeuSerHisSerPheLeu 80
               |||||||||||||||||||||||||||
Db         278 GGGGAGGTCCTGAGTCACTCCTTCTTA 304

RESULT 55
BM090808/c
LOCUS       BM090808                504 bp    mRNA    linear   EST 20-NOV-2001
DEFINITION  ig15e03.x1 Human Fetal Pancreas 1A Homo sapiens cDNA 3', mRNA
            sequence.
ACCESSION   BM090808
VERSION     BM090808.1  GI:17019774
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: ig15e03.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
```

```
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@imgate.wustl.edu)
            High quality sequence stop: 447.
EATURES             Location/Qualifiers
     source         1. .504
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /tissue_type="Fetal Pancreas (4 Pooled Donors, 18 - 20
                    weeks, Stratagene #738023)"
                    /dev_stage="Fetal Pancreas"
                    /clone_lib="Human Fetal Pancreas 1A"
                    /note="Vector: pBluescript SK(-); Site_1: NotI; Site_2:
                    XhoI; cDNA made by oligo-dT priming. Size-selected by
                    CHROMA SPIN-1000  (Clontech). Average insert size ~1kb. 5'
                    XhoI site was destroyed after directional cloning.
                    Amplified once.  Contact information: Hiroshi Inoue, MD,
                    Metabolism Div. (Alan Permutt Lab),  Washington University
                    School of Medicine, Box 8127, 660 South Euclid Ave., St.
                    Louis, MO 63110 E-mail: hinoue@imgate.wustl.edu Tel:
                    314-362-1916, Fax:314-747-2692."
RIGIN

lignment Scores:
red. No.:               305             Length:         504
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             2.9%            Indels:         0
B:                      2               Gaps:           0

S-10-821-670A-27 (1-307) x BM090808 (1-504)

y          79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||
o         400 TTTTTACTGATTCACAAAAAGGAAGAC 374

ESULT 56
M367597
OCUS        AW367597                507 bp    mRNA    linear   EST 04-FEB-2000
EFINITION   MR0-HT0164-151299-012-b02 HT0164 Homo sapiens cDNA, mRNA sequence.
CCESSION    AW367597
ERSION      AW367597.1  GI:6872247
EYWORDS     EST.
OURCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 507)
 AUTHORS    HCGP http://www.ludwig.org.br/ORESTES.
 TITLE      The FAPESP/LICR Human Cancer Genome Project
 JOURNAL    Unpublished (1999)
OMMENT      Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-HT0164-
            151299-012-b02&t3=1999-12-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 13
            High quality sequence stop: 95.
EATURES             Location/Qualifiers
```

```
     source         1. .507
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /dev_stage="Adult"
                    /clone_lib="HT0164"
                    /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                    Site_2: SmaI; A mini-library was made by cloning products
                    derived from  ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 -  Ludwig Institute for Cancer Research)
                    profiles into  the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              306             Length:         507
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.9%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-27 (1-307) x AW367597 (1-507)

Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
Db         106 TTTTTACTGATTCACAAAAAGGAAGAC 132

RESULT 57
AI554405/c
LOCUS       AI554405                510 bp    mRNA    linear   EST 13-MAY-1999
DEFINITION  tq11a12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2208478 3'
            similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION   AI554405
VERSION     AI554405.1  GI:4486768
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2025   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 404
            POLYA=No.
FEATURES            Location/Qualifiers
     source         1. .510
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2208478"
                    /tissue_type="poorly-differentiated endometrial
                    adenocarcinoma, 2 pooled tumors"
                    /lab_host="DH10B"
                    /clone_lib="NCI_CGAP_Ut3"
                    /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                    Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
```

```
                Average insert size 1.45 kb. Life Technologies catalog #:
                11541-018"
)RIGIN

\lignment Scores:
'zed. No.:              308             Length:         510
;core:                  9.00            Matches:        9
'ercent Similarity:     100.0%          Conservative:   0
!est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            2.9%            Indels:         0
)B:                     1               Gaps:           0

IS-10-821-670A-27 (1-307) x AI554405 (1-510)

)y          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
)b         403 TTTTTACTGATTCACAAAAAGGAAGAC 377

:ESULT 58
\V706519/c
;OCUS       AV706519                516 bp    mRNA    linear   EST 09-OCT-2000
)EFINITION  AV706519 ADB Homo sapiens cDNA clone ADBAVE10 5', mRNA sequence.
\CCESSION   AV706519
'ERSION     AV706519.1  GI:10723798
:EYWORDS    EST.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 516)
  AUTHORS   Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G.,
            Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z.,
            Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S.,
            Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
  TITLE     Homo sapiens cDNA ADB clones
  JOURNAL   Unpublished (2000)
:OMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
'EATURES             Location/Qualifiers
     source          1. .516
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ADBAVE10"
                     /tissue_type="Adrenal gland"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="ADB"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
)RIGIN

\lignment Scores:
'red. No.:              311             Length:         516
;core:                  9.00            Matches:        9
'ercent Similarity:     100.0%          Conservative:   0
!est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            2.9%            Indels:         0
)B:                     1               Gaps:           0

IS-10-821-670A-27 (1-307) x AV706519 (1-516)

)y          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
)b         143 TTTTTACTGATTCACAAAAAGGAAGAC 117
```

```
RESULT 59
DA098991/c
LOCUS       DA098991                546 bp    mRNA    linear   EST 02-NOV-2005
DEFINITION  DA098991 BRACE3 Homo sapiens cDNA clone BRACE3010218 5', mRNA
            sequence.
ACCESSION   DA098991
VERSION     DA098991.1  GI:78757572
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 546)
  AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE     Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
  PUBMED    16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES             Location/Qualifiers
     source          1. .546
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="BRACE3010218"
                     /tissue_type="cerebellum"
                     /clone_lib="BRACE3"
                     /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              327             Length:         546
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.9%            Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x DA098991 (1-546)

Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
Db          98 TTTTTACTGATTCACAAAAAGGAAGAC 72

RESULT 60
DB284546/c
LOCUS       DB284546                553 bp    mRNA    linear   EST 10-DEC-2005
DEFINITION  DB284546 UTERU3 Homo sapiens cDNA clone UTERU3012510 5', mRNA
            sequence.
ACCESSION   DB284546
VERSION     DB284546.1  GI:83439601
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 553)
 AUTHORS    Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE      Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
 JOURNAL    Genome Res. 16 (1), 55-65 (2006)
  PUBMED    16344560
OMMENT      Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
EATURES             Location/Qualifiers
     source         1. .553
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UTERU3012510"
                    /tissue_type="uterus"
                    /clone_lib="UTERU3"
                    /note="Vector: pME18SFL3"
RIGIN

lignment Scores:
red. No.:               331             Length:         553
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             2.9%            Indels:         0
B:                      9               Gaps:           0

S-10-821-670A-27 (1-307) x DB284546 (1-553)

y          79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||
b         483 TTTTTACTGATTCACAAAAAGGAAGAC 457

ESULT 61
A102042/c
OCUS        DA102042                561 bp    mRNA    linear   EST 01-NOV-2005
EFINITION   DA102042 BRACE3 Homo sapiens cDNA clone BRACE3014468 5', mRNA
            sequence.
CCESSION    DA102042
ERSION      DA102042.1  GI:78562825
EYWORDS     EST.
OURCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 561)
 AUTHORS    Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE      Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
 JOURNAL    Genome Res. 16 (1), 55-65 (2006)
  PUBMED    16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES            Location/Qualifiers
     source         1. .561
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="BRACE3014468"
                    /tissue_type="cerebellum"
                    /clone_lib="BRACE3"
                    /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:              335             Length:         561
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.9%            Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x DA102042 (1-561)

Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
Db         459 TTTTTACTGATTCACAAAAAGGAAGAC 433

RESULT 62
CW054731
LOCUS       CW054731                563 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  104_295_10516691_115_30176 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10516691, genomic survey
            sequence.
ACCESSION   CW054731
VERSION     CW054731.1  GI:54731461
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 295  row: k  column: 09
```

```
          Seq primer: M13/pUC Reverse
          Class: methylation filtered
          High quality sequence stop: 563.
'EATURES             Location/Qualifiers
     source          1. .563
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10516691"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
)RIGIN

.lignment Scores:
'red. No.:                336            Length:         563
:core:                    9.00           Matches:        9
'ercent Similarity:       100.0%         Conservative:   0
iest Local Similarity:    100.0%         Mismatches:     0
)uery Match:              2.9%           Indels:         0
)B:                       13             Gaps:           0

'S-10-821-670A-27 (1-307) x CW054731 (1-563)

)y          99 LysGluSerLysAsnLysIlePheLeu 107
               |||||||||||||||||||||||||||
)b         533 AAAGAATCAAAGAACAAGATCTTCTTA 559

:ESULT 63
)B349096
)OCUS        DB349096                 566 bp    mRNA    linear   EST 04-DEC-2005
)EFINITION   DB349096 TRACH3 Homo sapiens cDNA clone TRACH3005200 3', mRNA
             sequence.
.CCESSION    DB349096
'ERSION      DB349096.1  GI:83258035
:EYWORDS     EST.
:OURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
:EFERENCE    1  (bases 1 to 566)
  AUTHORS    Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
             Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
             Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
             Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
             Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
             Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
  TITLE      Diversification of Transcriptional Modulation: Large-scale
             Identification and Characterization of Putative Alternative
             Promoters of Human Genes
  JOURNAL    Genome Res. 16 (1), 55-65 (2006)
    PUBMED   16344560
:OMMENT      Contact: Takao Isogai
             FLJ Project (HRI Team)
             Helix Research Institute
             2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
             Tel: 81-438-52-3975
             Fax: 81-438-52-3986
             Email: flj-cdna@nifty.com
             NEDO human cDNA project (New Energy and Industrial Technology
             Developmental Organization, Japan); cDNA library construction:
             Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
             Research Association for Biotechnology (RAB) and Biotechnology
             Center, National Institute of Technology and Evaluation; 3'-end one
             pass sequencing: RAB.
'EATURES             Location/Qualifiers
     source          1. .566
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="TRACH3005200"
                     /tissue_type="trachea"
                     /clone_lib="TRACH3"
                     /note="Vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.:                337            Length:         566
Score:                    9.00           Matches:        9
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              2.9%           Indels:         0
DB:                       9              Gaps:           0

US-10-821-670A-27 (1-307) x DB349096 (1-566)

Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
Db         393 TTTTTACTGATTCACAAAAAGGAAGAC 419

RESULT 64
BM907722
LOCUS        BM907722                 572 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION   AGENCOURT_6618905 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5736102
             5', mRNA sequence.
ACCESSION    BM907722
VERSION      BM907722.1  GI:19358101
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 572)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: DCTD/DTP/Gazdar
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM12744  row: b  column: 07
             High quality sequence stop: 572.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5736102"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

Alignment Scores:
Pred. No.:                340            Length:         572
Score:                    9.00           Matches:        9
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              2.9%           Indels:         0
```

```
B:                    3             Gaps:          0

S-10-821-670A-27 (1-307) x BM907722 (1-572)

y         79 PheLeuLeuIleHisLysLysGluAsp 87
             |||||||||||||||||||||||||||
o        156 TTTTTACTGATTCACAAAAAGGAAGAC 182

ESULT 65
K818181/c
OCUS       CK818181                593 bp    mRNA    linear   EST 11-MAR-2004
EFINITION  ic21a08.y5 HR85 islet Homo sapiens cDNA clone IMAGE: 5', mRNA
           sequence.
CCESSION   CK818181
ERSION     CK818181.1  GI:44835106
EYWORDS    EST.
OURCE      Homo sapiens (human)
 ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
EFERENCE   1  (bases 1 to 593)
 AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
           Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
           Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
           McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
           Bowers,Y.
 TITLE     WashU-Harvard Pancreas EST Project
 JOURNAL   Unpublished (2000)
OMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
           Endocrine Pancreas Consortium
           Harvard University, Howard Hughes Medical Institute
           Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
           MA 02138
           Tel: 617-495-1812
           Fax: 617-495-8557
           Email: dmelton@biohp.harvard.edu
           This read is a 5' RESEQUENCE of a previously sequenced pancreas
           clone
           Good hit to opposite strand read. . .wrong orientation BUT PASSED FOR
           MOUSE-PANCREAS VERIFICATION
           Seq primer: -40UP from Gibco.
EATURES              Location/Qualifiers
    source           1. .593
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
RIGIN

lignment Scores:
red. No.:              351           Length:        593
core:                  9.00          Matches:       9
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            2.9%          Indels:        0
B:                     5             Gaps:          0

S-10-821-670A-27 (1-307) x CK818181 (1-593)

y         79 PheLeuLeuIleHisLysLysGluAsp 87
             |||||||||||||||||||||||||||
Db       408 TTTTTACTGATTCACAAAAAGGAAGAC 382

RESULT 66
CW136151/c
LOCUS       CW136151                624 bp    DNA     linear   GSS 29-OCT-2004
DEFINITION  104_521_11118228_148_34843_048 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 11118228, genomic survey
            sequence.
ACCESSION   CW136151
VERSION     CW136151.1  GI:54828698
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 624)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 521  row: b  column: 12
            Seq primer: SWfor Forward
            Class: methylation filtered
            High quality sequence stop: 624.
FEATURES             Location/Qualifiers
     source          1. .624
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="11118228"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:              367           Length:        624
Score:                  9.00          Matches:       9
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            2.9%          Indels:        0
DB:                     13            Gaps:          0

US-10-821-670A-27 (1-307) x CW136151 (1-624)

Qy         99 LysGluSerLysAsnLysIlePheLeu 107
              |||||||||||||||||||||||||
Db        324 AAAGAATCAAAGAACAAGATCTTCTTA 298

RESULT 67
CN207623
LOCUS       CN207623                628 bp    mRNA    linear   EST 30-APR-2004
DEFINITION  Tor8042 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
            sequence.
ACCESSION   CN207623
```

```
'ERSION     CN207623.1  GI:46904354
:EYWORDS    EST.
:OURCE      Tortula ruralis
  ORGANISM  Tortula ruralis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
            Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
:EFERENCE   1  (bases 1 to 628)
  AUTHORS   Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
  TITLE     The rehydration transcriptome of the desiccation-tolerant bryophyte
            Tortula ruralis: transcript classification and analysis
  JOURNAL   BMC Genomics 5 (1), 89 (2004)
    PUBMED  15546486
:OMMENT     Contact: Oliver Melvin J
            Plant Stress Lab
            USDA-ARS
            3810 4th St, Lubbock, TX 79415, USA
            Tel: 806-749-5560
            Fax: 806-723-5272
            Email: moliver@lbk.ars.usda.gov
            PCR PRimers
            FORWARD: GTTTTCCCAGTCACGAC
            BACKWARD: CAGGAAACAGCTATGAC.
'EATURES             Location/Qualifiers
     source          1. .628
                     /organism="Tortula ruralis"
                     /mol_type="mRNA"
                     /db_xref="taxon:38588"
                     /clone_lib="Gametophyte rehydration Library"
                     /note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
                     SalI; Site_2: NotI"
)RIGIN

.lignment Scores:
'red. No.:                 369             Length:         628
:core:                     9.00            Matches:        9
'ercent Similarity:        100.0%          Conservative:   0
!est Local Similarity:     100.0%          Mismatches:     0
)uery Match:               2.9%            Indels:         0
)B:                        8               Gaps:           0

!S-10-821-670A-27 (1-307) x CN207623 (1-628)

)y        145 GluValThrCysGlyAlaAlaThrLeu 153
              |||||||||||||||||||||||||||
)b        601 GAGGTGACATGTGGGGCGGCCACACTN 627

:ESULT 68
:W136150
:OCUS       CW136150                638 bp    DNA     linear   GSS 29-OCT-2004
)EFINITION  104_521_11118228_116_34847_048 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 11118228, genomic survey
            sequence.
:CCESSION   CW136150
'ERSION     CW136150.1  GI:54828697
:EYWORDS    GSS.
:OURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
:EFERENCE   1  (bases 1 to 638)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
    PUBMED  15660154
:OMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 521  row: b  column: 12
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 638.
FEATURES             Location/Qualifiers
     source          1. .638
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="11118228"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

Alignment Scores:
Pred. No.:                 375             Length:         638
Score:                     9.00            Matches:        9
Percent Similarity:        100.0%          Conservative:   0
Best Local Similarity:     100.0%          Mismatches:     0
Query Match:               2.9%            Indels:         0
DB:                        13              Gaps:           0

US-10-821-670A-27 (1-307) x CW136150 (1-638)

Qy         99 LysGluSerLysAsnLysIlePheLeu 107
              |||||||||||||||||||||||||||
Db        525 AAAGAATCAAAGAACAAGATCTTCTTA 551

RESULT 69
CL344654
LOCUS       CL344654                645 bp    DNA     linear   GSS 19-AUG-2004
DEFINITION  RPCI44_278P18.r RPCI-44 Sus scrofa genomic clone RPCI44_278P18,
            genomic survey sequence.
ACCESSION   CL344654
VERSION     CL344654.1  GI:51396622
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 645)
  AUTHORS   Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
            Beever,J.E. and Schook,L.B.
  TITLE     Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
            Through Comparative Genomics
  JOURNAL   Unpublished (2004)
COMMENT     Other_GSSs: RPCI44_278P18.f
            Contact: Lawrence B. Schook
            Department of Animal Sciences
            University of Illinois at Urbana Champaign
            1201 W. Gregory Dr., Urbana, IL 61801, USA
            Tel: 217 265 5326
            Fax: 217 244 5617
            Email: schook@uiuc.edu
            Clones are derived from the porcine BAC library RPCI-44
            (http://www.bacpac.chori.org/porcine242.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@chori.org).
            Clones may be purchased from BACPAC Resources
            (http://BACPACorders.chori.org). This work was undertaken as part
            of the International Swine Genome Sequencing Consortium by
            University of Illinois at Urbana Champaign, USA with funds provided
            by grant No. AG2002-34480-11828 from USDA-CSREES and
            AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
```

```
          Initiative)
          Plate: 278  row: P  column: 18
          Seq primer: SP6
          Class: BAC ends.
EATURES             Location/Qualifiers
    source          1. .645
                    /organism="Sus scrofa"
                    /mol_type="genomic DNA"
                    /strain="four pigs (breed: 37.5% Yorks Landrace and 25%
                    Meishan)"
                    /db_xref="taxon:9823"
                    /clone="RPCI44_278P18"
                    /sex="male"
                    /cell_type="blood"
                    /clone_lib="RPCI-44"
                    /note="Vector: pTARBAC2; Site_1: EcoRI; Site_2: EcoRI;
                    porcine male BAC library produced by Pieter de Jong"
RIGIN

lignment Scores:
red. No.:               378             Length:         645
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             2.9%            Indels:         0
B:                      13              Gaps:           0

S-10-821-670A-27 (1-307) x CL344654 (1-645)

Y         252 PheGlyValGlnValGlnGlyLysAsn 260
              |||||||||||||||||||||||||||
          29 TTTGGTGTTCAGGTTCAGGGCAAGAAC 55

ESULT 70
T874689/c
OCUS        DT874689                 648 bp    mRNA    linear   EST 18-SEP-2005
EFINITION   AGENCOURT_58684019 NIH_ZGC_5 Danio rerio cDNA clone IMAGE:8101578
            5', mRNA sequence.
CCESSION    DT874689
ERSION      DT874689.1  GI:75844429
EYWORDS     EST.
OURCE       Danio rerio (zebrafish)
 ORGANISM   Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
EFERENCE    1  (bases 1 to 648)
 AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
 TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL    Unpublished (1999)
OMMENT      Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: John Postlethwait, University of Oregon
             cDNA Library Preparation: Dr. Sumio Sugano
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM17510  row: o  column: 16
            High quality sequence start: 8
            High quality sequence stop: 559.
EATURES             Location/Qualifiers
    source          1. .648
                    /organism="Danio rerio"
                    /mol_type="mRNA"
                    /db_xref="taxon:7955"
                    /clone="IMAGE:8101578"
                    /tissue_type="contains eggs from one female, from all
                    stages of development as well as support cells"
                    /lab_host="DH10B TonA"
                    /clone_lib="NIH_ZGC_5"
                    /note="Organ: ovary; Vector: pME18S-FL3; Site_1: DraIII;
                    Site_2: DraIII; 1st strand cDNA was primed with an
                    oligo(dT) primer
                    [GCGGCTGAAGACGGCCTATGTGGCCTTTTTTTTTTTTTTTT];
                    double-stranded cDNA was ligated to a DraIII adaptor
                    [GGCCUACUGG], digested and directionally cloned into
                    distinct DraIII sites of the pME18S-FL3. Library was size
                    selected for 1.0 kb, with a average insert size of ~1.2kb.
                    Library constructed by Yutaka Suzuki (University of Tokyo
                    Institute of Medical Science). Custom primers recommended
                    for sequencing: 5' end primer 5'-GGATGTTGCCTTTACTTCTA-3'
                    and 3' end primer 5'-CGACCTGCAGCTCGAGCACA-3'. Note: This
                    is a Zebrafish Gene Collection (ZGC) library"
ORIGIN

Alignment Scores:
Pred. No.:              380             Length:         648
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.9%            Indels:         0
DB:                     10              Gaps:           0

US-10-821-670A-27 (1-307) x DT874689 (1-648)

Qy        203 ThrSerSerPhePheIleArgAspIle 211
              |||||||||||||||||||||||||
Db         29 ACGTCCTCTTTCTTCATTCGCGACATC 3

RESULT 71
CW374083/c
LOCUS       CW374083                 649 bp    DNA     linear   GSS 01-NOV-2004
DEFINITION  fsbb001f050m06k0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f050m06, genomic survey
            sequence.
ACCESSION   CW374083
VERSION     CW374083.1  GI:55092527
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f050  row: m  column: 06
            Seq primer: k Reverse
            Class: methylation filtered
            High quality sequence stop: 649.
FEATURES            Location/Qualifiers
     source         1. .649
                    /organism="Sorghum bicolor"
                    /mol_type="genomic DNA"
                    /cultivar="ATx623"
                    /db_xref="taxon:4558"
                    /clone="fsbb001f050m06"
                    /clone_lib="Sorghum methylation filtered library (LibID:
                    104)"
```

/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Alignment Scores:

Pred. No.:	380	Length:	649
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.9%	Indels:	0
DB:	13	Gaps:	0

US-10-821-670A-27 (1-307) x CW374083 (1-649)

```
Qy         99 LysGluSerLysAsnLysIlePheLeu 107
              |||||||||||||||||||||||||||
Db        323 AAAGAATCAAAGAACAAGATCTTCTTA 297
```

RESULT 72
BG696339
LOCUS BG696339 650 bp mRNA linear EST 07-MAY-2001
DEFINITION 602658709F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4801803 5', mRNA sequence.
ACCESSION BG696339
VERSION BG696339.1 GI:13961382
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 650)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10695 row: a column: 04
High quality sequence stop: 650.

FEATURES Location/Qualifiers
source 1. .650
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4801803"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.:	381	Length:	650
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.9%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-27 (1-307) x BG696339 (1-650)

```
Qy         79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||
Db        372 TTTTTACTGATTCACAAAAAGGAAGAC 398
```

RESULT 73
CL344592
LOCUS CL344592 657 bp DNA linear GSS 19-AUG-2004
DEFINITION RPCI44_278D6.r RPCI-44 Sus scrofa genomic clone RPCI44_278D6, genomic survey sequence.
ACCESSION CL344592
VERSION CL344592.1 GI:51396560
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 657)
AUTHORS Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M., Beever,J.E. and Schook,L.B.
TITLE Piggy-BACing the Human Genome: Constructing a Porcine Physical Map Through Comparative Genomics
JOURNAL Unpublished (2004)
COMMENT Other_GSSs: RPCI44_278D6.f
Contact: Lawrence B. Schook
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 265 5326
Fax: 217 244 5617
Email: schook@uiuc.edu
Clones are derived from the porcine BAC library RPCI-44 (http://www.bacpac.chori.org/porcine242.htm). For BAC library availability, please contact Pieter de Jong (pdejong@chori.org). Clones may be purchased from BACPAC Resources (http://BACPACorders.chori.org). This work was undertaken as part of the International Swine Genome Sequencing Consortium by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG2002-34480-11828 from USDA-CSREES and AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing Initiative)
Plate: 278 row: D column: 6
Seq primer: SP6
Class: BAC ends.

FEATURES Location/Qualifiers
source 1. .657
/organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="four pigs (breed: 37.5% Yorks Landrace and 25% Meishan)"
/db_xref="taxon:9823"
/clone="RPCI44_278D6"
/sex="male"
/cell_type="blood"
/clone_lib="RPCI-44"
/note="Vector: pTARBAC2; Site_1: EcoRI; Site_2: EcoRI; porcine male BAC library produced by Pieter de Jong"

ORIGIN

Alignment Scores:

Pred. No.:	384	Length:	657
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.9%	Indels:	0
DB:	13	Gaps:	0

US-10-821-670A-27 (1-307) x CL344592 (1-657)

```
Qy        252 PheGlyValGlnValGlnGlyLysAsn 260
              |||||||||||||||||||||||||||
Db         27 TTTGGTGTTCAGGTTCAGGGCAAGAAC 53
```

```
ESULT 74
J773963/c
OCUS        BU773963                661 bp    mRNA    linear   EST 23-OCT-2003
EFINITION   SJEGBC03 SJE Schistosoma japonicum cDNA similar to
            gi|639869|dbj|BAA07127.1| (D37885) choline kinase R2 [Rattus
            norvegicus], mRNA sequence.
CCESSION    BU773963
ERSION      BU773963.1  GI:28341279
EYWORDS     EST.
OURCE       Schistosoma japonicum
 ORGANISM   Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
EFERENCE    1  (bases 1 to 661)
 AUTHORS    Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
            Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
            Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
            McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
 TITLE      Evolutionary and biomedical implications of a Schistosoma japonicum
            complementary DNA resource
 JOURNAL    Nat. Genet. 35 (2), 139-147 (2003)
  PUBMED    12973349
OMMENT      Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn.
EATURES                 Location/Qualifiers
     source             1. .661
                        /organism="Schistosoma japonicum"
                        /mol_type="mRNA"
                        /db_xref="taxon:6182"
                        /tissue_type="Whole egg"
                        /dev_stage="egg"
                        /lab_host="rabbits"
                        /clone_lib="SJE"
RIGIN

lignment Scores:
red. No.:               386             Length:         661
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             2.9%            Indels:         0
B:                      3               Gaps:           0

S-10-821-670A-27 (1-307) x BU773963 (1-661)

Y          201 AsnTyrThrSerSerPhePheIleArg 209
               |||||||||||||||||||||||||
D          306 AACTACACTTCTAGTTTCTTCATAAGA 280

ESULT 75
W956339
OCUS        AW956339                677 bp    mRNA    linear   EST 01-JUN-2000
EFINITION   EST368409 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.
CCESSION    AW956339
ERSION      AW956339.1  GI:8146022
EYWORDS     EST.
OURCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 677)
 AUTHORS    Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
            Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
 TITLE      Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 90
            Seq primer: Reverse.
FEATURES                Location/Qualifiers
     source             1. .677
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone_lib="MAGE resequences, MAGD"
                        /note="Vector: pBluescriptSKm"
ORIGIN

Alignment Scores:
Pred. No.:              395             Length:         677
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.9%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-27 (1-307) x AW956339 (1-677)

Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
Db         330 TTTTTACTGATTCACAAAAAGGAAGAC 356

RESULT 76
DR724059
LOCUS       DR724059                683 bp    mRNA    linear   EST 15-JUL-2005
DEFINITION  AGENCOURT_55148409 NICHD_XGC_Emb9 Xenopus laevis cDNA clone
            IMAGE:7973954 3', mRNA sequence.
ACCESSION   DR724059
VERSION     DR724059.1  GI:70898171
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 683)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Igor Dawid
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM17094  row: i  column: 24
            High quality sequence start: 170
            High quality sequence stop: 404.
FEATURES                Location/Qualifiers
     source             1. .683
                        /organism="Xenopus laevis"
                        /mol_type="mRNA"
                        /db_xref="taxon:8355"
                        /clone="IMAGE:7973954"
                        /tissue_type="Embryonic stage 17/19"
                        /lab_host="DH10B TonA"
                        /clone_lib="NICHD_XGC_Emb9"
```

/note="Organ: embryo; Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI; cDNA was primed using oligo-dT primer: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection 1.4kb resulted in an average insert size of 2.1kb. This is a non-normalized primary library (normalized library is NICHD_XGC_Emb10) and was constructed by Express Genomics (Frederick, MD). Note: this is a Xenopus Gene Collection (http://xgc.nci.nih.gov/) library."

)RIGIN

.lignment Scores:

:ed. No.:	398	Length:	683
:core:	9.00	Matches:	9
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.9%	Indels:	0
B:	10	Gaps:	0

S-10-821-670A-27 (1-307) x DR724059 (1-683)

y 74 ValLeuSerHisSerPheLeuLeuIle 82
||||||||||||||||||||||||||||
b 457 GTTTTAAGTCACTCTTTTCTTCTTATT 483

ESULT 77
A413781
OCUS CA413781 688 bp mRNA linear EST 07-NOV-2002
EFINITION UI-H-EZ0-bat-p-08-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens cDNA clone UI-H-EZ0-bat-p-08-0-UI 3', mRNA sequence.
CCESSION CA413781
ERSION CA413781.1 GI:24776432
EYWORDS EST.
OURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
EFERENCE 1 (bases 1 to 688)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
OMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of Orthoapedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 313-608, >ALU
Seq primer: M13 FORWARD
POLYA=Yes.
EATURES Location/Qualifiers
source 1. .688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZ0-bat-p-08-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ch1"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_Ch1 is a cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCACGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ0
TAG_SEQ=ATCTAATATG"

ORIGIN

Alignment Scores:

Pred. No.:	400	Length:	688
Score:	9.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.9%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-27 (1-307) x CA413781 (1-688)

Qy 79 PheLeuLeuIleHisLysLysGluAsp 87
|||||||||||||||||||||||||||
Db 201 TTTTTACTGATTCACAAAAAGGAAGAC 227

RESULT 78
CW470377
LOCUS CW470377 692 bp DNA linear GSS 02-NOV-2004
DEFINITION fsbb001f223i17k0 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone fsbb001f223i17, genomic survey sequence.
ACCESSION CW470377
VERSION CW470377.1 GI:55218338
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 692)
AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and Martienssen,R.A.
TITLE Sorghum genome sequencing by methylation filtration
JOURNAL PLoS Biol. 3 (1), e13 (2005)
PUBMED 15660154
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: fsbb001f223 row: i column: 17
Seq primer: k Reverse
Class: methylation filtered
High quality sequence stop: 692.
FEATURES Location/Qualifiers
source 1. .692
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="fsbb001f223i17"
/clone_lib="Sorghum methylation filtered library (LibID: 104)"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a

```
                    methylation filtered library."
RIGIN

lignment Scores:
red. No.:               402             Length:         692
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             2.9%            Indels:         0
B:                      13              Gaps:           0

S-10-821-670A-27 (1-307) x CW470377 (1-692)

Y          99 LysGluSerLysAsnLysIlePheLeu 107
              |||||||||||||||||||||||||||
o          37 AAAGAATCAAAGAACAAGATCTTCTTA 63

ESULT 79
E387304
OCUS        BE387304                697 bp    mRNA    linear   EST 21-JUL-2000
EFINITION   601275594F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616655 5',
            mRNA sequence.
CCESSION    BE387304
ERSION      BE387304.1  GI:9332669
EYWORDS     EST.
OURCE       Homo sapiens (human)
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
EFERENCE    1  (bases 1 to 697)
 AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
 TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL    Unpublished (1999)
OMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM282  row: k  column: 24
            High quality sequence start: 82
            High quality sequence stop: 534.
EATURES             Location/Qualifiers
     source         1. .697
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:3616655"
                    /tissue_type="melanotic melanoma"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_20"
                    /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming.  Directionally
                    cloned into EcoRI/XhoI sites using the following 5'
                    adaptor: GGCACGAG(G).  Size-selected >500bp for average
                    insert size 1.8kb.  Library constructed by Ling Hong in
                    the laboratory of Gerald M. Rubin (University of
                    California, Berkeley) using  ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."
RIGIN

lignment Scores:
red. No.:               405             Length:         697
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             2.9%            Indels:         0
B:                      7               Gaps:           0

S-10-821-670A-27 (1-307) x BE387304 (1-697)
```

```
Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
Db         117 TTTTTACTGATTCACAAAAAGGAAGAC 143

RESULT 80
BQ009739/c
LOCUS       BQ009739                700 bp    mRNA    linear   EST 26-MAR-2002
DEFINITION  UI-H-ED0-aya-h-21-0-UI.s1 NCI_CGAP_ED0 Homo sapiens cDNA clone
            IMAGE:5836100 3', mRNA sequence.
ACCESSION   BQ009739
VERSION     BQ009739.1  GI:19734640
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             The following repetitive elements were found in this cDNA
            sequence: 11-306, >ALU (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES            Location/Qualifiers
     source         1. .700
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5836100"
                    /tissue_type="Chondrosarcoma"
                    /dev_stage="Adult"
                    /lab_host="DH10B (Life Technologies)"
                    /clone_lib="NCI_CGAP_ED0"
                    /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                    (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                    Site_2: Not I; NCI_CGAP_ED0 is a cDNA library containing
                    the following tissue(s): Chondrosarcoma cell line CS5. The
                    library was constructed according to Bonaldo, Lennon and
                    Soares, Genome Research, 6:791-806, 1996. First strand
                    cDNA synthesis was primed with an oligo-dT primer
                    containing a Not I site. Double stranded cDNA was ligated
                    to an EcoR I adaptor, digested with Not I, and cloned
                    directionally into pT7T3-Pac vector. The oligonucleotide
                    used to prime the synthesis of first-strand cDNA contains
                    a library tag sequence that is located between the Not I
                    site and the (dT)18 tail. The sequence tag for this
                    library is GCTCAAGGCT.
                    TAG_TISSUE=chondrosarcoma
                    TAG_LIB=UI-H-ED0
                    TAG_SEQ=CGTCAAGGCT"
ORIGIN

Alignment Scores:
Pred. No.:              406             Length:         700
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.9%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x BQ009739 (1-700)
```

```
)y          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
)b         418 TTTTTACTGATTCACAAAAAGGAAGAC 392

:ESULT 81
:N279085/c
:OCUS       CN279085                 707 bp    mRNA    linear   EST 16-MAY-2004
)EFINITION  17000424715748 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
\CCESSION   CN279085
'ERSION     CN279085.1  GI:47295499
:EYWORDS    EST.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 707)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
:OMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 707   Std Error: 0.00.
'EATURES             Location/Qualifiers
     source          1. .707
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, cell lines H1, H7, and
                     H9"
                     /clone_lib="GRN_ES"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from undifferentiated hES cell lines H1 (p32), H7 (p29),
                     and H9 (p26) maintained in feeder-free conditions"
)RIGIN

\lignment Scores:
'red. No.:                410           Length:         707
:core:                    9.00          Matches:        9
'ercent Similarity:       100.0%        Conservative:   0
)est Local Similarity:    100.0%        Mismatches:     0
)uery Match:              2.9%          Indels:         0
)B:                       8             Gaps:           0

)S-10-821-670A-27 (1-307) x CN279085 (1-707)

)y          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
)b         235 TTTTTACTGATTCACAAAAAGGAAGAC 209

:ESULT 82
:N412356
:OCUS       CN412356                 722 bp    mRNA    linear   EST 16-MAY-2004
)EFINITION  17000532543092 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
\CCESSION   CN412356
'ERSION     CN412356.1  GI:47399950
:EYWORDS    EST.
:OURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
:EFERENCE   1  (bases 1 to 722)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 722   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .722
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, cell lines H1, H7, and
                     H9"
                     /clone_lib="GRN_ES"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from undifferentiated hES cell lines H1 (p32), H7 (p29),
                     and H9 (p26) maintained in feeder-free conditions"
ORIGIN

Alignment Scores:
Pred. No.:                417           Length:         722
Score:                    9.00          Matches:        9
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              2.9%          Indels:         0
DB:                       8             Gaps:           0

US-10-821-670A-27 (1-307) x CN412356 (1-722)

Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
Db         395 TTTTTACTGATTCACAAAAAGGAAGAC 421

RESULT 83
BU633670/c
LOCUS       BU633670                 757 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FL1-bgv-k-06-0-UI.s1 NCI_CGAP_FL1 Homo sapiens cDNA clone
            UI-H-FL1-bgv-k-06-0-UI 3', mRNA sequence.
ACCESSION   BU633670
VERSION     BU633670.1  GI:23300919
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 21-151, >MER20#DNA/MER1_type 302-597, >ALU (matched
            compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
```

```
EATURES             Location/Qualifiers
    source          1. .757
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UI-H-FL1-bgv-k-06-0-UI"
                    /tissue_type="Cell lines"
                    /dev_stage="Adult"
                    /lab_host="DH10B (Life Technologies)"
                    /clone_lib="NCI_CGAP_FL1"
                    /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                    (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                    Site_2: Not I; NCI_CGAP_FL1 is a normalized cDNA library
                    derived from a pool of mRNA obtained from 4 cell lines
                    from grade III chondrosarcoma tissues. The library was
                    constructed according to Bonaldo, Lennon and Soares,
                    Genome Research, 6:791-806, 1996. First strand cDNA
                    synthesis was primed with an oligo-dT primer containing a
                    Not I site.  Double stranded cDNA was ligated to an EcoR I
                    adaptor, digested with Not I, and cloned directionally
                    into pT7T3-Pac vector. The oligonucleotide used to prime
                    the synthesis of first-strand cDNA contains a library tag
                    sequence that is located between the Not I site and the
                    (dT)18 tail. The sequence tag for this library is
                    GAGGTCGGTG. The cell lines were provided by Dr. James
                    Martin from the University of Iowa.
                    TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
                    TAG_LIB=UI-H-FL1
                    TAG_SEQ=GAGGTCGGTG"
RIGIN

lignment Scores:
red. No.:               435             Length:         757
core:                   9.00            Matches:        9
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             2.9%            Indels:         0
B:                      3               Gaps:           0

S-10-821-670A-27 (1-307) x BU633670 (1-757)

y          79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||
o         709 TTTTTACTGATTCACAAAAAGGAAGAC 683

ESULT 84
P446084/c
OCUS        BP446084                763 bp    mRNA    linear   EST 30-DEC-2003
EFINITION   BP446084 full-length enriched swine cDNA library, adult liver Sus
            scrofa cDNA clone LVR010002F10 5', mRNA sequence.
CCESSION    BP446084
ERSION      BP446084.1  GI:40436151
EYWORDS     EST.
OURCE       Sus scrofa (pig)
 ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
EFERENCE    1  (bases 1 to 763)
 AUTHORS    Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
            Okumura,N., Hamasima,N. and Awata,T.
 TITLE      PEDE (Pig EST Data Explorer): construction of a database for ESTs
            derived from porcine full-length cDNA libraries
 JOURNAL    Nucleic Acids Res. 32 (1), D484-D488 (2004)
  PUBMED    14681463
OMMENT      Contact: Hirohide Uenishi
            Animal Genome Laboratory, Genome Research Department
            National Institute of Agrobiological Sciences
            2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
            Tel: +81-29-838-8627
            Fax: +81-29-838-8627
            Email: huenishi@affrc.go.jp
            EST project with full-length enriched cDNA libraries carried out in
            Animal Genome Research Program (Japan) by National Institute of
            Agrobiological Sciences and STAFF-Institute
            Single pass sequencing of clones derived from oligo-capped cDNA
            library
            Vector sequences were eliminated by RepeatMasker version 2002/07/13
            and crossmatch version 0.990319
            Low quality bases were trimmed based on the quality values.
FEATURES            Location/Qualifiers
     source         1. .763
                    /organism="Sus scrofa"
                    /mol_type="mRNA"
                    /db_xref="taxon:9823"
                    /clone="LVR010002F10"
                    /tissue_type="liver"
                    /dev_stage="adult"
                    /clone_lib="full-length enriched swine cDNA library, adult
                    liver"
ORIGIN

Alignment Scores:
Pred. No.:              438             Length:         763
Score:                  9.00            Matches:        9
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.9%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x BP446084 (1-763)

Qy          42 GlnSerSerGluValLeuGlySerGly 50
               |||||||||||||||||||||||||||
Db         646 CAATCCTCAGAGGTACTTGGGAGCGGA 620

RESULT 85
BU375548
LOCUS       BU375548                780 bp    mRNA    linear   EST 28-NOV-2002
DEFINITION  603807808F1 CSEQCHN74 Gallus gallus cDNA clone ChEST789p2 5', mRNA
            sequence.
ACCESSION   BU375548
VERSION     BU375548.1  GI:25883549
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES            Location/Qualifiers
     source         1. .780
                    /organism="Gallus gallus"
                    /mol_type="mRNA"
                    /strain="Compton Line 15I"
                    /db_xref="taxon:9031"
                    /clone="ChEST789p2"
                    /sex="Female"
                    /dev_stage="adult"
                    /lab_host="DH10B"
                    /clone_lib="CSEQCHN74"
                    /note="Organ: kidney + adrenal; Vector: pBluescript II
                    KS(+); Site_1: EcoRI; Site_2: Not1; This normalized
```

library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

)RIGIN

.lignment Scores:
'red. No.: 447 Length: 780
:core: 9.00 Matches: 9
'ercent Similarity: 100.0% Conservative: 0
iest Local Similarity: 100.0% Mismatches: 0
)uery Match: 2.9% Indels: 0
)B: 3 Gaps: 0

IS-10-821-670A-27 (1-307) x BU375548 (1-780)

)y 179 ProAlaAlaGluGluSerLeuProIle 187
||||||||||||||||||||||||||||
)b 682 CCTGCCGCGGAAGAGAGCTTGCCTATC 708

:ESULT 86
)Z056171/c
.OCUS BZ056171 796 bp DNA linear GSS 09-OCT-2002
)EFINITION llb95f10.b1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
.CCESSION BZ056171
'ERSION BZ056171.1 GI:23661434
:EYWORDS GSS.
:OURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
:EFERENCE 1 (bases 1 to 796)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
:OMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: llb95 row: f column: 10
Seq primer: -21UPpOT forward
Class: shotgun
High quality sequence start: 23
High quality sequence stop: 551.
'EATURES Location/Qualifiers
source 1. .796
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

)RIGIN

.lignment Scores:
'red. No.: 455 Length: 796
:core: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.9% Indels: 0
DB: 11 Gaps: 0

US-10-821-670A-27 (1-307) x BZ056171 (1-796)

Qy 51 LysThrLeuThrIleGlnValLysGlu 59
|||||||||||||||||||||||||||||
Db 651 AAAACATTAACAATCCAAGTGAAAGAA 625

RESULT 87
BZ020584
LOCUS BZ020584 798 bp DNA linear GSS 08-OCT-2002
DEFINITION oeg90c01.b1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION BZ020584
VERSION BZ020584.1 GI:23580317
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 798)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeg90 row: c column: 01
Seq primer: -21UPpOT forward
Class: shotgun
High quality sequence start: 120
High quality sequence stop: 335.
FEATURES Location/Qualifiers
source 1. .798
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Alignment Scores:
Pred. No.: 456 Length: 798
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.9% Indels: 0
DB: 11 Gaps: 0

US-10-821-670A-27 (1-307) x BZ020584 (1-798)

Qy 195 HisLysLeuLysTyrGluAsnTyrThr 203
|||||||||||||||||||||||||||
Db 687 CATAAGTTAAAATATGAAAATTATACT 713

RESULT 88
CT202661/c
LOCUS CT202661 798 bp DNA linear GSS 02-NOV-2005
DEFINITION Sus scrofa genomic clone CH242-149M11, genomic survey sequence.
ACCESSION CT202661
VERSION CT202661.1 GI:79718123

```
EYWORDS    GSS.
OURCE      Sus scrofa (pig)
 ORGANISM  Sus scrofa
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
           Sus.
EFERENCE   1  (bases 1 to 798)
 AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
 TITLE     Direct Submission
 JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
           Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
           humquery@sanger.ac.uk Unpublished
OMMENT     This sequence was generated from the SP6 end of BAC 149M11. 149M11
           is part of the CHORI-242 BAC Library created by P. de Jong. Further
           details: http://www.sanger.ac.uk/Projects/S_scrofa/.
EATURES              Location/Qualifiers
    source           1. .798
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-149M11"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
IGIN

lignment Scores:
red. No.:              456          Length:        798
core:                  9.00         Matches:       9
ercent Similarity:     100.0%       Conservative:  0
est Local Similarity:  100.0%       Mismatches:    0
uery Match:            2.9%         Indels:        0
B:                     14           Gaps:          0

S-10-821-670A-27 (1-307) x CT202661 (1-798)

y          78 SerPheLeuLeuIleHisLysLysGlu 86
              ||||||||||||||||||||||||||||
b         728 TCTTTTTTACTCATCCATAAAAAAGAA 702

ESULT 89
N518405/c
OCUS       DN518405                 802 bp    mRNA    linear   EST 10-MAR-2005
EFINITION  1259097 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
CCESSION   DN518405
ERSION     DN518405.1  GI:60728595
EYWORDS    EST.
OURCE      Bos taurus (cattle)
 ORGANISM  Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
           Pecora; Bovidae; Bovinae; Bos.
EFERENCE   1  (bases 1 to 802)
 AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
           Wray,J.E. and Keele,J.W.
 TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
 JOURNAL   Unpublished (2003)
OMMENT     Contact: Smith TPL
           USDA, ARS, US Meat Animal Research Center
           PO Box 166, Clay Center, NE 68933-0166, USA
           Tel: 402 762 4366
           Fax: 402 762 4390
           Email: smith@email.marc.usda.gov
           Single pass sequencing. Bases called with phred v0.020425.c and
           trimmed with the aid of the trim_alt option. Vector identified with
           cross_match v0.990329.
           Plate: RLK8037  row: F  column: 24
           Seq primer: TAGAAGGCACAGTCGAGG.
EATURES              Location/Qualifiers
    source           1. .802
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 7BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including ovary, hindbrain, uterus, and day-30 whole
                     embryos."
ORIGIN

Alignment Scores:
Pred. No.:             458          Length:        802
Score:                 9.00         Matches:       9
Percent Similarity:    100.0%       Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:           2.9%         Indels:        0
DB:                    9            Gaps:          0

US-10-821-670A-27 (1-307) x DN518405 (1-802)

Qy          47 LeuGlySerGlyLysThrLeuThrIle 55
               |||||||||||||||||||||||||||
Db         312 TTGGGATCAGGGAAAACATTAACCATT 286

RESULT 90
DN521145
LOCUS      DN521145                 819 bp    mRNA    linear   EST 11-MAR-2005
DEFINITION 1263973 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  DN521145
VERSION    DN521145.1  GI:60961723
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
  ORGANISM Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
           Pecora; Bovidae; Bovinae; Bos.
REFERENCE  1  (bases 1 to 819)
  AUTHORS  Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
           Wray,J.E. and Keele,J.W.
  TITLE    A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL  Unpublished (2003)
COMMENT    Contact: Smith TPL
           USDA, ARS, US Meat Animal Research Center
           PO Box 166, Clay Center, NE 68933-0166, USA
           Tel: 402 762 4366
           Fax: 402 762 4390
           Email: smith@email.marc.usda.gov
           Single pass sequencing. Bases called with phred v0.020425.c and
           trimmed with the aid of the trim_alt option. Vector identified with
           cross_match v0.990329.
           Plate: RLK8037  row: F  column: 24
           Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .819
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 7BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including ovary, hindbrain, uterus, and day-30 whole
                     embryos."
ORIGIN

Alignment Scores:
Pred. No.:             466          Length:        819
Score:                 9.00         Matches:       9
Percent Similarity:    100.0%       Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:           2.9%         Indels:        0
DB:                    9            Gaps:          0
```

```
S-10-821-670A-27 (1-307) x DN521145 (1-819)

y         47 LeuGlySerGlyLysThrLeuThrIle 55
             |||||||||||||||||||||||||||
b        512 TTGGGATCAGGGAAAACATTAACCATT 538

ESULT 91
G582789/c
OCUS       BG582789                841 bp    mRNA    linear   EST 11-APR-2001
EFINITION  EST484535 GVN Medicago truncatula cDNA clone pGVN-70P19 5' end,
           mRNA sequence.
CCESSION   BG582789
ERSION     BG582789.1  GI:13597853
EYWORDS    EST.
OURCE      Medicago truncatula (barrel medic)
  ORGANISM Medicago truncatula
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
           Medicago.
EFERENCE   1  (bases 1 to 841)
  AUTHORS  Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S.,
           Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
  TITLE    ESTs from one month old nitrogen-fixing root nodules of Medicago
           truncatula, 2001
  JOURNAL  Unpublished (2001)
OMMENT     Contact: Carroll P. Vance
           Department of Agronomy and Plant Genetics
           University of Minnesota
           411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
           Tel: 612 625 5715
           Fax: 651-649-5058
           Email: vance004@maroon.tc.umn.edu
           University of Minnesota name: M383861e TIGR sequence name:
           MTCDY94TK More information is available at: http://www.medicago.org
           Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
EATURES              Location/Qualifiers
     source          1. .841
                     /organism="Medicago truncatula"
                     /mol_type="mRNA"
                     /cultivar="genotype A17"
                     /db_xref="taxon:3880"
                     /clone="pGVN-70P19"
                     /tissue_type="N2-fixing root nodules"
                     /dev_stage="effective root nodules harvested one month
                     post inoculation with Sinorhizobium meliloti"
                     /lab_host="E. coli strain XLOLR"
                     /clone_lib="GVN"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; cDNA was prepared from polyA+ enriched RNA from
                     effective root nodules harvested one month post
                     inoculation with Sinorhizobium meliloti. The cDNA was
                     directionally ligated into the Uni-ZAP XR vector from
                     Stratagene and packaged using Gigapack III Gold packaging
                     extracts. Plasmids containing cDNA inserts were excised
                     from the recombinant lambda-ZAP phage using Ex-Assist
                     helper phage and propagated in XLOLR cells."
RIGIN

lignment Scores:
red. No.:              477          Length:        841
core:                  9.00         Matches:       9
ercent Similarity:     100.0%       Conservative:  0
est Local Similarity:  100.0%       Mismatches:    0
uery Match:            2.9%         Indels:        0
B:                     2            Gaps:          0

S-10-821-670A-27 (1-307) x BG582789 (1-841)

y        259 LysAsnAsnArgGluLysLysAspArg 267
             |||||||||||||||||||||||||
b        136 AAAAACAATAGAGAAAAAAAAGATAGA 110
```

```
RESULT 92
CR551254/c
LOCUS       CR551254                864 bp    mRNA    linear   EST 24-MAR-2005
DEFINITION  CR551254 Normalized and Subtracted bovine embryonic and
            extraembryonic tissues (bcaz/BE03) Bos taurus cDNA clone
            bcaz0001.m.23 5', mRNA sequence.
ACCESSION   CR551254
VERSION     CR551254.2  GI:61760533
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   Renard,J.P., Lewin,H.A., Yang,J., Hernandez,A., Degrelle,S.,
            Everts,R.E. and Hue,I.
  TITLE     Embryonic ESTs (bcaz)
  JOURNAL   Unpublished (2004)
COMMENT     On Jul 12, 2004 this sequence version replaced gi:50246164.
            Contact: Renard JP
            Biologie du Developpement et Reproduction
            INRA
            Domaine de Vilvert 78350 Jouy en Josas, FRANCE
            Email: jean-paul.renard@jouy.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence. AGENAE Resource centre. Francois PIUMI,
            Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
            genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
            FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
            Plate: bcaz0001a  row: m  column: 23.
FEATURES             Location/Qualifiers
     source          1. .864
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="bcaz0001.m.23"
                     /tissue_type="embryo (day 36 and day 64), extra-embryonic
                     tissue (day 14 to 25)"
                     /lab_host="DH10B"
                     /clone_lib="Normalized and Subtracted bovine embryonic and
                     extraembryonic tissues (bcaz/BE03)"
                     /note="Vector: pGEMZf11; Funding for EST sequencing was
                     provided by funds dedicated to J.P.RENARD (BDR, Inra).
                     Funding for construction and subtraction of the cDNA
                     library was provided by USDA ARS contract No 58-1275-2-020
                     to H. A. Lewin The cDNA library was constructed,
                     normalized and subtracted by Dr. A. Hernandez (W.M. Keck
                     Center, University of Illinois Urbana-Champaign) and S.
                     Degrelle (BDR, Inra) as described in Bonaldo et al.(1996),
                     Genome Research 6, 791-806. BE03 library is a normalized
                     library of embryonic tissues subtracted with 7800 known
                     EST sequences. The double-stranded cDNA was size selected
                     (>450 bp), adaptored with EcoRI adaptors at both ends and
                     digested with NotI. The cDNA was then directionally cloned
                     into EcoRI-NotI digested pGEM11Zf(+) phagemid vector.
                     Insert size was between 450-2200 bp. Tagged oligo-dT was
                     used to identify the origin of the ESTs where possible.
                     (A18)TGCGT = extraembryonic tissue; (A18)TCGGT = 36-day
                     oldfetus; (A18)TGCGA = 64-day old fetus (organs);
                     (A18)TCGGA = 64-day old fetus (body)"
ORIGIN

Alignment Scores:
Pred. No.:              488          Length:        864
Score:                  9.00         Matches:       9
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.9%         Indels:        0
DB:                     8            Gaps:          0

US-10-821-670A-27 (1-307) x CR551254 (1-864)
```

```
Qy         77 HisSerPheLeuLeuIleHisLysLys 85
              ||||||||||||||||||||||||||
Db        791 CATTCATTTCTTTTAATTCACAAAAAG 765

RESULT 93
BI258748
LOCUS       BI258748                894 bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  602970329F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109966 5',
            mRNA sequence.
ACCESSION   BI258748
VERSION     BI258748.1  GI:14815408
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11266  row: i  column: 07
            High quality sequence stop: 851.
FEATURES             Location/Qualifiers
     source          1. .894
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5109966"
                     /tissue_type="cervical carcinoma cell line"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_12"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.4 kb. Library prepared by Life
                     Technologies."
ORIGIN

Alignment Scores:
Pred. No.:                503           Length:         894
Score:                    9.00          Matches:        9
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              2.9%          Indels:         0
DB:                       2             Gaps:           0

US-10-821-670A-27 (1-307) x BI258748 (1-894)

Qy         79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||
Db        699 TTTTTACTGATTCACAAAAAGGAAGAC 725

RESULT 94
BI088766
LOCUS       BI088766                895 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  602851556F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4993380 5',
            mRNA sequence.
ACCESSION   BI088766
VERSION     BI088766.1  GI:14507096
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11013  row: o  column: 13
            High quality sequence stop: 623.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4993380"
                     /cell_line="MGC36"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_10"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5 kb. Library prepared by Life
                     Technologies."
ORIGIN

Alignment Scores:
Pred. No.:                504           Length:         895
Score:                    9.00          Matches:        9
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              2.9%          Indels:         0
DB:                       2             Gaps:           0

US-10-821-670A-27 (1-307) x BI088766 (1-895)

Qy         257 GlnGlyLysAsnAsnArgGluLysLys 265
               |||||||||||||||||||||||||
Db         837 CAGGGGAAAAACAATAGAGAGAAGAAA 863

RESULT 95
CF409178/c
LOCUS       CF409178                913 bp    mRNA    linear   EST 02-SEP-2003
DEFINITION  CH3#059_B01T7 Canine heart normalized cDNA Library in pBluescript
            Canis familiaris cDNA clone CH3#059_B01 5', mRNA sequence.
ACCESSION   CF409178
VERSION     CF409178.1  GI:34410424
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Yi,Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.
  TITLE     Expressed sequence tags from Canine heart
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: CH3#059_B01T3
            Contact: George AL
            Division of Genetic Medicine
            Vanderbilt University
            529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
            Tel: 615 936 2660
            Fax: 615 936 2661
            Email: al.george@vanderbilt.edu
            Insert Length: 2300   Std Error: 0.00
            Seq primer: T7: TAATACGACTCACTATAGGG
```

```
          High quality sequence start: 41
          High quality sequence stop: 823.
'EATURES             Location/Qualifiers
     source          1. .913
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="CH3#059_B01"
                     /tissue_type="heart"
                     /cell_type="heart"
                     /dev_stage="mixed developmental stages (adult, 30 day - 40
                     day fetal)"
                     /clone_lib="Canine heart normalized cDNA Library in
                     pBluescript"
                     /note="Organ: heart; Vector: pBluescript; Site_1: 5' of
                     vector NotI; Site_2: 3' of vector EcoRI; Tissue source:
                     dog heart (adult, 30 day - 40 day fetal), right and left
                     atria and ventricle. Dog breed - mixed (beagle, German
                     shepherd,  pointer, Irish setter). Library construction:
                     oligo-dT primed"
)RIGIN

.lignment Scores:
'red. No.:                512            Length:         913
:core:                    9.00           Matches:        9
'ercent Similarity:       100.0%         Conservative:   0
)est Local Similarity:    100.0%         Mismatches:     0
)uery Match:              2.9%           Indels:         0
)B:                       5              Gaps:           0

)S-10-821-670A-27 (1-307) x CF409178 (1-913)

)y          42 GlnSerSerGluValLeuGlySerGly 50
               ||||||||||||||||||||||||||
)b         641 CAATCCTCAGAGGTACTCGGGAGCGGA 615

:ESULT 96
)N565372
:OCUS       DN565372                 923 bp    mRNA    linear   EST 14-MAR-2005
)EFINITION  90930534 Sea Urchin primary mesenchyme cell cDNA library
            Strongylocentrotus purpuratus cDNA clone PMCSPR2-133L23 3', mRNA
            sequence.
.CCESSION   DN565372
'ERSION     DN565372.1  GI:61124411
:EYWORDS    EST.
:OURCE      Strongylocentrotus purpuratus
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
:EFERENCE   1  (bases 1 to 923)
  AUTHORS   Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
            Ettensohn,C.A.
  TITLE     A large scale analysis of mRNAs expressed by primary mesenchyme
            cells of the sea urchin embryo
  JOURNAL   Development 128 (13), 2615-2627 (2001)
   PUBMED   11493577
:OMMENT     Contact: Erica Sodergren
            Human Genome Sequencing Center
            Baylor College of Medicine
            One Baylor Plaza, Houston, TX 77030, USA
            Tel: 713-798-7676
            Fax: 713-798-6977
            Email: ericas@bcm.tmc.edu
            NCBI Trace Archive: 490837216
            Insert Length: 1750   Std Error: 0.25
            Plate: 133  row: L  column: 23.
'EATURES             Location/Qualifiers
     source          1. .923
                     /organism="Strongylocentrotus purpuratus"
                     /mol_type="mRNA"
                     /db_xref="taxon:7668"
                     /clone="PMCSPR2-133L23"
                     /tissue_type="embryo"
                     /cell_type="primary mesenchyme cells"
                     /lab_host="E.coli"
                     /clone_lib="Sea Urchin primary mesenchyme cell cDNA
                     library"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: MluI; oligo
                     dt priming from poly A+ RNA, directionally cloned"
ORIGIN

Alignment Scores:
Pred. No.:                517            Length:         923
Score:                    9.00           Matches:        9
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              2.9%           Indels:         0
DB:                       9              Gaps:           0

US-10-821-670A-27 (1-307) x DN565372 (1-923)

Qy         223 LysProLeuLysAsnSerArgHisVal 231
               |||||||||||||||||||||||||||
Db          58 AAACCTTTAAAAAACAGTCGGCACGTT 84

RESULT 97
DN786150
LOCUS       DN786150                 937 bp    mRNA    linear   EST 07-APR-2005
DEFINITION  94044776 Sea Urchin primary mesenchyme cell cDNA library
            Strongylocentrotus purpuratus cDNA clone PMCSPR2-149D22 5', mRNA
            sequence.
ACCESSION   DN786150
VERSION     DN786150.1  GI:62386916
KEYWORDS    EST.
SOURCE      Strongylocentrotus purpuratus
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1  (bases 1 to 937)
  AUTHORS   Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
            Ettensohn,C.A.
  TITLE     A large-scale analysis of mRNAs expressed by primary mesenchyme
            cells of the sea urchin embryo
  JOURNAL   Development 128 (13), 2615-2627 (2001)
   PUBMED   11493577
COMMENT     Contact: Erica Sodergren
            Human Genome Sequencing Center
            Baylor College of Medicine
            One Baylor Plaza, Houston, TX 77030, USA
            Tel: 713-798-7676
            Fax: 713-798-6977
            Email: ericas@bcm.tmc.edu
            NCBI Trace Archive: 508345780
            Insert Length: 1750   Std Error: 0.25
            Plate: 149  row: D  column: 22.
FEATURES             Location/Qualifiers
     source          1. .937
                     /organism="Strongylocentrotus purpuratus"
                     /mol_type="mRNA"
                     /db_xref="taxon:7668"
                     /clone="PMCSPR2-149D22"
                     /tissue_type="embryo"
                     /cell_type="primary mesenchyme cells"
                     /lab_host="E.coli"
                     /clone_lib="Sea Urchin primary mesenchyme cell cDNA
                     library"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: MluI; oligo
                     dt priming from poly A+ RNA, directionally cloned"
ORIGIN

Alignment Scores:
Pred. No.:                524            Length:         937
Score:                    9.00           Matches:        9
Percent Similarity:       100.0%         Conservative:   0
```

```
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            2.9%            Indels:         0
B:                     9               Gaps:           0

S-10-821-670A-27 (1-307) x DN786150 (1-937)

Y         99 LysGluSerLysAsnLysIlePheLeu 107
             |||||||||||||||||||||||||||
D        586 AAGGAAAGTAAAAATAAAATTTTTCTT 612

ESULT 98
U365640
OCUS       DU365640                943 bp    DNA     linear   GSS 05-OCT-2005
EFINITION  1098313079446 CHORI-243 Ovis aries genomic clone CH243-22I12,
           genomic survey sequence.
CCESSION   DU365640
ERSION     DU365640.1  GI:77095502
EYWORDS    GSS.
OURCE      Ovis aries (sheep)
 ORGANISM  Ovis aries
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
           Pecora; Bovidae; Caprinae; Ovis.
EFERENCE   1  (bases 1 to 943)
 AUTHORS   Kirkness,E., Shetty,J., de Jong,P., McEwan,J.C., Oddy,H. and
           Cockett,N.
 TITLE     Ovine BAC End Sequences from Library CHORI-243
 JOURNAL   Unpublished (2004)
.MMENT     Other_GSSs: 1098268383532
           Contact: Ewen Kirkness
           The Institute for Genomic Research (TIGR; www.tigr.org)
           9712 Medical Center Drive, Rockville, MD 20850, USA
           Tel: 301-795-7536
           Email: ekirknes@tigr.org
           Sequences generated at the J. Craig Venter Institute Joint
           Technology Center (JCVIJTC; http://www.venterinstitute.org/).
           Original Trace: 1098313079446 Trace TI: gnl|ti|918903956
           Insert Length: 184000   Std Error: 0.00  row: I  column: 12
           Seq primer: SP6
           Class: BAC ends.
EATURES              Location/Qualifiers
    source           1. .943
                     /organism="Ovis aries"
                     /mol_type="genomic DNA"
                     /strain="Texel breed"
                     /db_xref="taxon:9940"
                     /clone="CH243-22I12"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-243"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     The CHORI-243 sheep (M) (Ovis aries) BAC library produced
                     by Pieter de Jong's lab at CHORI
                     http://bacpac.chori.org/library.php?id=162"
RIGIN

lignment Scores:
red. No.:              527             Length:         943
core:                  9.00            Matches:        9
ercent Similarity:     100.0%          Conservative:   0
est Local Similarity:  100.0%          Mismatches:     0
uery Match:            2.9%            Indels:         0
B:                     13              Gaps:           0

S-10-821-670A-27 (1-307) x DU365640 (1-943)

Y        147 ThrCysGlyAlaAlaThrLeuSerAla 155
             |||||||||||||||||||||||||||
D        695 ACCTGTGGAGCAGCCACCCTCTCTGCT 721

ESULT 99
G035474
OCUS       BG035474                960 bp    mRNA    linear   EST 24-JAN-2001

DEFINITION  602325507F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413864 5',
            mRNA sequence.
ACCESSION   BG035474
VERSION     BG035474.1  GI:12429618
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 960)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10140  row: m  column: 01
            High quality sequence stop: 682.
FEATURES              Location/Qualifiers
     source           1. .960
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4413864"
                      /tissue_type="adenocarcinoma, cell line"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_90"
                      /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                      Average insert size 1.7 kb. Library enriched for
                      full-length clones and constructed by Life Technologies.
                      Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:             535             Length:         960
Score:                 9.00            Matches:        9
Percent Similarity:    100.0%          Conservative:   0
Best Local Similarity: 100.0%          Mismatches:     0
Query Match:           2.9%            Indels:         0
DB:                    2               Gaps:           0

US-10-821-670A-27 (1-307) x BG035474 (1-960)

Qy         79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||
Db        416 TTTTTACTGATTCACAAAAAGGAAGAC 442

RESULT 100
BG027599
LOCUS       BG027599                986 bp    mRNA    linear   EST 24-JAN-2001
DEFINITION  602294475F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4389115 5',
            mRNA sequence.
ACCESSION   BG027599
VERSION     BG027599.1  GI:12416387
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM10076  row: e  column: 20
          High quality sequence stop: 671.
'EATURES             Location/Qualifiers
     source          1. .986
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4389115"
                     /tissue_type="osteosarcoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_86"
                     /note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.533 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
)RIGIN

.lignment Scores:
'ced. No.:               548            Length:         986
core:                    9.00           Matches:        9
'ercent Similarity:      100.0%         Conservative:   0
)est Local Similarity:   100.0%         Mismatches:     0
)uery Match:             2.9%           Indels:         0
)B:                      2              Gaps:           0

)S-10-821-670A-27 (1-307) x BG027599 (1-986)

)y          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
)b         347 TTTTTACTGATTCACAAAAAGGAAGAC 373


)earch completed: June 10, 2006, 16:34:06
'ob time : 4282.81 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

)M protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:43:45 ; Search time 175.01 Seconds
(without alignments)
4923.420 Million cell updates/sec

Title: US-10-821-670A-27
Perfect score: 307
Sequence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2800955

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110458_27682/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.p2n.200scores.rni
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=200 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05p
-USER=US10821670_@CGN_1_1_677_@runat_07062006_110458_27682 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	307	100.0	921	3	US-09-917-265A-26	Sequence 26, Appl
c	2	307	100.0	921	3	US-09-917-265A-28	Sequence 28, Appl
	3	307	100.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	4	307	100.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
	5	307	100.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	6	307	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
	7	206	67.1	921	3	US-09-011-143-6	Sequence 6, Appli
	8	206	67.1	921	3	US-09-011-143-7	Sequence 7, Appli
	9	206	67.1	921	3	US-09-302-495-6	Sequence 6, Appli
	10	206	67.1	921	3	US-09-302-495-7	Sequence 7, Appli
	11	206	67.1	921	3	US-10-079-616-6	Sequence 6, Appli
	12	206	67.1	921	3	US-10-079-616-7	Sequence 7, Appli
	13	206	67.1	987	3	US-09-917-265A-29	Sequence 29, Appl
c	14	206	67.1	987	3	US-09-917-265A-31	Sequence 31, Appl
	15	206	67.1	2193	3	US-09-011-143-5	Sequence 5, Appli
	16	206	67.1	2193	3	US-09-302-495-5	Sequence 5, Appli
	17	206	67.1	2193	3	US-10-079-616-5	Sequence 5, Appli
	18	205	66.8	985	3	US-09-917-265A-55	Sequence 55, Appl
c	19	205	66.8	985	3	US-09-917-265A-57	Sequence 57, Appl
	20	37	12.1	921	3	US-09-917-265A-52	Sequence 52, Appl
c	21	37	12.1	921	3	US-09-917-265A-54	Sequence 54, Appl
	22	37	12.1	987	3	US-09-917-265A-58	Sequence 58, Appl
c	23	37	12.1	987	3	US-09-917-265A-60	Sequence 60, Appl
	24	37	12.1	990	3	US-09-079-984A-1	Sequence 1, Appli
	25	37	12.1	990	3	US-09-079-984A-11	Sequence 11, Appl
	26	37	12.1	990	3	US-09-390-729-1	Sequence 1, Appli
	27	37	12.1	990	3	US-09-390-729-11	Sequence 11, Appl
	28	37	12.1	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	29	37	12.1	1533	3	US-09-917-265A-68	Sequence 68, Appl
	30	37	12.1	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	31	37	12.1	1599	3	US-09-917-265A-63	Sequence 63, Appl
	32	37	12.1	2267	3	US-09-917-265A-107	Sequence 107, App
c	33	37	12.1	2267	3	US-09-917-265A-109	Sequence 109, App
	34	35	11.4	987	2	US-08-186-529-1	Sequence 1, Appli
	35	35	11.4	987	2	US-08-640-386A-1	Sequence 1, Appli
	36	35	11.4	1018	2	US-08-184-009-194	Sequence 194, App
	37	35	11.4	1018	2	US-08-458-356-194	Sequence 194, App
	38	35	11.4	1018	3	US-08-460-736-194	Sequence 194, App
	39	35	11.4	1018	3	US-09-535-370-194	Sequence 194, App
	40	35	11.4	1018	3	US-09-663-667-194	Sequence 194, App
	41	35	11.4	1389	3	US-09-634-368-4	Sequence 4, Appli
	42	35	11.4	1399	2	US-08-751-767A-3	Sequence 3, Appli
	43	35	11.4	1560	2	US-08-751-767A-11	Sequence 11, Appl
	44	35	11.4	1623	2	US-08-751-767A-9	Sequence 9, Appli
	45	35	11.4	2307	3	US-09-949-016-5452	Sequence 5452, Ap
	46	35	11.4	2362	2	US-08-265-087-1	Sequence 1, Appli
	47	35	11.4	2362	2	US-08-621-493-1	Sequence 1, Appli
	48	35	11.4	2362	2	US-08-965-688-1	Sequence 1, Appli
	49	35	11.4	2362	3	US-09-260-173-1	Sequence 1, Appli
	50	35	11.4	2362	3	US-09-924-703-3	Sequence 3, Appli
	51	35	11.4	6139	2	US-08-751-767A-7	Sequence 7, Appli
	52	23	7.5	987	3	US-08-848-760B-24	Sequence 24, Appl
	53	23	7.5	987	3	US-09-826-025-24	Sequence 24, Appl
	54	23	7.5	1870	3	US-09-310-842-4	Sequence 4, Appli
	55	23	7.5	2318	3	US-09-851-062-3	Sequence 3, Appli
	56	23	7.5	2318	3	US-09-949-016-315	Sequence 315, App
	57	22	7.2	16002	3	US-09-949-016-12057	Sequence 12057, A
	58	22	7.2	16003	3	US-09-949-016-17194	Sequence 17194, A
	59	17	5.5	73	3	US-09-823-549-77	Sequence 77, Appl
c	60	17	5.5	601	3	US-09-949-016-24253	Sequence 24253, A
c	61	17	5.5	601	3	US-09-949-016-190686	Sequence 190686,
	62	17	5.5	1061	2	US-08-385-335A-13	Sequence 13, Appl
	63	17	5.5	1409	3	US-09-634-368-3	Sequence 3, Appli
	64	17	5.5	1472	3	US-09-634-368-2	Sequence 2, Appli
	65	17	5.5	1569	3	US-09-634-368-12	Sequence 12, Appl
	66	17	5.5	2013	3	US-09-634-368-11	Sequence 11, Appl
	67	17	5.5	2709	3	US-09-634-368-13	Sequence 13, Appl
	68	17	5.5	6295	2	US-08-659-206A-4	Sequence 4, Appli
	69	17	5.5	7287	2	US-08-659-206A-1	Sequence 1, Appli
	70	12	3.9	38	3	US-09-011-143-12	Sequence 12, Appl
	71	12	3.9	38	3	US-09-302-495-12	Sequence 12, Appl
	72	12	3.9	38	3	US-10-079-616-12	Sequence 12, Appl
c	73	12	3.9	601	3	US-09-949-016-24250	Sequence 24250, A
c	74	12	3.9	601	3	US-09-949-016-24251	Sequence 24251, A
c	75	12	3.9	601	3	US-09-949-016-190683	Sequence 190683,
c	76	12	3.9	601	3	US-09-949-016-190684	Sequence 190684,
	77	9	2.9	532	3	US-09-513-999C-4018	Sequence 4018, Ap
	78	8	2.6	25	3	US-09-887-145-37	Sequence 37, Appl
c	79	8	2.6	25	3	US-09-917-265A-86	Sequence 86, Appl
c	80	8	2.6	32	3	US-09-011-143-13	Sequence 13, Appl

c 81	8	2.6	32	3	US-09-302-495-13	Sequence 13, Appl
c 82	8	2.6	32	3	US-10-079-616-13	Sequence 13, Appl
83	8	2.6	44	3	US-09-011-143-14	Sequence 14, Appl
84	8	2.6	44	3	US-09-302-495-14	Sequence 14, Appl
85	8	2.6	44	3	US-10-079-616-14	Sequence 14, Appl
86	8	2.6	601	3	US-09-949-016-70299	Sequence 70299, A
87	8	2.6	601	3	US-09-949-016-87513	Sequence 87513, A
c 88	8	2.6	601	3	US-09-949-016-202770	Sequence 202770,
89	8	2.6	633	5	US-09-974-300-5194	Sequence 5194, Ap
c 90	8	2.6	830	3	US-09-621-976-1463	Sequence 1463, Ap
91	8	2.6	885	3	US-09-328-352-1423	Sequence 1423, Ap
c 92	8	2.6	2961	3	US-09-949-016-2226	Sequence 2226, Ap
93	8	2.6	3342	2	US-08-254-989-1	Sequence 1, Appli
94	8	2.6	6758	3	US-09-902-540-1033	Sequence 1033, Ap
95	8	2.6	7173	3	US-09-949-016-17491	Sequence 17491, A
96	8	2.6	28976	3	US-09-949-002-689	Sequence 689, App
97	8	2.6	28976	3	US-09-949-002-698	Sequence 698, App
98	8	2.6	41815	3	US-09-949-016-17447	Sequence 17447, A
c 99	8	2.6	68444	3	US-09-949-016-13968	Sequence 13968, A
c 100	8	2.6	72843	3	US-09-949-016-12574	Sequence 12574, A
c 101	8	2.6	81927	3	US-09-949-016-15623	Sequence 15623, A
c 102	8	2.6	87350	3	US-08-781-891-79	Sequence 79, Appl
c 103	8	2.6	87350	3	US-09-618-166-79	Sequence 79, Appl
c 104	8	2.6	87543	3	US-09-791-211-3	Sequence 3, Appli
105	8	2.6	104428	3	US-09-949-016-12737	Sequence 12737, A
106	8	2.6	104429	3	US-09-949-016-13814	Sequence 13814, A
c 107	8	2.6	145320	3	US-09-949-016-15858	Sequence 15858, A
108	8	2.6	168575	3	US-09-426-290-1	Sequence 1, Appli
c 109	8	2.6	393753	3	US-09-949-016-14573	Sequence 14573, A
c 110	8	2.6	393753	3	US-09-949-016-14574	Sequence 14574, A
111	8	2.6	670689	3	US-09-949-016-12505	Sequence 12505, A
112	8	2.6	670690	3	US-09-949-016-14207	Sequence 14207, A
c 113	8	2.6	784019	3	US-09-949-016-14033	Sequence 14033, A
c 114	8	2.6	818128	3	US-09-949-016-14546	Sequence 14546, A
c 115	8	2.6	818128	3	US-09-949-016-14547	Sequence 14547, A
c 116	8	2.6	818128	3	US-09-949-016-14548	Sequence 14548, A
c 117	8	2.6	818128	3	US-09-949-016-14549	Sequence 14549, A
c 118	8	2.6	818128	3	US-09-949-016-14550	Sequence 14550, A
c 119	8	2.6	818128	3	US-09-949-016-14551	Sequence 14551, A
c 120	8	2.6	818128	3	US-09-949-016-14552	Sequence 14552, A
c 121	8	2.6	818128	3	US-09-949-016-14553	Sequence 14553, A
c 122	8	2.6	818128	3	US-09-949-016-14554	Sequence 14554, A
c 123	8	2.6	818128	3	US-09-949-016-14555	Sequence 14555, A
c 124	8	2.6	818128	3	US-09-949-016-14556	Sequence 14556, A
c 125	8	2.6	818128	3	US-09-949-016-14557	Sequence 14557, A
c 126	8	2.6	818128	3	US-09-949-016-14558	Sequence 14558, A
c 127	8	2.6	818128	3	US-09-949-016-14559	Sequence 14559, A
c 128	8	2.6	818128	3	US-09-949-016-14560	Sequence 14560, A
c 129	8	2.6	818128	3	US-09-949-016-14561	Sequence 14561, A
c 130	8	2.6	818128	3	US-09-949-016-14562	Sequence 14562, A
c 131	8	2.6	818128	3	US-09-949-016-14564	Sequence 14564, A
c 132	8	2.6	818128	3	US-09-949-016-14565	Sequence 14565, A
c 133	8	2.6	818128	3	US-09-949-016-14566	Sequence 14566, A
c 134	8	2.6	818128	3	US-09-949-016-14567	Sequence 14567, A
c 135	8	2.6	828152	3	US-09-949-016-12777	Sequence 12777, A
136	8	2.6	1830121	3	US-09-557-884-1	Sequence 1, Appli
137	8	2.6	1830121	3	US-09-643-990A-1	Sequence 1, Appli
138	8	2.6	1830121	3	US-10-158-865-1	Sequence 1, Appli
139	7	2.3	24	3	US-09-823-549-48	Sequence 48, Appl
c 140	7	2.3	25	3	US-09-917-265A-88	Sequence 88, Appl
141	7	2.3	25	3	US-09-396-196G-42419	Sequence 42419, A
142	7	2.3	25	3	US-09-396-196G-42420	Sequence 42420, A
c 143	7	2.3	39	3	US-09-079-984A-14	Sequence 14, Appl
c 144	7	2.3	39	3	US-09-390-729-14	Sequence 14, Appl
145	7	2.3	44	2	US-08-823-516-115	Sequence 115, App
146	7	2.3	44	3	US-08-759-038-123	Sequence 123, App
147	7	2.3	44	3	US-08-758-314-123	Sequence 123, App
148	7	2.3	44	3	US-09-684-938-123	Sequence 123, App
149	7	2.3	44	3	US-09-308-825A-123	Sequence 123, App
150	7	2.3	44	3	US-09-940-244-115	Sequence 115, App
151	7	2.3	44	3	US-09-381-212-115	Sequence 115, App
152	7	2.3	44	3	US-09-713-601A-115	Sequence 115, App
153	7	2.3	45	3	US-09-777-430C-60	Sequence 60, Appl
154	7	2.3	50	2	US-08-823-516-118	Sequence 118, App
155	7	2.3	50	3	US-08-759-038-126	Sequence 126, App
156	7	2.3	50	3	US-08-758-314-126	Sequence 126, App
157	7	2.3	50	3	US-09-940-244-118	Sequence 118, App
158	7	2.3	50	3	US-09-381-212-118	Sequence 118, App
159	7	2.3	50	3	US-09-713-601A-118	Sequence 118, App
160	7	2.3	51	3	US-09-684-938-126	Sequence 126, App
161	7	2.3	51	3	US-09-308-825A-126	Sequence 126, App
162	7	2.3	178	3	US-09-513-999C-35523	Sequence 35523, A
163	7	2.3	186	3	US-09-489-039A-260	Sequence 260, App
164	7	2.3	241	3	US-09-270-767-8558	Sequence 8558, Ap
165	7	2.3	241	3	US-09-270-767-23840	Sequence 23840, A
c 166	7	2.3	259	3	US-09-513-999C-29666	Sequence 29666, A
167	7	2.3	287	3	US-09-313-294A-2940	Sequence 2940, Ap
168	7	2.3	300	4	US-09-297-648-247	Sequence 247, App
169	7	2.3	326	3	US-08-916-576B-16	Sequence 16, Appl
170	7	2.3	326	3	US-10-078-337-16	Sequence 16, Appl
c 171	7	2.3	327	3	US-09-513-999C-320	Sequence 320, App
c 172	7	2.3	331	3	US-09-513-999C-33699	Sequence 33699, A
c 173	7	2.3	338	3	US-09-513-999C-30716	Sequence 30716, A
c 174	7	2.3	378	3	US-09-513-999C-21946	Sequence 21946, A
c 175	7	2.3	383	3	US-09-621-976-15609	Sequence 15609, A
176	7	2.3	405	3	US-09-270-767-8945	Sequence 8945, Ap
177	7	2.3	405	3	US-09-270-767-24227	Sequence 24227, A
178	7	2.3	421	4	US-09-880-107-3615	Sequence 3615, Ap
179	7	2.3	423	5	US-09-974-300-6739	Sequence 6739, Ap
c 180	7	2.3	430	3	US-09-621-976-1556	Sequence 1556, Ap
181	7	2.3	431	3	US-09-513-999C-32365	Sequence 32365, A
182	7	2.3	448	2	US-08-616-368A-29	Sequence 29, Appl
183	7	2.3	448	3	US-09-054-298-29	Sequence 29, Appl
184	7	2.3	448	3	US-08-818-655-29	Sequence 29, Appl
185	7	2.3	448	3	US-09-305-839-29	Sequence 29, Appl
186	7	2.3	450	3	US-09-854-133-340	Sequence 340, App
c 187	7	2.3	457	3	US-09-270-767-6682	Sequence 6682, Ap
c 188	7	2.3	457	3	US-09-270-767-21964	Sequence 21964, A
c 189	7	2.3	467	3	US-09-621-976-12583	Sequence 12583, A
190	7	2.3	468	3	US-09-252-991A-16394	Sequence 16394, A
c 191	7	2.3	475	3	US-09-621-976-3718	Sequence 3718, Ap
192	7	2.3	482	3	US-09-621-976-99	Sequence 99, Appl
c 193	7	2.3	483	3	US-09-902-540-6648	Sequence 6648, Ap
c 194	7	2.3	486	3	US-09-489-039A-5766	Sequence 5766, Ap
c 195	7	2.3	495	3	US-09-252-991A-13925	Sequence 13925, A
c 196	7	2.3	497	3	US-09-621-976-10651	Sequence 10651, A
197	7	2.3	505	3	US-08-916-576B-18	Sequence 18, Appl
198	7	2.3	505	3	US-10-078-337-18	Sequence 18, Appl
c 199	7	2.3	507	3	US-09-621-976-3715	Sequence 3715, Ap
c 200	7	2.3	537	3	US-09-107-532A-2913	Sequence 2913, Ap

ALIGNMENTS

```
RESULT 1
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
```

LOCATION: (1)..(921)
US-09-917-265A-26

Alignment Scores:

Pred. No.:	0	Length:	921
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265A-26 (1-921)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 2
US-09-917-265A-28/c
; Sequence 28, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-28

Alignment Scores:

Pred. No.:	0	Length:	921
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265A-28 (1-921)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

y          201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

y          221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

y          241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

y          261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

y          281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

y          301 TrpAlaSerValSerCysSer 307
                 ||||||||||||||||||||
b           21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 3
US-09-917-265A-43
 Sequence 43, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 43
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1533)
US-09-917-265A-43

Alignment Scores:
Pred. No.:              0           Length:        1533
Score:                  307.00      Matches:       307
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            100.0%      Indels:        0
DB:                     3           Gaps:          0

US-10-821-670A-27 (1-307) x US-09-917-265A-43 (1-1533)

y            1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b            1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

y           21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

y           41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy          61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy          81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         301 TrpAlaSerValSerCysSer 307
                 ||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 4
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
```

S-09-917-265A-45

Alignment Scores:

Pred. No.:	0	Length:	1533
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265A-45 (1-1533)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

RESULT 5
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:

Pred. No.:	0	Length:	1599
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265A-38 (1-1599)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
```

```
y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

y       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

y       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

y       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

y       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

y       301 TrpAlaSerValSerCysSer 307
            |||||||||||||||||||||
b       967 TGGGCATCCGTGTCCTGCAGT 987

ESULT 6
S-09-917-265A-40/c
 Sequence 40, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 40
   LENGTH: 1599
   TYPE: DNA
   ORGANISM: Felis catus
S-09-917-265A-40

lignment Scores:
red. No.:               0           Length:         1599
core:                   307.00      Matches:        307
ercent Similarity:      100.0%      Conservative:   0
st Local Similarity:    100.0%      Mismatches:     0
ery Match:              100.0%      Indels:         0
:                       3           Gaps:           0

--10-821-670A-27 (1-307) x US-09-917-265A-40 (1-1599)

y         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

y        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

y        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db       633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 7
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/011,143
      FILING DATE:  04-FEB-1998
      CLASSIFICATION:  536
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  PCT/JP97/01824
      FILING DATE:  29-MAY-1997
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  JP 165249/1996
      FILING DATE:  04-JUN-1996
    ATTORNEY/AGENT INFORMATION:
      NAME:  BROWDY, Roger L.
      REGISTRATION NUMBER:  25,618
      REFERENCE/DOCKET NUMBER:  IMAMURA=1
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  202-628-5197
      TELEFAX:  202-737-3528
  INFORMATION FOR SEQ ID NO:  6:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  921 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
IS-09-011-143-6

Alignment Scores:
Pred. No.:              2.48e-214      Length:          921
Score:                  206.00         Matches:         306
Percent Similarity:     99.7%          Conservative:    0
Best Local Similarity:  99.7%          Mismatches:      1
Query Match:            67.1%          Indels:          0
DB:                     3              Gaps:            0

IS-10-821-670A-27 (1-307) x US-09-011-143-6 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 8
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
```

```
      LENGTH:  921 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
S-09-011-143-7

lignment Scores:
red. No.:              2.48e-214      Length:        921
core:                  206.00         Matches:       306
ercent Similarity:     99.7%          Conservative:  0
est Local Similarity:  99.7%          Mismatches:    1
uery Match:            67.1%          Indels:        0
B:                     3              Gaps:          0

S-10-821-670A-27 (1-307) x US-09-011-143-7 (1-921)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
b        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy       301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
Db       901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 9
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

Alignment Scores:
Pred. No.:              2.48e-214      Length:        921
Score:                  206.00         Matches:       306
Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            67.1%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-302-495-6 (1-921)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
```

```
Qy          21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy          41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy          61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy          81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
               ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         301 TrpAlaSerValSerCysSer 307
               |||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921
```

```
RESULT 10
US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-302-495-7

Alignment Scores:
Pred. No.:                2.48e-214       Length:          921
Score:                    206.00          Matches:         306
Percent Similarity:       99.7%           Conservative:    0
Best Local Similarity:    99.7%           Mismatches:      1
Query Match:              67.1%           Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-27 (1-307) x US-09-302-495-7 (1-921)

Qy           1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy          21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy          41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy          61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy          81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
```

```
y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
            ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
b        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
t        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
t        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
t        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
t        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

y        301 TrpAlaSerValSerCysSer 307
            |||||||||||||||||||||
b        901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 11
S-10-079-616-6
 Sequence 6, Application US/10079616
 Patent No. 6566097
   GENERAL INFORMATION:
        APPLICANT: IMAMURA, Takayuki
                   MAEDA, Hiroaki
                   FUJIYASU, Takeshi
                   IMAGAWA, Yoshitaka
                   TOKIYOSHI, Sachio
        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
        NUMBER OF SEQUENCES: 26
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: BROWDY AND NEIMARK
             STREET: 419 Seventh Street, N.W., Suite 300
             CITY: Washington
             STATE: D.C.
             COUNTRY: USA
             ZIP: 20004
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/10/079,616
             FILING DATE: 22-Feb-2002
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 09/011,143
             FILING DATE: 04-FEB-1998
             APPLICATION NUMBER: PCT/JP97/01824
             FILING DATE: 29-MAY-1997
             APPLICATION NUMBER: JP 165249/1996
             FILING DATE: 04-JUN-1996
        ATTORNEY/AGENT INFORMATION:
             NAME: BROWDY, Roger L.
             REGISTRATION NUMBER: 25,618
             REFERENCE/DOCKET NUMBER: IMAMURA=1
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: 202-628-5197
             TELEFAX: 202-737-3528
   INFORMATION FOR SEQ ID NO: 6:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 921 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

Alignment Scores:
Pred. No.:                2.48e-214      Length:          921
Score:                    206.00         Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              67.1%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-10-079-616-6 (1-921)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
```

```
Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 12
US-10-079-616-7
  Sequence 7, Application US/10079616
  Patent No. 6566097
    GENERAL INFORMATION:
        APPLICANT: IMAMURA, Takayuki
                   MAEDA, Hiroaki
                   FUJIYASU, Takeshi
                   IMAGAWA, Yoshitaka
                   TOKIYOSHI, Sachio
        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
        NUMBER OF SEQUENCES: 26
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: BROWDY AND NEIMARK
             STREET: 419 Seventh Street, N.W., Suite 300
             CITY: Washington
             STATE: D.C.
             COUNTRY: USA
             ZIP: 20004
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/10/079,616
             FILING DATE: 22-Feb-2002
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 09/011,143
             FILING DATE: 04-FEB-1998
             APPLICATION NUMBER: PCT/JP97/01824
             FILING DATE: 29-MAY-1997
             APPLICATION NUMBER: JP 165249/1996
             FILING DATE: 04-JUN-1996
        ATTORNEY/AGENT INFORMATION:
             NAME: BROWDY, Roger L.
             REGISTRATION NUMBER: 25,618
             REFERENCE/DOCKET NUMBER: IMAMURA=1
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: 202-628-5197
             TELEFAX: 202-737-3528
    INFORMATION FOR SEQ ID NO: 7:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 921 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7
```

```
Alignment Scores:
Pred. No.:                2.48e-214      Length:          921
Score:                    206.00         Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              67.1%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-10-079-616-7 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

```
ESULT 13
S-09-917-265A-29
 Sequence 29, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 29
   LENGTH: 987
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(987)
S-09-917-265A-29

lignment Scores:
red. No.:              2.65e-214      Length:          987
core:                  206.00         Matches:         306
ercent Similarity:     99.7%          Conservative:    0
est Local Similarity:  99.7%          Mismatches:      1
uery Match:            67.1%          Indels:          0
B:                     3              Gaps:            0

S-10-821-670A-27 (1-307) x US-09-917-265A-29 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 14
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

Alignment Scores:
Pred. No.:             2.65e-214      Length:          987
Score:                 206.00         Matches:         306
Percent Similarity:    99.7%          Conservative:    0
Best Local Similarity: 99.7%          Mismatches:      1
Query Match:           67.1%          Indels:          0
DB:                    3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-917-265A-31 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
)b        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

)y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

)y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

)y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

)y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
)b        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

)y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

)y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

)y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

)y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

)y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

)y        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
)b         21 TGGGCATCCGTGTCCTGCAGT 1

!ESULT 15
)S-09-011-143-5
· Sequence 5, Application US/09011143
· Patent No. 6472509
:  GENERAL INFORMATION:
·    APPLICANT:  IMAMURA, Takayuki
:    APPLICANT:  MAEDA, Hiroaki
:    APPLICANT:  FUJIYASU, Takeshi
:    APPLICANT:  IMAGAWA, Yoshitaka
:    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
·    NUMBER OF SEQUENCES:  26
:    CORRESPONDENCE ADDRESS:
:      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
·      CITY:  Washington
·      STATE:  D.C.
·      COUNTRY:  USA
·      ZIP:  20004
·    COMPUTER READABLE FORM:
·      MEDIUM TYPE:  Floppy disk
·      COMPUTER:  IBM PC compatible
·      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

Alignment Scores:
Pred. No.:                5.78e-214       Length:          2193
Score:                    206.00          Matches:         306
Percent Similarity:       99.7%           Conservative:    0
Best Local Similarity:    99.7%           Mismatches:      1
Query Match:              67.1%           Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-27 (1-307) x US-09-011-143-5 (1-2193)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669
```

```
y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

y       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

y       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

y       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

y       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

y       301 TrpAlaSerValSerCysSer 307
            |||||||||||||||||||||
b      1030 TGGGCATCCGTGTCCTGCAGT 1050

ESULT 16
S-09-302-495-5
 Sequence 5, Application US/09302495
 Patent No. 6518045
   GENERAL INFORMATION:
        APPLICANT: IMAMURA, Takayuki
                   MAEDA, Hiroaki
                   FUJIYASU, Takeshi
                   IMAGAWA, Yoshitaka
                   TOKIYOSHI, Sachio
        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
        NUMBER OF SEQUENCES: 26
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: BROWDY AND NEIMARK
             STREET: 419 Seventh Street, N.W., Suite 300
             CITY: Washington
             STATE: D.C.
             COUNTRY: USA
             ZIP: 20004
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/302,495
             FILING DATE: 30-Apr-1999
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: US/09/011,143
             FILING DATE: 04-FEB-1998
             APPLICATION NUMBER: PCT/JP97/01824
             FILING DATE: 29-MAY-1997
             APPLICATION NUMBER: JP 165249/1996
             FILING DATE: 04-JUN-1996
        ATTORNEY/AGENT INFORMATION:
             NAME: BROWDY, Roger L.
             REGISTRATION NUMBER: 25,618
             REFERENCE/DOCKET NUMBER: IMAMURA=1
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: 202-628-5197
             TELEFAX: 202-737-3528
   INFORMATION FOR SEQ ID NO: 5:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 2193 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

Alignment Scores:
Pred. No.:                5.78e-214      Length:          2193
Score:                    206.00         Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              67.1%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-302-495-5 (1-2193)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969
```

```
Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050

RESULT 17
US-10-079-616-5
  Sequence 5, Application US/10079616
  Patent No. 6566097
    GENERAL INFORMATION:
         APPLICANT: IMAMURA, Takayuki
                    MAEDA, Hiroaki
                    FUJIYASU, Takeshi
                    IMAGAWA, Yoshitaka
                    TOKIYOSHI, Sachio
         TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
         NUMBER OF SEQUENCES: 26
         CORRESPONDENCE ADDRESS:
              ADDRESSEE: BROWDY AND NEIMARK
              STREET: 419 Seventh Street, N.W., Suite 300
              CITY: Washington
              STATE: D.C.
              COUNTRY: USA
              ZIP: 20004
         COMPUTER READABLE FORM:
              MEDIUM TYPE: Floppy disk
              COMPUTER: IBM PC compatible
              OPERATING SYSTEM: PC-DOS/MS-DOS
              SOFTWARE: PatentIn Release #1.0, Version #1.30
         CURRENT APPLICATION DATA:
              APPLICATION NUMBER: US/10/079,616
              FILING DATE: 22-Feb-2002
              CLASSIFICATION: <Unknown>
         PRIOR APPLICATION DATA:
              APPLICATION NUMBER: 09/011,143
              FILING DATE: 04-FEB-1998
              APPLICATION NUMBER: PCT/JP97/01824
              FILING DATE: 29-MAY-1997
              APPLICATION NUMBER: JP 165249/1996
              FILING DATE: 04-JUN-1996
         ATTORNEY/AGENT INFORMATION:
              NAME: BROWDY, Roger L.
              REGISTRATION NUMBER: 25,618
              REFERENCE/DOCKET NUMBER: IMAMURA=1
         TELECOMMUNICATION INFORMATION:
              TELEPHONE: 202-628-5197
              TELEFAX: 202-737-3528
    INFORMATION FOR SEQ ID NO: 5:
         SEQUENCE CHARACTERISTICS:
              LENGTH: 2193 base pairs
              TYPE: nucleic acid
              STRANDEDNESS: single
              TOPOLOGY: linear
         MOLECULE TYPE: cDNA
         SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.:                5.78e-214      Length:          2193
Score:                    206.00         Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              67.1%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-10-079-616-5 (1-2193)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050

RESULT 18
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
```

```
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 55
   LENGTH: 985
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(984)
S-09-917-265A-55

lignment Scores:
red. No.:              3.24e-213      Length:         985
core:                  205.00         Matches:        305
ercent Similarity:     99.7%          Conservative:   0
est Local Similarity:  99.7%          Mismatches:     1
uery Match:            66.8%          Indels:         0
B:                     3              Gaps:           0

S-10-821-670A-27 (1-307) x US-09-917-265A-55 (1-985)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
b        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy       301 TrpAlaSerValSerCys 306
             ||||||||||||||||||
Db       967 TGGGCATCCGTGTCCTGC 984

RESULT 19
US-09-917-265A-57/c
; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57

Alignment Scores:
Pred. No.:              3.24e-213      Length:         985
Score:                  205.00         Matches:        305
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            66.8%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-57 (1-985)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500
```

```
)y        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
)b        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

)y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

)y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

)y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

)y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

)y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

)y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

)y        301 TrpAlaSerValSerCys 306
              ||||||||||||||||||
)b         19 TGGGCATCCGTGTCCTGC 2

:ESULT 20
IS-09-917-265A-52
· Sequence 52, Application US/09917265A
· Patent No. 6818444
· GENERAL INFORMATION:
·  APPLICANT: Wonderling, Ramani S.
·  APPLICANT:  Boroughs, Karen L.
·  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
·  TITLE OF INVENTION:  THEREOF
·  FILE REFERENCE: IM-5
·  CURRENT APPLICATION NUMBER: US/09/917,265A
·  CURRENT FILING DATE:  2001-07-27
·  PRIOR APPLICATION NUMBER: 60/223,016
·  PRIOR FILING DATE: 2000-08-04
·  NUMBER OF SEQ ID NOS: 111
·  SOFTWARE: PatentIn version 3.2
· SEQ ID NO 52
:   LENGTH: 921
·   TYPE: DNA
:   ORGANISM: Canis familiaris
·   FEATURE:
·   NAME/KEY: CDS
·   LOCATION: (1)..(921)
IS-09-917-265A-52

\lignment Scores:
>red. No.:                1.76e-30        Length:         921
;core:                    37.00           Matches:        37
>ercent Similarity:       100.0%          Conservative:   0
3est Local Similarity:    100.0%          Mismatches:     0
)uery Match:              12.1%           Indels:         0
)B:                       3               Gaps:           0

IS-10-821-670A-27 (1-307) x US-09-917-265A-52 (1-921)

)y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 21
US-09-917-265A-54/c
; Sequence 54, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-54

Alignment Scores:
Pred. No.:                1.76e-30        Length:         921
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-54 (1-921)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 22
US-09-917-265A-58
; Sequence 58, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-58

Alignment Scores:
```

```
red. No.:              1.88e-30       Length:         987
core:                  37.00          Matches:        37
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            12.1%          Indels:         0
B:                     3              Gaps:           0

S-10-821-670A-27 (1-307) x US-09-917-265A-58 (1-987)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 23
S-09-917-265A-60/c
 Sequence 60, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 60
   LENGTH: 987
   TYPE: DNA
   ORGANISM: Canis familiaris
S-09-917-265A-60

lignment Scores:
red. No.:              1.88e-30       Length:         987
core:                  37.00          Matches:        37
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            12.1%          Indels:         0
B:                     3              Gaps:           0

S-10-821-670A-27 (1-307) x US-09-917-265A-60 (1-987)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

ESULT 24
S-09-079-984A-1
 Sequence 1, Application US/09079984A
 Patent No. 6231850
  GENERAL INFORMATION:
    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
    APPLICANT:  Yamada, Katsushige
    TITLE OF INVENTION:  Canine interleukin 12, a production method
    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
    TITLE OF INVENTION:  method using it
    NUMBER OF SEQUENCES:  16
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Miller & Christenbury Intellectual Property
      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
      STREET:  1600 Market Street, 39th Floor
      CITY:  Philadelphia
      STATE:  PA
      COUNTRY:  USA
      ZIP:  19103
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy Disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  WordPerfect 5.1
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/079,984A
      FILING DATE:  15-MAY-1998
    ATTORNEY/AGENT INFORMATION:
      NAME:  Austin R. Miller
      REGISTRATION NUMBER:  16,602
      REFERENCE/DOCKET NUMBER:  1051-98
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (215) 563-1810
      TELEFAX:  (215) 568-6946
  INFORMATION FOR SEQ ID NO:  1:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  990 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA to mRNA
    ORIGINAL SOURCE:
      ORGANISM:  Canis familiaris
    FEATURE:
      NAME/KEY:  Canine IL12
      LOCATION:  1 to 987
      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

Alignment Scores:
Pred. No.:             1.89e-30       Length:         990
Score:                 37.00          Matches:        37
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           12.1%          Indels:         0
DB:                    3              Gaps:           0

US-10-821-670A-27 (1-307) x US-09-079-984A-1 (1-990)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 25
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
```

```
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  WordPerfect 5.1
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/079,984A
      FILING DATE:  15-MAY-1998
    ATTORNEY/AGENT INFORMATION:
      NAME:  Austin R. Miller
      REGISTRATION NUMBER:  16,602
      REFERENCE/DOCKET NUMBER:  1051-98
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (215) 563-1810
      TELEFAX:  (215) 568-6946
  INFORMATION FOR SEQ ID NO:  11:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  990 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA to mRNA
    ORIGINAL SOURCE:
      ORGANISM:  Canis familiaris
    FEATURE:
      NAME/KEY:  Canine IL12
      LOCATION:  1 to 987
      IDENTIFICATION METHOD:  Similarity
IS-09-079-984A-11

Alignment Scores:
Pred. No.:                1.89e-30        Length:         990
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-079-984A-11 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 26
US-09-390-729-1
 Sequence 1, Application US/09390729
 Patent No. 6562334
  GENERAL INFORMATION:
    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
    APPLICANT:  Yamada, Katsushige
    TITLE OF INVENTION:  Canine interleukin 12, a production method
    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
    TITLE OF INVENTION:  method using it
    NUMBER OF SEQUENCES:  16
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Miller & Christenbury Intellectual Property
      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
      STREET:  1600 Market Street, 39th Floor
      CITY:  Philadelphia
      STATE:  PA
      COUNTRY:  USA
      ZIP:  19103
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy Disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  WordPerfect 5.1
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/390,729
      FILING DATE:
    PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  09/079,984
;     FILING DATE:  15-MAY-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Austin R. Miller
;     REGISTRATION NUMBER:  16,602
;     REFERENCE/DOCKET NUMBER:  1051-98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-1810
;     TELEFAX:  (215) 568-6946
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  990 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM:  Canis familiaris
;   FEATURE:
;     NAME/KEY:  Canine IL12
;     LOCATION:  1 to 987
;     IDENTIFICATION METHOD:  Similarity
US-09-390-729-1

Alignment Scores:
Pred. No.:                1.89e-30        Length:         990
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-390-729-1 (1-990)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 27
US-09-390-729-11
; Sequence 11, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
```

```
      NAME:  Austin R. Miller
      REGISTRATION NUMBER:  16,602
      REFERENCE/DOCKET NUMBER:  1051-98
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (215) 563-1810
      TELEFAX:  (215) 568-6946
  INFORMATION FOR SEQ ID NO:  11:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  990 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA to mRNA
    ORIGINAL SOURCE:
      ORGANISM:  Canis familiaris
    FEATURE:
      NAME/KEY:  Canine IL12
      LOCATION:  1 to 987
      IDENTIFICATION METHOD:  Similarity
S-09-390-729-11

lignment Scores:
red. No.:               1.89e-30       Length:         990
core:                   37.00          Matches:        37
ercent Similarity:      100.0%         Conservative:   0
est Local Similarity:   100.0%         Mismatches:     0
uery Match:             12.1%          Indels:         0
B:                      3              Gaps:           0

S-10-821-670A-27 (1-307) x US-09-390-729-11 (1-990)

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
b       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 28
S-09-917-265A-66
 Sequence 66, Application US/09917265A
 Patent No. 6818444
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265A
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 66
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1533)
S-09-917-265A-66

lignment Scores:
red. No.:               2.89e-30       Length:         1533
core:                   37.00          Matches:        37
ercent Similarity:      100.0%         Conservative:   0
est Local Similarity:   100.0%         Mismatches:     0
uery Match:             12.1%          Indels:         0
B:                      3              Gaps:           0

S-10-821-670A-27 (1-307) x US-09-917-265A-66 (1-1533)

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 29
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

Alignment Scores:
Pred. No.:              2.89e-30       Length:         1533
Score:                  37.00          Matches:        37
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            12.1%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-68 (1-1533)

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 30
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61
```

```
Alignment Scores:
Pred. No.:                3.01e-30        Length:         1599
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-61 (1-1599)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 31
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

Alignment Scores:
Pred. No.:                3.01e-30        Length:         1599
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-63 (1-1599)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 32
US-09-917-265A-107
; Sequence 107, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
US-09-917-265A-107

Alignment Scores:
Pred. No.:                4.24e-30        Length:         2267
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-107 (1-2267)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 33
US-09-917-265A-109/c
; Sequence 109, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-109

Alignment Scores:
Pred. No.:                4.24e-30        Length:         2267
Score:                    37.00           Matches:        37
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              12.1%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-109 (1-2267)

Qy         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

RESULT 34
US-08-186-529-1
; Sequence 1, Application US/08186529
; Patent No. 5573764
```

```
  GENERAL INFORMATION:
    APPLICANT:  Sykes, Megan
    APPLICANT:  Wolf, Stanley F.
    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
    NUMBER OF SEQUENCES:  4
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
      STREET:  87 CambridgePark Drive
      CITY:  Cambridge
      STATE:  MA
      COUNTRY:  USA
      ZIP:  02140
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/186,529
      FILING DATE:
      CLASSIFICATION:  424
    ATTORNEY/AGENT INFORMATION:
      NAME:  McDaniels, Patricia A.
      REGISTRATION NUMBER:  33,194
      REFERENCE/DOCKET NUMBER:  GI 5225
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  617-498-8401
      TELEFAX:  617-876-5851
  INFORMATION FOR SEQ ID NO:  1:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  987 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
    ORIGINAL SOURCE:
      ORGANISM:  Homo sapiens
      CELL TYPE:  Lymphoblast
      CELL LINE:  RPMI 8866
    FEATURE:
      NAME/KEY:  CDS
      LOCATION:  1..987
S-08-186-529-1

lignment Scores:
red. No.:              2.82e-28       Length:        987
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     2              Gaps:          0

S-10-821-670A-27 (1-307) x US-08-186-529-1 (1-987)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 35
S-08-640-386A-1
 Sequence 1, Application US/08640386A
 Patent No. 5756085
  GENERAL INFORMATION:
    APPLICANT:  Sykes, Megan
    APPLICANT:  Wolf, Stanley F.
    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1

Alignment Scores:
Pred. No.:              2.82e-28       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-27 (1-307) x US-08-640-386A-1 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 36
US-08-184-009-194
; Sequence 194, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
```

```
      ZIP:  10036
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/184,009
      FILING DATE:  19-JAN-1994
      CLASSIFICATION:  435
    ATTORNEY/AGENT INFORMATION:
      NAME:  Frommer, William S.
      REGISTRATION NUMBER:  25,506
      REFERENCE/DOCKET NUMBER:  454310-2530
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (212) 840-3333
      TELEFAX:  (212) 840-0712
      TELEX:  425066CURTMS
  INFORMATION FOR SEQ ID NO:  194:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  1018 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
)S-08-184-009-194

\lignment Scores:
)red. No.:                2.91e-28        Length:         1018
;core:                    35.00           Matches:        35
)ercent Similarity:       100.0%          Conservative:   0
)est Local Similarity:    100.0%          Mismatches:     0
)uery Match:              11.4%           Indels:         0
)B:                       2               Gaps:           0

)S-10-821-670A-27 (1-307) x US-08-184-009-194 (1-1018)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
)b        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

(ESULT 37
)S-08-458-356-194
  Sequence 194, Application US/08458356
  Patent No. 5942235
  GENERAL INFORMATION:
    APPLICANT:  Paoletti, Enzo
    APPLICANT:  Tartaglia, James
    APPLICANT:  Cox, William I.
    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
    NUMBER OF SEQUENCES:  217
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Curtis, Morris & Safford
      STREET:  530 Fifth Avenue
      CITY:  New York
      STATE:  NY
      COUNTRY:  USA
      ZIP:  10036
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/458,356
      FILING DATE:  02-JUN-1995
      CLASSIFICATION:  424
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  US 08/184,009
;       FILING DATE:  19-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Frommer, William S.
;       REGISTRATION NUMBER:  25,506
;       REFERENCE/DOCKET NUMBER:  454310-2530
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 840-3333
;       TELEFAX:  (212) 840-0712
;       TELEX:  425066CURTMS
;   INFORMATION FOR SEQ ID NO:  194:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1018 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-458-356-194

Alignment Scores:
Pred. No.:                2.91e-28        Length:         1018
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-27 (1-307) x US-08-458-356-194 (1-1018)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 38
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
```

```
  INFORMATION FOR SEQ ID NO:  194:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  1018 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
S-08-460-736-194

lignment Scores:
red. No.:              2.91e-28       Length:         1018
core:                  35.00          Matches:        35
ercent Similarity:     100.0%         Conservative:   0
est Local Similarity:  100.0%         Mismatches:     0
uery Match:            11.4%          Indels:         0
B:                     3              Gaps:           0

S-10-821-670A-27 (1-307) x US-08-460-736-194 (1-1018)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
b        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

ESULT 39
S-09-535-370-194
 Sequence 194, Application US/09535370
 Patent No. 6537594
   GENERAL INFORMATION:
        APPLICANT: Paoletti, Enzo
                   Tartaglia, James
                   Cox, William I.
        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
        NUMBER OF SEQUENCES: 217
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: Curtis, Morris & Safford
             STREET: 530 Fifth Avenue
             CITY: New York
             STATE: NY
             COUNTRY: USA
             ZIP: 10036
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.25
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/535,370
             FILING DATE: 24-Mar-2000
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 08/460,736
             FILING DATE: <Unknown>
        ATTORNEY/AGENT INFORMATION:
             NAME: Frommer, William S.
             REGISTRATION NUMBER: 25,506
             REFERENCE/DOCKET NUMBER: 454310-2530
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (212) 840-3333
             TELEFAX: (212) 840-0712
             TELEX: 425066CURTMS
   INFORMATION FOR SEQ ID NO: 194:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 1018 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 194:
S-09-535-370-194

Alignment Scores:
Pred. No.:             2.91e-28       Length:         1018
Score:                 35.00          Matches:        35
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           11.4%          Indels:         0
DB:                    3              Gaps:           0

US-10-821-670A-27 (1-307) x US-09-535-370-194 (1-1018)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
             |||||||||||||||||||||||||||||||||||||||||||||
Db       737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 40
US-09-663-667-194
; Sequence 194, Application US/09663667
; Patent No. 6780407
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,667
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/184,009
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 194:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1018 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-663-667-194

Alignment Scores:
Pred. No.:             2.91e-28       Length:         1018
Score:                 35.00          Matches:        35
Percent Similarity:    100.0%         Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:           11.4%          Indels:         0
DB:                    3              Gaps:           0
```

```
)S-10-821-670A-27 (1-307) x US-09-663-667-194 (1-1018)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
)b        737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

(ESULT 41
)S-09-634-368-4
 Sequence 4, Application US/09634368
 Patent No. 6617135
 GENERAL INFORMATION:
  APPLICANT:  Gillies, Stephen
  APPLICANT:  Lo, Kin Ming
  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
  FILE REFERENCE:  LEX-010
  CURRENT APPLICATION NUMBER: US/09/634,368
  CURRENT FILING DATE:  2000-08-09
  PRIOR APPLICATION NUMBER:  60/147,924
  PRIOR FILING DATE:  1999-08-09
  NUMBER OF SEQ ID NOS:  32
  SOFTWARE:  PatentIn Ver. 2.0
 SEQ ID NO 4
   LENGTH: 1389
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Description of Artificial Sequence: human
   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
)S-09-634-368-4

\lignment Scores:
>red. No.:                3.94e-28        Length:         1389
;core:                    35.00           Matches:        35
>ercent Similarity:       100.0%          Conservative:   0
;est Local Similarity:    100.0%          Mismatches:     0
)uery Match:              11.4%           Indels:         0
)B:                       3               Gaps:           0

)S-10-821-670A-27 (1-307) x US-09-634-368-4 (1-1389)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
)b        706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

(ESULT 42
)S-08-751-767A-3
 Sequence 3, Application US/08751767A
 Patent No. 5994104
  GENERAL INFORMATION:
    APPLICANT:  ANDERSON, ROBERT J.
    APPLICANT:  GRANT, HUGH
    APPLICANT:  MACDONALD, IAN D.
    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
    NUMBER OF SEQUENCES:  80
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  NIXON & VANDERHYE P.C.
      STREET:  1100 NORTH GLEBE ROAD
      CITY:  ARLINGTON
      STATE:  VA
      COUNTRY:  USA
      ZIP:  22201
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/751,767A
      FILING DATE:  08-NOV-1996
      CLASSIFICATION:  536
    ATTORNEY/AGENT INFORMATION:
      NAME:  SADOFF, B.J.
      REGISTRATION NUMBER:  36,663
      REFERENCE/DOCKET NUMBER:  117-221
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  7038164091
      TELEFAX:  7038164100
  INFORMATION FOR SEQ ID NO:  3:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  1399 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
    FEATURE:
      NAME/KEY:  CDS
      LOCATION:  43..1026
US-08-751-767A-3

Alignment Scores:
Pred. No.:                3.97e-28        Length:         1399
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-27 (1-307) x US-08-751-767A-3 (1-1399)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

RESULT 43
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
```

```
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  7038164091
      TELEFAX:  7038164100
  INFORMATION FOR SEQ ID NO:  11:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  1560 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
    FEATURE:
      NAME/KEY:  CDS
      LOCATION:  1..1557
S-08-751-767A-11

lignment Scores:
red. No.:               4.41e-28       Length:        1560
core:                   35.00          Matches:       35
ercent Similarity:      100.0%         Conservative:  0
est Local Similarity:   100.0%         Mismatches:    0
uery Match:             11.4%          Indels:        0
B:                      2              Gaps:          0

S-10-821-670A-27 (1-307) x US-08-751-767A-11 (1-1560)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        583 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 642

y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b        643 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 687

ESULT 44
S-08-751-767A-9
 Sequence 9, Application US/08751767A
 Patent No. 5994104
  GENERAL INFORMATION:
    APPLICANT:  ANDERSON, ROBERT J.
    APPLICANT:  GRANT, HUGH
    APPLICANT:  MACDONALD, IAN D.
    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
    NUMBER OF SEQUENCES:  80
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  NIXON & VANDERHYE P.C.
      STREET:  1100 NORTH GLEBE ROAD
      CITY:  ARLINGTON
      STATE:  VA
      COUNTRY:  USA
      ZIP:  22201
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/751,767A
      FILING DATE:  08-NOV-1996
      CLASSIFICATION:  536
    ATTORNEY/AGENT INFORMATION:
      NAME:  SADOFF, B.J.
      REGISTRATION NUMBER:  36,663
      REFERENCE/DOCKET NUMBER:  117-221
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  7038164091
      TELEFAX:  7038164100
  INFORMATION FOR SEQ ID NO:  9:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  1623 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

Alignment Scores:
Pred. No.:              4.58e-28       Length:        1623
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-27 (1-307) x US-08-751-767A-9 (1-1623)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 45
US-09-949-016-5452
; Sequence 5452, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5452
;   LENGTH: 2307
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5452

Alignment Scores:
Pred. No.:              6.46e-28       Length:        2307
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-949-016-5452 (1-2307)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       648 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 707

Qy       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db       708 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 752

RESULT 46
US-08-265-087-1
; Sequence 1, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
```

```
    TITLE OF INVENTION:  Compositions and Methods for Use of
    TITLE OF INVENTION:  IL-12 as an Adjuvant
    NUMBER OF SEQUENCES:  4
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Howson and Howson
      STREET:  Spring House Corporate Center, PO Box 457
      CITY:  Spring House
      STATE:  Pennsylvania
      COUNTRY:  USA
      ZIP:  19477
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/265,087
      FILING DATE:
      CLASSIFICATION:  424
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  US 08/229,282
      FILING DATE:  18-APR-1994
    ATTORNEY/AGENT INFORMATION:
      NAME:  Bak, Mary E.
      REGISTRATION NUMBER:  31,215
      REFERENCE/DOCKET NUMBER:  WST51AUSA
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  215-540-9206
      TELEFAX:  215-540-5818
  INFORMATION FOR SEQ ID NO:  1:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  2362 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  unknown
    MOLECULE TYPE:  cDNA
    FEATURE:
      NAME/KEY:  CDS
      LOCATION:  33..1016
)S-08-265-087-1

\lignment Scores:
)red. No.:              6.61e-28        Length:         2362
)core:                  35.00           Matches:        35
)ercent Similarity:     100.0%          Conservative:   0
)est Local Similarity:  100.0%          Mismatches:     0
)uery Match:            11.4%           Indels:         0
)B:                     2               Gaps:           0

)S-10-821-670A-27 (1-307) x US-08-265-087-1 (1-2362)

)y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

)y        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
)b        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

(ESULT 47
)S-08-621-493-1
  Sequence 1, Application US/08621493
  Patent No. 5723127
   GENERAL INFORMATION:
     APPLICANT:  Scott, Phillip
     APPLICANT:  Trinchieri, Giorgio
     TITLE OF INVENTION:  Compositions and Methods for Use of
     TITLE OF INVENTION:  IL-12 as an Adjuvant
     NUMBER OF SEQUENCES:  4
     CORRESPONDENCE ADDRESS:
       ADDRESSEE:  Howson and Howson
       STREET:  Spring House Corporate Center, PO Box 457
       CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-621-493-1

Alignment Scores:
Pred. No.:              6.61e-28        Length:         2362
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x US-08-621-493-1 (1-2362)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 48
US-08-965-688-1
; Sequence 1, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/965,688
      FILING DATE:
      CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  08/621,493
      FILING DATE:  25-MAR-1996
      APPLICATION NUMBER:  08/265,087
      FILING DATE:  17-JUN-1994
      APPLICATION NUMBER:  US 08/229,282
      FILING DATE:  18-APR-1994
    ATTORNEY/AGENT INFORMATION:
      NAME:  Bak, Mary E.
      REGISTRATION NUMBER:  31,215
      REFERENCE/DOCKET NUMBER:  WST51AUSA
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  215-540-9206
      TELEFAX:  215-540-5818
  INFORMATION FOR SEQ ID NO:  1:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  2362 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  unknown
    MOLECULE TYPE:  cDNA
    FEATURE:
      NAME/KEY:  CDS
      LOCATION:  33..1016
S-08-965-688-1

lignment Scores:
red. No.:               6.61e-28        Length:         2362
core:                   35.00           Matches:        35
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             11.4%           Indels:         0
B:                      2               Gaps:           0

S-10-821-670A-27 (1-307) x US-08-965-688-1 (1-2362)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

ESULT 49
S-09-260-173-1
 Sequence 1, Application US/09260173
 Patent No. 6168923
   GENERAL INFORMATION:
        APPLICANT: Scott, Phillip
                   Trinchieri, Giorgio
        TITLE OF INVENTION: Compositions and Methods for Use of
                            IL-12 as an Adjuvant
        NUMBER OF SEQUENCES: 4
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: Howson and Howson
             STREET: Spring House Corporate Center, PO Box 457
             CITY: Spring House
             STATE: Pennsylvania
             COUNTRY: USA
             ZIP: 19477
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2362 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  33..1016
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

Alignment Scores:
Pred. No.:              6.61e-28        Length:         2362
Score:                  35.00           Matches:        35
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            11.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-260-173-1 (1-2362)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 50
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
```

```
  PRIOR FILING DATE: 1990-09-18
  PRIOR APPLICATION NUMBER: 07/307,817
  PRIOR FILING DATE: 1989-02-07
  PRIOR APPLICATION NUMBER: 07/269,945
  PRIOR FILING DATE: 1988-11-10
  NUMBER OF SEQ ID NOS: 19
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
    LENGTH: 2362
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
    OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
    NAME/KEY: CDS
    LOCATION: (33)..(1016)
US-09-924-703-3

Alignment Scores:
Pred. No.:                6.61e-28        Length:         2362
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-924-703-3 (1-2362)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 51
US-08-751-767A-7
 Sequence 7, Application US/08751767A
 Patent No. 5994104
  GENERAL INFORMATION:
    APPLICANT:  ANDERSON, ROBERT J.
    APPLICANT:  GRANT, HUGH
    APPLICANT:  MACDONALD, IAN D.
    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
    NUMBER OF SEQUENCES:  80
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  NIXON & VANDERHYE P.C.
      STREET:  1100 NORTH GLEBE ROAD
      CITY:  ARLINGTON
      STATE:  VA
      COUNTRY:  USA
      ZIP:  22201
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/751,767A
      FILING DATE:  08-NOV-1996
      CLASSIFICATION:  536
    ATTORNEY/AGENT INFORMATION:
      NAME:  SADOFF, B.J.
      REGISTRATION NUMBER:  36,663
      REFERENCE/DOCKET NUMBER:  117-221
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  7038164091
      TELEFAX:  7038164100
  INFORMATION FOR SEQ ID NO:  7:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  6139 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  both
      TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
    FEATURE:
      NAME/KEY:  CDS
      LOCATION:  3222..4841
US-08-751-767A-7

Alignment Scores:
Pred. No.:                1.68e-27        Length:         6139
Score:                    35.00           Matches:        35
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              11.4%           Indels:         0
DB:                       2               Gaps:           0

US-10-821-670A-27 (1-307) x US-08-751-767A-7 (1-6139)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3867 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3926

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db       3927 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3971

RESULT 52
US-08-848-760B-24
; Sequence 24, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24

Alignment Scores:
Pred. No.:                3.2e-15         Length:         987
```

```
core:                 23.00          Matches:       23
ercent Similarity:    100.0%         Conservative:  0
est Local Similarity: 100.0%         Mismatches:    0
uery Match:           7.5%           Indels:        0
B:                    3              Gaps:          0

S-10-821-670A-27 (1-307) x US-08-848-760B-24 (1-987)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y       215 AspProPro 217
            |||||||||
b       706 GACCCACCC 714

ESULT 53
S-09-826-025-24
 Sequence 24, Application US/09826025
 Patent No. 6730512
   GENERAL INFORMATION:
        APPLICANT: Chang, Lung-Ji
        TITLE OF INVENTION: Combination Immunogene Therapy
        NUMBER OF SEQUENCES: 25
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: Medlen & Carroll, LLP
             STREET: 220 Montgomery Street, Suite 2200
             CITY: San Francisco
             STATE: California
             COUNTRY: United States of America
             ZIP: 94104
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/826,025
             FILING DATE: 04-Apr-2001
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 08/838,702
             FILING DATE: <Unknown>
        ATTORNEY/AGENT INFORMATION:
             NAME: Ingolia, Diane E.
             REGISTRATION NUMBER: 40,027
             REFERENCE/DOCKET NUMBER: CHANG-02687
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: (415) 705-8410
             TELEFAX: (415) 397-8338
   INFORMATION FOR SEQ ID NO: 24:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 987 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: double
             TOPOLOGY: linear
        MOLECULE TYPE: other nucleic acid
             DESCRIPTION: /desc = "DNA"
        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
S-09-826-025-24

lignment Scores:
red. No.:             3.2e-15        Length:        987
core:                 23.00          Matches:       23
ercent Similarity:    100.0%         Conservative:  0
est Local Similarity: 100.0%         Mismatches:    0
uery Match:           7.5%           Indels:        0
B:                    3              Gaps:          0

S-10-821-670A-27 (1-307) x US-09-826-025-24 (1-987)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy      215 AspProPro 217
            |||||||||
Db      706 GACCCACCC 714

RESULT 54
US-09-310-842-4
; Sequence 4, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

Alignment Scores:
Pred. No.:            5.97e-15       Length:        1870
Score:                23.00          Matches:       23
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          7.5%           Indels:        0
DB:                   3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-310-842-4 (1-1870)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1278 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 1337

Qy      215 AspProPro 217
            |||||||||
Db     1338 GACCCACCC 1346

RESULT 55
US-09-851-062-3
; Sequence 3, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
```

```
  CURRENT FILING DATE:  2001-05-07
  NUMBER OF SEQ ID NOS: 87
 SEQ ID NO 3
   LENGTH: 2318
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (14)...(1000)
US-09-851-062-3

Alignment Scores:
Pred. No.:                7.36e-15       Length:          2318
Score:                    23.00          Matches:         23
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              7.5%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-851-062-3 (1-2318)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 718

Qy        215 AspProPro 217
              |||||||||
Db        719 GACCCACCC 727

RESULT 56
US-09-949-016-315
 Sequence 315, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   FILE REFERENCE: CL001307
   CURRENT APPLICATION NUMBER: US/09/949,016
   CURRENT FILING DATE:  2000-04-14
   PRIOR APPLICATION NUMBER: 60/241,755
   PRIOR FILING DATE: 2000-10-20
   PRIOR APPLICATION NUMBER: 60/237,768
   PRIOR FILING DATE: 2000-10-03
   PRIOR APPLICATION NUMBER: 60/231,498
   PRIOR FILING DATE: 2000-09-08
   NUMBER OF SEQ ID NOS: 207012
   SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 315
    LENGTH: 2318
    TYPE: DNA
    ORGANISM: Human
US-09-949-016-315

Alignment Scores:
Pred. No.:                7.36e-15       Length:          2318
Score:                    23.00          Matches:         23
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              7.5%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-949-016-315 (1-2318)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 718

Qy        215 AspProPro 217
              |||||||||
Db        719 GACCCACCC 727

RESULT 57
US-09-949-016-12057
; Sequence 12057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12057
;   LENGTH: 16002
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12057

Alignment Scores:
Pred. No.:                5.91e-13       Length:          16002
Score:                    22.00          Matches:         22
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              7.2%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-949-016-12057 (1-16002)

Qy        231 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9948 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 10007

Qy        251 ThrPhe 252
              ||||||
Db      10008 ACATTC 10013

RESULT 58
US-09-949-016-17194
; Sequence 17194, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17194
;   LENGTH: 16003
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17194

Alignment Scores:
Pred. No.:                5.91e-13       Length:          16003
Score:                    22.00          Matches:         22
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              7.2%           Indels:          0
```

```
B:                     3              Gaps:          0

S-10-821-670A-27 (1-307) x US-09-949-016-17194 (1-16003)

y        231 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 250
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       9948 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 10007

y        251 ThrPhe 252
             ||||||
b      10008 ACATTC 10013

ESULT 59
S-09-823-549-77
 Sequence 77, Application US/09823549
 Patent No. 6664442
 GENERAL INFORMATION:
  APPLICANT: McConlogue, Lisa  C
  APPLICANT:  Games, Kate D.
  APPLICANT:  Yednock, Theodore A.
  APPLICANT:  Hua, Tan
  APPLICANT:  Messersmith, Elizabeth
  APPLICANT:  Bard, Frederique
  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
  FILE REFERENCE: 015270-009110US
  CURRENT APPLICATION NUMBER: US/09/823,549
  CURRENT FILING DATE:  2001-03-30
  PRIOR APPLICATION NUMBER: US 60/193,847
  PRIOR FILING DATE: 2000-03-30
  NUMBER OF SEQ ID NOS: 85
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 77
   LENGTH: 73
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: IL-12 p40, #1 marker
S-09-823-549-77

lignment Scores:
red. No.:              8.54e-10       Length:        73
core:                  17.00          Matches:       17
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            5.5%           Indels:        0
B:                     3              Gaps:          0

S-10-821-670A-27 (1-307) x US-09-823-549-77 (1-73)

y        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
b          9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59

ESULT 60
S-09-949-016-24253/c
 Sequence 24253, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
  APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
  CURRENT APPLICATION NUMBER: US/09/949,016
  CURRENT FILING DATE:  2000-04-14
  PRIOR APPLICATION NUMBER: 60/241,755
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/237,768
  PRIOR FILING DATE: 2000-10-03
  PRIOR APPLICATION NUMBER: 60/231,498
  PRIOR FILING DATE: 2000-09-08
  NUMBER OF SEQ ID NOS: 207012
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 24253
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24253

Alignment Scores:
Pred. No.:             6.65e-09       Length:        601
Score:                 17.00          Matches:       17
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           5.5%           Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-949-016-24253 (1-601)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIle 211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       102 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATC 52

RESULT 61
US-09-949-016-190686/c
; Sequence 190686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190686
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190686

Alignment Scores:
Pred. No.:             6.65e-09       Length:        601
Score:                 17.00          Matches:       17
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           5.5%           Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-949-016-190686 (1-601)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIle 211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       102 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATC 52

RESULT 62
US-08-385-335A-13
; Sequence 13, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
```

ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,335A
FILING DATE: 08-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1061 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-385-335A-13

Alignment Scores:

Pred. No.:	1.16e-08	Length:	1061
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.5%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-27 (1-307) x US-08-385-335A-13 (1-1061)

```
Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 766
```

RESULT 63
US-09-634-368-3
Sequence 3, Application US/09634368
Patent No. 6617135
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/09/634,368
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1409
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-09-634-368-3

Alignment Scores:

Pred. No.:	1.53e-08	Length:	1409
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.5%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-634-368-3 (1-1409)

```
Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740
```

RESULT 64
US-09-634-368-2
; Sequence 2, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/09/634,368
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-2

Alignment Scores:

Pred. No.:	1.59e-08	Length:	1472
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.5%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-634-368-2 (1-1472)

```
Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740
```

RESULT 65
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/09/634,368
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

Alignment Scores:

Pred. No.:	1.69e-08	Length:	1569
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.5%	Indels:	0

```
E:                    3              Gaps:          0

S-10-821-670A-27 (1-307) x US-09-634-368-12 (1-1569)

y        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

ESULT 66
S-09-634-368-11
 Sequence 11, Application US/09634368
 Patent No. 6617135
 GENERAL INFORMATION:
  APPLICANT:  Gillies, Stephen
  APPLICANT:  Lo, Kin Ming
  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
  FILE REFERENCE:  LEX-010
  CURRENT APPLICATION NUMBER: US/09/634,368
  CURRENT FILING DATE:  2000-08-09
  PRIOR APPLICATION NUMBER:  60/147,924
  PRIOR FILING DATE:  1999-08-09
  NUMBER OF SEQ ID NOS:  32
  SOFTWARE:  PatentIn Ver. 2.0
 SEQ ID NO 11
   LENGTH: 2013
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Description of Artificial Sequence: murine
   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
S-09-634-368-11

lignment Scores:
red. No.:             2.16e-08       Length:        2013
core:                 17.00          Matches:       17
ercent Similarity:    100.0%         Conservative:  0
est Local Similarity: 100.0%         Mismatches:    0
uery Match:           5.5%           Indels:        0
B:                    3              Gaps:          0

S-10-821-670A-27 (1-307) x US-09-634-368-11 (1-2013)

y        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

ESULT 67
S-09-634-368-13
 Sequence 13, Application US/09634368
 Patent No. 6617135
 GENERAL INFORMATION:
  APPLICANT:  Gillies, Stephen
  APPLICANT:  Lo, Kin Ming
  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
  FILE REFERENCE:  LEX-010
  CURRENT APPLICATION NUMBER: US/09/634,368
  CURRENT FILING DATE:  2000-08-09
  PRIOR APPLICATION NUMBER:  60/147,924
  PRIOR FILING DATE:  1999-08-09
  NUMBER OF SEQ ID NOS:  32
  SOFTWARE:  PatentIn Ver. 2.0
 SEQ ID NO 13
   LENGTH: 2709
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Description of Artificial Sequence: murine
   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
   OTHER INFORMATION: sequence
S-09-634-368-13

lignment Scores:
red. No.:             2.88e-08       Length:        2709
Score:                17.00          Matches:       17
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          5.5%           Indels:        0
DB:                   3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-634-368-13 (1-2709)

Qy       205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1927 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1977

RESULT 68
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2377..3384
;      OTHER INFORMATION:  /product= "p40 gene product"
US-08-659-206A-4

Alignment Scores:
Pred. No.:            6.55e-08       Length:        6295
Score:                17.00          Matches:       17
Percent Similarity:   100.0%         Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:          5.5%           Indels:        0
DB:                   2              Gaps:          0

US-10-821-670A-27 (1-307) x US-08-659-206A-4 (1-6295)

Qy       205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       3046 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 3096

RESULT 69
US-08-659-206A-1
  Sequence 1, Application US/08659206A
  Patent No. 5922685
   GENERAL INFORMATION:
     APPLICANT:  Rakhmilevich, Alexander
     TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
     NUMBER OF SEQUENCES:  6
     CORRESPONDENCE ADDRESS:
       ADDRESSEE:  Quarles & Brady
       STREET:  1 South Pinckney Street
       CITY:  Madison
       STATE:  WI
       COUNTRY:  US
       ZIP:  53703
     COMPUTER READABLE FORM:
       MEDIUM TYPE:  Floppy disk
       COMPUTER:  IBM PC compatible
       OPERATING SYSTEM:  PC-DOS/MS-DOS
       SOFTWARE:  PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
       APPLICATION NUMBER:  US/08/659,206A
       FILING DATE:
       CLASSIFICATION:  435
     ATTORNEY/AGENT INFORMATION:
       NAME:  Seay, Nicholas J
       REGISTRATION NUMBER:  27386
       REFERENCE/DOCKET NUMBER:  110229.91144
     TELECOMMUNICATION INFORMATION:
       TELEPHONE:  608-251-5000
       TELEFAX:  608-251-9166
   INFORMATION FOR SEQ ID NO:  1:
     SEQUENCE CHARACTERISTICS:
       LENGTH:  7287 base pairs
       TYPE:  nucleic acid
       STRANDEDNESS:  double
       TOPOLOGY:  circular
     MOLECULE TYPE:  other nucleic acid
       DESCRIPTION:  /desc = "Plasmid DNA"
     IMMEDIATE SOURCE:
       CLONE:  pWRG3169
     FEATURE:
       NAME/KEY:  promoter
       LOCATION:  1..628
     FEATURE:
       NAME/KEY:  iDNA
       LOCATION:  629..810
     FEATURE:
       NAME/KEY:  CDS
       LOCATION:  join(953..1258, 1332..1673)
       OTHER INFORMATION:  /product= "p35 gene product"
     FEATURE:
       NAME/KEY:  polyA_site
       LOCATION:  1797..2024
     FEATURE:
       NAME/KEY:  promoter
       LOCATION:  2110..2737
     FEATURE:
       NAME/KEY:  iDNA
       LOCATION:  2738..2919
     FEATURE:
       NAME/KEY:  CDS
       LOCATION:  2983..3990
       OTHER INFORMATION:  /product= "p40 gene product"
     FEATURE:
       NAME/KEY:  polyA_site
       LOCATION:  4075..4306
US-08-659-206A-1

Alignment Scores:
Pred. No.:              7.56e-08        Length:         7287
Score:                  17.00           Matches:        17
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.5%            Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x US-08-659-206A-1 (1-7287)

Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3652 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 3702

RESULT 70
US-09-011-143-12
; Sequence 12, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-12

Alignment Scores:
Pred. No.:              0.000124        Length:         38
Score:                  12.00           Matches:        12
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.9%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-011-143-12 (1-38)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGlu 12
```

```
                ||||||||||||||||||||||||||||||||||||
b          1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36

ESULT 71
S-09-302-495-12
 Sequence 12, Application US/09302495
 Patent No. 6518045
   GENERAL INFORMATION:
        APPLICANT: IMAMURA, Takayuki
                   MAEDA, Hiroaki
                   FUJIYASU, Takeshi
                   IMAGAWA, Yoshitaka
                   TOKIYOSHI, Sachio
        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
        NUMBER OF SEQUENCES: 26
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: BROWDY AND NEIMARK
             STREET: 419 Seventh Street, N.W., Suite 300
             CITY: Washington
             STATE: D.C.
             COUNTRY: USA
             ZIP: 20004
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/302,495
             FILING DATE: 30-Apr-1999
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: US/09/011,143
             FILING DATE: 04-FEB-1998
             APPLICATION NUMBER: PCT/JP97/01824
             FILING DATE: 29-MAY-1997
             APPLICATION NUMBER: JP 165249/1996
             FILING DATE: 04-JUN-1996
        ATTORNEY/AGENT INFORMATION:
             NAME: BROWDY, Roger L.
             REGISTRATION NUMBER: 25,618
             REFERENCE/DOCKET NUMBER: IMAMURA=1
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: 202-628-5197
             TELEFAX: 202-737-3528
    INFORMATION FOR SEQ ID NO: 12:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 38 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
S-09-302-495-12

lignment Scores:
red. No.:               0.000124        Length:         38
core:                   12.00           Matches:        12
ercent Similarity:      100.0%          Conservative:   0
est Local Similarity:   100.0%          Mismatches:     0
uery Match:             3.9%            Indels:         0
B:                      3               Gaps:           0

S-10-821-670A-27 (1-307) x US-09-302-495-12 (1-38)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGlu 12
             ||||||||||||||||||||||||||||||||||||
b          1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36

ESULT 72
S-10-079-616-12
 Sequence 12, Application US/10079616
 Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 38 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-079-616-12

Alignment Scores:
Pred. No.:              0.000124        Length:         38
Score:                  12.00           Matches:        12
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            3.9%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-079-616-12 (1-38)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGlu 12
             ||||||||||||||||||||||||||||||||||||
Db         1 ATCTGGGARCTSGARAARAACGTSTACGTSGTSGAR 36

RESULT 73
US-09-949-016-24250/c
; Sequence 24250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
```

```
  PRIOR APPLICATION NUMBER: 60/241,755
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/237,768
  PRIOR FILING DATE: 2000-10-03
  PRIOR APPLICATION NUMBER: 60/231,498
  PRIOR FILING DATE: 2000-09-08
  NUMBER OF SEQ ID NOS: 207012
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 24250
    LENGTH: 601
    TYPE: DNA
    ORGANISM: Human
US-09-949-016-24250

Alignment Scores:
Pred. No.:                0.00183        Length:          601
Score:                    12.00          Matches:         12
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              3.9%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-949-016-24250 (1-601)

Qy          17 ProAspAlaProGlyGluMetValValLeuThrCys 28
               ||||||||||||||||||||||||||||||||||||
Db          81 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 46

RESULT 74
US-09-949-016-24251/c
  Sequence 24251, Application US/09949016
  Patent No. 6812339
  GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   FILE REFERENCE: CL001307
   CURRENT APPLICATION NUMBER: US/09/949,016
   CURRENT FILING DATE:  2000-04-14
   PRIOR APPLICATION NUMBER: 60/241,755
   PRIOR FILING DATE: 2000-10-20
   PRIOR APPLICATION NUMBER: 60/237,768
   PRIOR FILING DATE: 2000-10-03
   PRIOR APPLICATION NUMBER: 60/231,498
   PRIOR FILING DATE: 2000-09-08
   NUMBER OF SEQ ID NOS: 207012
   SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 24251
    LENGTH: 601
    TYPE: DNA
    ORGANISM: Human
US-09-949-016-24251

Alignment Scores:
Pred. No.:                0.00183        Length:          601
Score:                    12.00          Matches:         12
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              3.9%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-949-016-24251 (1-601)

Qy          17 ProAspAlaProGlyGluMetValValLeuThrCys 28
               ||||||||||||||||||||||||||||||||||||
Db         100 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 65

RESULT 75
US-09-949-016-190683/c
  Sequence 190683, Application US/09949016
  Patent No. 6812339
  GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190683
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-190683

Alignment Scores:
Pred. No.:                0.00183        Length:          601
Score:                    12.00          Matches:         12
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              3.9%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-949-016-190683 (1-601)

Qy          17 ProAspAlaProGlyGluMetValValLeuThrCys 28
               ||||||||||||||||||||||||||||||||||||
Db          81 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 46

RESULT 76
US-09-949-016-190684/c
; Sequence 190684, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190684
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-190684

Alignment Scores:
Pred. No.:                0.00183        Length:          601
Score:                    12.00          Matches:         12
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              3.9%           Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-949-016-190684 (1-601)

Qy          17 ProAspAlaProGlyGluMetValValLeuThrCys 28
               ||||||||||||||||||||||||||||||||||||
Db         100 CCGGATGCCCCTGGAGAAATGGTGGTCCTCACCTGT 65

RESULT 77
```

```
S-09-513-999C-4018
 Sequence 4018, Application US/09513999C
 Patent No. 6783961
 GENERAL INFORMATION:
  APPLICANT: Dumas Milne Edwards, J.B.
  APPLICANT:  Duclert, A.
  APPLICANT:  Giordano, J.Y.
  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 Patent No. 6783961
  FILE REFERENCE: 59.US2.REG
  CURRENT APPLICATION NUMBER: US/09/513,999C
  CURRENT FILING DATE:  2000-02-24
  PRIOR APPLICATION NUMBER: US 60/122,487
  PRIOR FILING DATE: 1999-02-26
  NUMBER OF SEQ ID NOS: 36681
  SOFTWARE: Patent.pm
 SEQ ID NO 4018
    LENGTH: 532
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: CDS
    LOCATION: 144..503
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 29
    OTHER INFORMATION: n=a, g, c or t
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 30
    OTHER INFORMATION: n=a, g, c or t
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 289
    OTHER INFORMATION: k=g or t
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 460
    OTHER INFORMATION: n=a, g, c or t
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 461
    OTHER INFORMATION: n=a, g, c or t
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 503
    OTHER INFORMATION: k=g or t
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 513
    OTHER INFORMATION: r=a or g
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 518
    OTHER INFORMATION: r=a or g
    FEATURE:
    NAME/KEY: UNSURE
    LOCATION: 49
    OTHER INFORMATION: Xaa=Leu or Arg
    FEATURE:
    NAME/KEY: UNSURE
    LOCATION: 106
    OTHER INFORMATION: Xaa=Ile or Lys or Met or Asn or Arg or Ser or Thr
S-09-513-999C-4018

lignment Scores:
red. No.:               2.98          Length:         532
core:                   9.00          Matches:        9
ercent Similarity:      100.0%        Conservative:   0
est Local Similarity:   100.0%        Mismatches:     0
uery Match:             2.9%          Indels:         0
B:                      3             Gaps:           0
```

```
US-10-821-670A-27 (1-307) x US-09-513-999C-4018 (1-532)

Qy          79 PheLeuLeuIleHisLysLysGluAsp 87
               |||||||||||||||||||||||||||
Db         462 TTTTTACTGATTCACAAAAAGGAAGAC 488

RESULT 78
US-09-887-145-37
; Sequence 37, Application US/09887145
; Patent No. 6780641
;   GENERAL INFORMATION:
;        APPLICANT: Kim, Seung U
;        TITLE OF INVENTION: Immortalized human microglia
;                            cell and continuous cell line
;        NUMBER OF SEQUENCES: 54
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: David Prashker, Esq.
;             STREET: P.O. Box 5387
;             CITY: Magnolia
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 01930
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
;             COMPUTER: Dell PC
;             OPERATING SYSTEM: MS DOS
;             SOFTWARE: Microsoft Word version 97
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/887,145
;             FILING DATE: 22-Jun-2001
;             CLASSIFICATION: Unknown
;        ATTORNEY/AGENT INFORMATION:
;             NAME: David Prashker, Esq.
;             REGISTRATION NUMBER: 29,693
;             REFERENCE/DOCKET NUMBER: UBC-002
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (978) 525-3794
;   INFORMATION FOR SEQ ID NO: 37:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 25 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-887-145-37

Alignment Scores:
Pred. No.:              1.86          Length:         25
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.6%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-27 (1-307) x US-09-887-145-37 (1-25)

Qy          69 HisLysGlyGlyGluValLeuSer 76
               |||||||||||||||||||||||
Db           2 CACAAAGGAGGCGAGGTTCTAAGC 25

RESULT 79
US-09-917-265A-86/c
; Sequence 86, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
```

PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 86
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Primer
IS-09-917-265A-86

Alignment Scores:

Pred. No.:	1.86	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265A-86 (1-25)

```
Qy        299 SerAsnTrpAlaSerValSerCys 306
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 80
US-09-011-143-13/c
Sequence 13, Application US/09011143
Patent No. 6472509
GENERAL INFORMATION:
APPLICANT: IMAMURA, Takayuki
APPLICANT: MAEDA, Hiroaki
APPLICANT: FUJIYASU, Takeshi
APPLICANT: IMAGAWA, Yoshitaka
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,143
FILING DATE: 04-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/01824
FILING DATE: 29-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 165249/1996
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: IMAMURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-011-143-13

Alignment Scores:

Pred. No.:	2.36	Length:	32
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-011-143-13 (1-32)

```
Qy        154 SerAlaGluLysValArgValAsp 161
              ||||||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGTCGAC 9
```

RESULT 81
US-09-302-495-13/c
; Sequence 13, Application US/09302495
; Patent No. 6518045
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/302,495
; FILING DATE: 30-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,143
; FILING DATE: 04-FEB-1998
; APPLICATION NUMBER: PCT/JP97/01824
; FILING DATE: 29-MAY-1997
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: IMAMURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-302-495-13

Alignment Scores:

Pred. No.:	2.36	Length:	32
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0

```
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            2.6%            Indels:        0
B:                     3               Gaps:          0

S-10-821-670A-27 (1-307) x US-09-302-495-13 (1-32)

y        154 SerAlaGluLysValArgValAsp 161
             |||||||||||||||||||||||
b         32 TCAGCAGAGAAGGTCAGAGTCGAC 9

ESULT 82
S-10-079-616-13/c
 Sequence 13, Application US/10079616
 Patent No. 6566097
   GENERAL INFORMATION:
        APPLICANT: IMAMURA, Takayuki
                   MAEDA, Hiroaki
                   FUJIYASU, Takeshi
                   IMAGAWA, Yoshitaka
                   TOKIYOSHI, Sachio
        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
        NUMBER OF SEQUENCES: 26
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: BROWDY AND NEIMARK
             STREET: 419 Seventh Street, N.W., Suite 300
             CITY: Washington
             STATE: D.C.
             COUNTRY: USA
             ZIP: 20004
        COMPUTER READABLE FORM:
             MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/10/079,616
             FILING DATE: 22-Feb-2002
             CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
             APPLICATION NUMBER: 09/011,143
             FILING DATE: 04-FEB-1998
             APPLICATION NUMBER: PCT/JP97/01824
             FILING DATE: 29-MAY-1997
             APPLICATION NUMBER: JP 165249/1996
             FILING DATE: 04-JUN-1996
        ATTORNEY/AGENT INFORMATION:
             NAME: BROWDY, Roger L.
             REGISTRATION NUMBER: 25,618
             REFERENCE/DOCKET NUMBER: IMAMURA=1
        TELECOMMUNICATION INFORMATION:
             TELEPHONE: 202-628-5197
             TELEFAX: 202-737-3528
     INFORMATION FOR SEQ ID NO: 13:
        SEQUENCE CHARACTERISTICS:
             LENGTH: 32 base pairs
             TYPE: nucleic acid
             STRANDEDNESS: single
             TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
S-10-079-616-13

lignment Scores:
red. No.:              2.36            Length:        32
core:                  8.00            Matches:       8
ercent Similarity:     100.0%          Conservative:  0
est Local Similarity:  100.0%          Mismatches:    0
uery Match:            2.6%            Indels:        0
B:                     3               Gaps:          0

S-10-821-670A-27 (1-307) x US-10-079-616-13 (1-32)

y        154 SerAlaGluLysValArgValAsp 161
             |||||||||||||||||||||||
Db        32 TCAGCAGAGAAGGTCAGAGTCGAC 9

RESULT 83
US-09-011-143-14
; Sequence 14, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-14

Alignment Scores:
Pred. No.:             3.22            Length:        44
Score:                 8.00            Matches:       8
Percent Similarity:    100.0%          Conservative:  0
Best Local Similarity: 100.0%          Mismatches:    0
Query Match:           2.6%            Indels:        0
DB:                    3               Gaps:          0

US-10-821-670A-27 (1-307) x US-09-011-143-14 (1-44)

Qy       160 ValAspAsnArgAspTyrLysLys 167
             ||||||||||||||||||||||
Db        21 GTCGACAACAGGGATTATAAGAAG 44

RESULT 84
US-09-302-495-14
; Sequence 14, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
```

```
                    MAEDA, Hiroaki
                    FUJIYASU, Takeshi
                    IMAGAWA, Yoshitaka
                    TOKIYOSHI, Sachio
          TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
          NUMBER OF SEQUENCES: 26
          CORRESPONDENCE ADDRESS:
               ADDRESSEE: BROWDY AND NEIMARK
               STREET: 419 Seventh Street, N.W., Suite 300
               CITY: Washington
               STATE: D.C.
               COUNTRY: USA
               ZIP: 20004
          COMPUTER READABLE FORM:
               MEDIUM TYPE: Floppy disk
               COMPUTER: IBM PC compatible
               OPERATING SYSTEM: PC-DOS/MS-DOS
               SOFTWARE: PatentIn Release #1.0, Version #1.30
          CURRENT APPLICATION DATA:
               APPLICATION NUMBER: US/09/302,495
               FILING DATE: 30-Apr-1999
               CLASSIFICATION: <Unknown>
          PRIOR APPLICATION DATA:
               APPLICATION NUMBER: US/09/011,143
               FILING DATE: 04-FEB-1998
               APPLICATION NUMBER: PCT/JP97/01824
               FILING DATE: 29-MAY-1997
               APPLICATION NUMBER: JP 165249/1996
               FILING DATE: 04-JUN-1996
          ATTORNEY/AGENT INFORMATION:
               NAME: BROWDY, Roger L.
               REGISTRATION NUMBER: 25,618
               REFERENCE/DOCKET NUMBER: IMAMURA=1
          TELECOMMUNICATION INFORMATION:
               TELEPHONE: 202-628-5197
               TELEFAX: 202-737-3528
     INFORMATION FOR SEQ ID NO: 14:
          SEQUENCE CHARACTERISTICS:
               LENGTH: 44 base pairs
               TYPE: nucleic acid
               STRANDEDNESS: single
               TOPOLOGY: linear
          MOLECULE TYPE: cDNA
          SEQUENCE DESCRIPTION: SEQ ID NO: 14:
IS-09-302-495-14

Alignment Scores:
Pred. No.:                3.22          Length:          44
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              2.6%          Indels:          0
DB:                       3             Gaps:            0

IS-10-821-670A-27 (1-307) x US-09-302-495-14 (1-44)

Qy         160 ValAspAsnArgAspTyrLysLys 167
               |||||||||||||||||||||||
Db          21 GTCGACAACAGGGATTATAAGAAG 44

RESULT 85
IS-10-079-616-14
  Sequence 14, Application US/10079616
  Patent No. 6566097
    GENERAL INFORMATION:
          APPLICANT: IMAMURA, Takayuki
                     MAEDA, Hiroaki
                     FUJIYASU, Takeshi
                     IMAGAWA, Yoshitaka
                     TOKIYOSHI, Sachio
          TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
          NUMBER OF SEQUENCES: 26
          CORRESPONDENCE ADDRESS:
               ADDRESSEE: BROWDY AND NEIMARK
               STREET: 419 Seventh Street, N.W., Suite 300
               CITY: Washington
               STATE: D.C.
               COUNTRY: USA
               ZIP: 20004
          COMPUTER READABLE FORM:
               MEDIUM TYPE: Floppy disk
               COMPUTER: IBM PC compatible
               OPERATING SYSTEM: PC-DOS/MS-DOS
               SOFTWARE: PatentIn Release #1.0, Version #1.30
          CURRENT APPLICATION DATA:
               APPLICATION NUMBER: US/10/079,616
               FILING DATE: 22-Feb-2002
               CLASSIFICATION: <Unknown>
          PRIOR APPLICATION DATA:
               APPLICATION NUMBER: 09/011,143
               FILING DATE: 04-FEB-1998
               APPLICATION NUMBER: PCT/JP97/01824
               FILING DATE: 29-MAY-1997
               APPLICATION NUMBER: JP 165249/1996
               FILING DATE: 04-JUN-1996
          ATTORNEY/AGENT INFORMATION:
               NAME: BROWDY, Roger L.
               REGISTRATION NUMBER: 25,618
               REFERENCE/DOCKET NUMBER: IMAMURA=1
          TELECOMMUNICATION INFORMATION:
               TELEPHONE: 202-628-5197
               TELEFAX: 202-737-3528
     INFORMATION FOR SEQ ID NO: 14:
          SEQUENCE CHARACTERISTICS:
               LENGTH: 44 base pairs
               TYPE: nucleic acid
               STRANDEDNESS: single
               TOPOLOGY: linear
          MOLECULE TYPE: cDNA
          SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-079-616-14

Alignment Scores:
Pred. No.:                3.22          Length:          44
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              2.6%          Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-079-616-14 (1-44)

Qy         160 ValAspAsnArgAspTyrLysLys 167
               |||||||||||||||||||||||
Db          21 GTCGACAACAGGGATTATAAGAAG 44

RESULT 86
US-09-949-016-70299
; Sequence 70299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70299
```

```
   LENGTH: 601
   TYPE: DNA
   ORGANISM: Human
S-09-949-016-70299

lignment Scores:
red. No.:              41.1          Length:        601
core:                  8.00          Matches:       8
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            2.6%          Indels:        0
B:                     3             Gaps:          0

S-10-821-670A-27 (1-307) x US-09-949-016-70299 (1-601)

y         75 LeuSerHisSerPheLeuLeuIle 82
             |||||||||||||||||||||||||
b        506 CTCAGTCATTCTTTTTTACTAATT 529

ESULT 87
S-09-949-016-87513
 Sequence 87513, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
  APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
  CURRENT APPLICATION NUMBER: US/09/949,016
  CURRENT FILING DATE:  2000-04-14
  PRIOR APPLICATION NUMBER: 60/241,755
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/237,768
  PRIOR FILING DATE: 2000-10-03
  PRIOR APPLICATION NUMBER: 60/231,498
  PRIOR FILING DATE: 2000-09-08
  NUMBER OF SEQ ID NOS: 207012
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 87513
   LENGTH: 601
   TYPE: DNA
   ORGANISM: Human
S-09-949-016-87513

lignment Scores:
red. No.:              41.1          Length:        601
core:                  8.00          Matches:       8
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            2.6%          Indels:        0
B:                     3             Gaps:          0

S-10-821-670A-27 (1-307) x US-09-949-016-87513 (1-601)

y         75 LeuSerHisSerPheLeuLeuIle 82
             |||||||||||||||||||||||||
b        440 CTATCACATTCCTTTCTCTTAATC 463

ESULT 88
S-09-949-016-202770/c
 Sequence 202770, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
  APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
  CURRENT APPLICATION NUMBER: US/09/949,016
  CURRENT FILING DATE:  2000-04-14
  PRIOR APPLICATION NUMBER: 60/241,755
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/237,768
  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 202770
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-202770

Alignment Scores:
Pred. No.:             41.1          Length:        601
Score:                 8.00          Matches:       8
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           2.6%          Indels:        0
DB:                    3             Gaps:          0

US-10-821-670A-27 (1-307) x US-09-949-016-202770 (1-601)

Qy         71 GlyGlyGluValLeuSerHisSer 78
              |||||||||||||||||||||||
Db        411 GGTGGGGAGGTGTTATCCCATAGC 388

RESULT 89
US-09-974-300-5194
; Sequence 5194, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
;  APPLICANT: Berka, Randy M.
;  APPLICANT:  Clausen, Ib Groth
;  TITLE OF INVENTION: Methods For Monitoring Multiple Gene
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: 10085.500-US
;  CURRENT APPLICATION NUMBER: US/09/974,300
;  CURRENT FILING DATE:  2001-10-05
;  PRIOR APPLICATION NUMBER: 09/680,598
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: 60/279,526
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 8481
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5194
;   LENGTH: 633
;   TYPE: DNA
;   ORGANISM: Bacillus clausii
US-09-974-300-5194

Alignment Scores:
Pred. No.:             43.2          Length:        633
Score:                 8.00          Matches:       8
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           2.6%          Indels:        0
DB:                    5             Gaps:          0

US-10-821-670A-27 (1-307) x US-09-974-300-5194 (1-633)

Qy         58 LysGluPheAlaAspAlaGlyGln 65
              |||||||||||||||||||||||
Db        391 AAAGAGTTTGCTGATGCCGGGCAA 414

RESULT 90
US-09-621-976-1463/c
; Sequence 1463, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
```

```
  CURRENT FILING DATE:  2000-07-21
  NUMBER OF SEQ ID NOS: 19335
  SOFTWARE: Patent.pm
 SEQ ID NO 1463
   LENGTH: 830
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: 138..671
   NAME/KEY: sig_peptide
   LOCATION: 138..416
   OTHER INFORMATION: Von Heijne matrix
   OTHER INFORMATION: score 7.59999990463257
   OTHER INFORMATION: seq LPDLLLLAGPAXX/ER
US-09-621-976-1463

Alignment Scores:
Pred. No.:                56.3          Length:          830
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              2.6%          Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-27 (1-307) x US-09-621-976-1463 (1-830)

Qy         42 GlnSerSerGluValLeuGlySer 49
              |||||||||||||||||||||||
Db        695 CAGAGTTCAGAGGTCTTGGGGTCA 672

RESULT 91
US-09-328-352-1423
  Sequence 1423, Application US/09328352
  Patent No. 6562958
  GENERAL INFORMATION:
   APPLICANT: Gary L. Breton et al.
   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
   TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
   FILE REFERENCE: GTC99-03PA
   CURRENT APPLICATION NUMBER: US/09/328,352
   CURRENT FILING DATE: 1999-06-04
   NUMBER OF SEQ ID NOS: 8252
  SEQ ID NO 1423
    LENGTH: 885
    TYPE: DNA
    ORGANISM: Acinetobacter baumannii
US-09-328-352-1423

Alignment Scores:
Pred. No.:                59.9          Length:          885
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              2.6%          Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-27 (1-307) x US-09-328-352-1423 (1-885)

Qy         217 ProLysAsnLeuGlnLeuLysPro 224
               |||||||||||||||||||||||
Db         556 CCTAAAAACTTACAATTAAAACCT 579

RESULT 92
US-09-949-016-2226/c
  Sequence 2226, Application US/09949016
  Patent No. 6812339
  GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   FILE REFERENCE: CL001307
   CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2226
;   LENGTH: 2961
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2226

Alignment Scores:
Pred. No.:                194           Length:          2961
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              2.6%          Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-27 (1-307) x US-09-949-016-2226 (1-2961)

Qy         221 GlnLeuLysProLeuLysAsnSer 228
               ||||||||||||||||||||||||
Db        1567 CAGCTGAAACCTCTAAAAAATTCT 1544

RESULT 93
US-08-254-989-1
; Sequence 1, Application US/08254989
; Patent No. 5859307
;  GENERAL INFORMATION:
;    APPLICANT:  Mombaerts, Peter
;    APPLICANT:  Tonegawa, Susumu
;    APPLICANT:  Johnson, Randall S.
;    APPLICANT:  Papaioannou, Virginia
;    TITLE OF INVENTION:  Mutant RAG-1 Deficient Animals Having No
;    TITLE OF INVENTION:  Mature B and T Lymphocytes
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kilpatrick & Cody
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  U.S.
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/254,989
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/830831
;      FILING DATE:  04-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  MIT5783
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 815-6508
;      TELEFAX:  (404) 815-6555
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3342 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

```
    MOLECULE TYPE:  DNA (genomic)
    HYPOTHETICAL:  NO
    ANTI-SENSE:  NO
    ORIGINAL SOURCE:
      ORGANISM:  Mouse
S-08-254-989-1

lignment Scores:
red. No.:              219           Length:        3342
core:                  8.00          Matches:       8
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            2.6%          Indels:        0
B:                     2             Gaps:          0

S-10-821-670A-27 (1-307) x US-08-254-989-1 (1-3342)

y         55 IleGlnValLysGluPheAlaAsp 62
             |||||||||||||||||||||||
b       1331 ATTCAAGTCAAAGAATTTGCTGAC 1354

ESULT 94
S-09-902-540-1033
 Sequence 1033, Application US/09902540
 Patent No. 6833447
 GENERAL INFORMATION:
  APPLICANT: Goldman, Barry S.
  APPLICANT:  Hinkle, Gregory J.
  APPLICANT:  Slater, Steven C.
  APPLICANT:  Wiegand, Roger C.
  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
  FILE REFERENCE: 38-10(15849)B
  CURRENT APPLICATION NUMBER: US/09/902,540
  CURRENT FILING DATE:  2001-07-10
  PRIOR APPLICATION NUMBER: 60/217,883
  PRIOR FILING DATE: 2000-07-10
  NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 1033
   LENGTH: 6758
   TYPE: DNA
   ORGANISM: Myxococcus xanthus
S-09-902-540-1033

lignment Scores:
red. No.:              434           Length:        6758
core:                  8.00          Matches:       8
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            2.6%          Indels:        0
B:                     3             Gaps:          0

S-10-821-670A-27 (1-307) x US-09-902-540-1033 (1-6758)

y        134 ValLysSerSerArgGlySerSer 141
             |||||||||||||||||||||||
b       4617 GTGAAGTCATCGAGAGGGTCGTCG 4640

ESULT 95
S-09-949-016-17491
 Sequence 17491, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
  APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
  CURRENT APPLICATION NUMBER: US/09/949,016
  CURRENT FILING DATE:  2000-04-14
  PRIOR APPLICATION NUMBER: 60/241,755
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/237,768
  PRIOR FILING DATE: 2000-10-03
  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17491
;   LENGTH: 7173
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17491

Alignment Scores:
Pred. No.:             460           Length:        7173
Score:                 8.00          Matches:       8
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           2.6%          Indels:        0
DB:                    3             Gaps:          0

US-10-821-670A-27 (1-307) x US-09-949-016-17491 (1-7173)

Qy         84 LysLysGluAspGlyIleTrpSer 91
              |||||||||||||||||||||||
Db       4555 AAGAAAGAAGACGGGATTTGGAGC 4578

RESULT 96
US-09-949-002-689
; Sequence 689, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 689
;   LENGTH: 28976
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-002-689

Alignment Scores:
Pred. No.:             1.79e+03      Length:        28976
Score:                 8.00          Matches:       8
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           2.6%          Indels:        0
DB:                    3             Gaps:          0

US-10-821-670A-27 (1-307) x US-09-949-002-689 (1-28976)

Qy        102 LysAsnLysIlePheLeuLysCys 109
              |||||||||||||||||||||||
Db          2 AAAAATAAAATATTTCTTAAATGC 25

RESULT 97
US-09-949-002-698
; Sequence 698, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/09/949,002
;  CURRENT FILING DATE:  2000-01-28
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
```

NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 698
LENGTH: 28976
TYPE: DNA
ORGANISM: Human
US-09-949-002-698

Alignment Scores:

Pred. No.:	1.79e+03	Length:	28976
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-949-002-698 (1-28976)

```
Qy        102 LysAsnLysIlePheLeuLysCys 109
              ||||||||||||||||||||||||
Db          2 AAAAATAAAATATTTCTTAAATGC 25
```

RESULT 98
US-09-949-016-17447
Sequence 17447, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17447
LENGTH: 41815
TYPE: DNA
ORGANISM: Human
US-09-949-016-17447

Alignment Scores:

Pred. No.:	2.56e+03	Length:	41815
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-949-016-17447 (1-41815)

```
Qy         71 GlyGlyGluValLeuSerHisSer 78
              |||||||||||||||||||||||
Db      24855 GGTGGGGAGGTGTTATCCCATAGC 24878
```

RESULT 99
US-09-949-016-13968/c
Sequence 13968, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13968
LENGTH: 68444
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(68444)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13968

Alignment Scores:

Pred. No.:	4.14e+03	Length:	68444
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-949-016-13968 (1-68444)

```
Qy        221 GlnLeuLysProLeuLysAsnSer 228
              ||||||||||||||||||||||||
Db      65050 CAGCTGAAACCTCTAAAAAATTCT 65027
```

RESULT 100
US-09-949-016-12574/c
Sequence 12574, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12574
LENGTH: 72843
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(72843)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12574

Alignment Scores:

Pred. No.:	4.39e+03	Length:	72843
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.6%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-949-016-12574 (1-72843)

```
Qy        200 GluAsnTyrThrSerSerPhePhe 207
              |||||||||||||||||||||||
Db      25305 GAAAATTACACATCTTCTTTTTTT 25282
```

earch completed: June 10, 2006, 04:50:28
:b time : 272.01 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

)M protein - nucleic search, using frame_plus_p2n model

Run on: June 11, 2006, 22:10:55 ; Search time 1482.59 Seconds
(without alignments)
3816.589 Million cell updates/sec

Title: US-10-821-670A-27
Perfect score: 307
Sequence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size: 1

Total number of hits satisfying chosen parameters: 37767826

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110503_27781/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap
-SUFFIX=oligo.p2n.200scores.rnpbm -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10821670_@CGN_1_1_4932_@runat_07062006_110503_27781 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	307	100.0	921	3	US-09-917-265-26	Sequence 26, Appl
c 2	307	100.0	921	3	US-09-917-265-28	Sequence 28, Appl
3	307	100.0	921	9	US-10-821-670-26	Sequence 26, Appl
c 4	307	100.0	921	9	US-10-821-670-28	Sequence 28, Appl
5	307	100.0	1533	3	US-09-917-265-43	Sequence 43, Appl
c 6	307	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
7	307	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
c 8	307	100.0	1533	9	US-10-821-670-45	Sequence 45, Appl
9	307	100.0	1599	3	US-09-917-265-38	Sequence 38, Appl
c 10	307	100.0	1599	3	US-09-917-265-40	Sequence 40, Appl
11	307	100.0	1599	9	US-10-821-670-38	Sequence 38, Appl
c 12	307	100.0	1599	9	US-10-821-670-40	Sequence 40, Appl
13	206	67.1	921	6	US-10-079-616-6	Sequence 6, Appli
14	206	67.1	921	6	US-10-079-616-7	Sequence 7, Appli
15	206	67.1	987	3	US-09-917-265-29	Sequence 29, Appl
c 16	206	67.1	987	3	US-09-917-265-31	Sequence 31, Appl
17	206	67.1	987	9	US-10-821-670-29	Sequence 29, Appl
c 18	206	67.1	987	9	US-10-821-670-31	Sequence 31, Appl
19	206	67.1	990	7	US-10-041-672C-1	Sequence 1, Appli
20	206	67.1	2193	6	US-10-079-616-5	Sequence 5, Appli
21	206	67.1	4522	7	US-10-041-672C-10	Sequence 10, Appl
22	205	66.8	985	3	US-09-917-265-55	Sequence 55, Appl
c 23	205	66.8	985	3	US-09-917-265-57	Sequence 57, Appl
24	205	66.8	985	9	US-10-821-670-55	Sequence 55, Appl
c 25	205	66.8	985	9	US-10-821-670-57	Sequence 57, Appl
26	37	12.1	921	3	US-09-917-265-52	Sequence 52, Appl
c 27	37	12.1	921	3	US-09-917-265-54	Sequence 54, Appl
28	37	12.1	921	9	US-10-821-670-52	Sequence 52, Appl
c 29	37	12.1	921	9	US-10-821-670-54	Sequence 54, Appl
30	37	12.1	987	3	US-09-917-265-58	Sequence 58, Appl
c 31	37	12.1	987	3	US-09-917-265-60	Sequence 60, Appl
32	37	12.1	987	9	US-10-821-670-58	Sequence 58, Appl
c 33	37	12.1	987	9	US-10-821-670-60	Sequence 60, Appl
34	37	12.1	1533	3	US-09-917-265-66	Sequence 66, Appl
c 35	37	12.1	1533	3	US-09-917-265-68	Sequence 68, Appl
36	37	12.1	1533	9	US-10-821-670-66	Sequence 66, Appl
c 37	37	12.1	1533	9	US-10-821-670-68	Sequence 68, Appl
38	37	12.1	1599	3	US-09-917-265-61	Sequence 61, Appl
c 39	37	12.1	1599	3	US-09-917-265-63	Sequence 63, Appl
40	37	12.1	1599	9	US-10-821-670-61	Sequence 61, Appl
c 41	37	12.1	1599	9	US-10-821-670-63	Sequence 63, Appl
42	37	12.1	2267	3	US-09-917-265-107	Sequence 107, App
c 43	37	12.1	2267	3	US-09-917-265-109	Sequence 109, App
44	37	12.1	2267	9	US-10-821-670-107	Sequence 107, App
c 45	37	12.1	2267	9	US-10-821-670-109	Sequence 109, App
46	35	11.4	987	3	US-09-754-014-2	Sequence 2, Appli
47	35	11.4	987	3	US-09-754-014-3	Sequence 3, Appli
48	35	11.4	987	3	US-09-754-014-4	Sequence 4, Appli
49	35	11.4	987	3	US-09-836-866-2	Sequence 2, Appli
50	35	11.4	1007	8	US-10-221-975A-1	Sequence 1, Appli
51	35	11.4	1018	7	US-10-267-384-194	Sequence 194, App
52	35	11.4	1389	8	US-10-603-064-4	Sequence 4, Appli
53	35	11.4	1397	7	US-10-349-507-2	Sequence 2, Appli
54	35	11.4	1397	7	US-10-267-565-2	Sequence 2, Appli
55	35	11.4	1399	10	US-10-929-182-22	Sequence 22, Appl
56	35	11.4	2347	7	US-10-429-802-44	Sequence 44, Appl
57	35	11.4	2347	7	US-10-430-503-35	Sequence 35, Appl
58	35	11.4	2362	3	US-09-924-703-3	Sequence 3, Appli
59	35	11.4	2362	8	US-10-358-395-3	Sequence 3, Appli
60	35	11.4	5686	7	US-10-136-837-1	Sequence 1, Appli
61	35	11.4	11569	10	US-10-511-237-1	Sequence 1, Appli
62	28	9.1	2390	10	US-10-528-644A-53	Sequence 53, Appl
63	23	7.5	987	3	US-09-826-025-24	Sequence 24, Appl
64	23	7.5	987	9	US-10-785-577-24	Sequence 24, Appl
65	23	7.5	1005	7	US-10-373-456-18	Sequence 18, Appl
66	23	7.5	1017	7	US-10-373-456-20	Sequence 20, Appl
67	23	7.5	1580	9	US-10-742-405-7	Sequence 7, Appli
68	23	7.5	1828	7	US-10-373-456-2	Sequence 2, Appli
69	23	7.5	1870	6	US-10-228-811-4	Sequence 4, Appli
70	23	7.5	2318	6	US-10-172-399-7	Sequence 7, Appli
71	23	7.5	2318	9	US-10-476-961-3	Sequence 3, Appli
72	23	7.5	2466	7	US-10-373-456-1	Sequence 1, Appli
73	23	7.5	8578	3	US-09-828-825-1	Sequence 1, Appli
74	23	7.5	8578	3	US-09-828-825-3	Sequence 3, Appli

	75	23	7.5	8608	3	US-09-828-825-7	Sequence 7, Appli
	76	23	7.5	8623	3	US-09-828-825-5	Sequence 5, Appli
	77	23	7.5	8629	3	US-09-828-825-15	Sequence 15, Appl
	78	23	7.5	8638	3	US-09-828-825-9	Sequence 9, Appli
	79	23	7.5	8644	3	US-09-828-825-13	Sequence 13, Appl
	80	23	7.5	8659	3	US-09-828-825-11	Sequence 11, Appl
	81	23	7.5	11453	10	US-10-511-237-3	Sequence 3, Appli
	82	22	7.2	18340	8	US-10-240-376A-130	Sequence 130, App
c	83	20	6.5	270	7	US-10-029-386-16833	Sequence 16833, A
	84	20	6.5	399	16	US-11-128-061-661	Sequence 661, App
	85	20	6.5	399	16	US-11-128-061-4303	Sequence 4303, Ap
	86	20	6.5	399	16	US-11-128-049-661	Sequence 661, App
	87	20	6.5	399	16	US-11-128-049-4303	Sequence 4303, Ap
c	88	20	6.5	556	7	US-10-029-386-3133	Sequence 3133, Ap
	89	17	5.5	73	3	US-09-823-549-77	Sequence 77, Appl
	90	17	5.5	73	9	US-10-685-992-77	Sequence 77, Appl
	91	17	5.5	600	16	US-11-136-527-4408	Sequence 4408, Ap
	92	17	5.5	1024	16	US-11-136-527-312	Sequence 312, App
	93	17	5.5	1409	8	US-10-603-064-3	Sequence 3, Appli
	94	17	5.5	1472	8	US-10-603-064-2	Sequence 2, Appli
	95	17	5.5	1569	8	US-10-603-064-12	Sequence 12, Appl
	96	17	5.5	1610	9	US-10-742-405-5	Sequence 5, Appli
	97	17	5.5	1840	6	US-10-172-399-3	Sequence 3, Appli
	98	17	5.5	2013	8	US-10-603-064-11	Sequence 11, Appl
	99	17	5.5	2709	8	US-10-603-064-13	Sequence 13, Appl
	100	17	5.5	5966	7	US-10-136-837-3	Sequence 3, Appli
	101	17	5.5	11458	10	US-10-511-237-2	Sequence 2, Appli
	102	12	3.9	38	6	US-10-079-616-12	Sequence 12, Appl
	103	10	3.3	21925	7	US-10-017-161-2415	Sequence 2415, Ap
	104	10	3.3	21925	7	US-10-292-798-2055	Sequence 2055, Ap
	105	10	3.3	26184	7	US-10-017-161-2043	Sequence 2043, Ap
	106	10	3.3	26184	7	US-10-292-798-1689	Sequence 1689, Ap
	107	9	2.9	30	8	US-10-240-376A-9	Sequence 9, Appli
	108	9	2.9	353	9	US-10-357-930-7460	Sequence 7460, Ap
c	109	9	2.9	381	3	US-09-796-692-7886	Sequence 7886, Ap
c	110	9	2.9	381	6	US-10-040-862-7886	Sequence 7886, Ap
c	111	9	2.9	381	7	US-10-057-475B-7886	Sequence 7886, Ap
c	112	9	2.9	381	7	US-10-154-884B-7886	Sequence 7886, Ap
c	113	9	2.9	381	9	US-10-764-324-7886	Sequence 7886, Ap
	114	9	2.9	400	8	US-10-242-535A-51196	Sequence 51196, A
	115	9	2.9	400	8	US-10-085-783A-51196	Sequence 51196, A
	116	9	2.9	419	8	US-10-240-376A-1	Sequence 1, Appli
	117	9	2.9	419	8	US-10-240-376A-2	Sequence 2, Appli
	118	9	2.9	426	9	US-10-357-930-37422	Sequence 37422, A
c	119	9	2.9	540	4	US-09-925-065A-564824	Sequence 564824,
c	120	9	2.9	540	5	US-09-925-065A-564824	Sequence 564824,
	121	9	2.9	600	10	US-10-972-079-50704	Sequence 50704, A
	122	9	2.9	858	6	US-10-198-846-9631	Sequence 9631, Ap
	123	9	2.9	2256	9	US-10-357-930-22505	Sequence 22505, A
	124	9	2.9	2256	9	US-10-357-930-24790	Sequence 24790, A
	125	9	2.9	2256	9	US-10-357-930-28340	Sequence 28340, A
c	126	9	2.9	2433	7	US-10-369-493-24162	Sequence 24162, A
	127	9	2.9	2659	6	US-10-198-846-13710	Sequence 13710, A
c	128	9	2.9	3284	7	US-10-108-260A-630	Sequence 630, App
	129	9	2.9	1503841	3	US-09-795-668-1	Sequence 1, Appli
	130	9	2.9	1503841	3	US-09-795-686-1	Sequence 1, Appli
	131	9	2.9	1503841	3	US-09-946-807-1	Sequence 1, Appli
	132	9	2.9	1503841	10	US-10-995-011-1	Sequence 1, Appli
c	133	8	2.6	25	3	US-09-917-265-86	Sequence 86, Appl
	134	8	2.6	25	3	US-09-887-145-37	Sequence 37, Appl
	135	8	2.6	25	8	US-10-719-956-231796	Sequence 231796,
c	136	8	2.6	25	9	US-10-821-670-86	Sequence 86, Appl
	137	8	2.6	25	13	US-11-036-317-431048	Sequence 431048,
	138	8	2.6	25	16	US-11-136-527-18285	Sequence 18285, A
	139	8	2.6	25	16	US-11-136-527-18288	Sequence 18288, A
	140	8	2.6	30	7	US-10-349-507-39	Sequence 39, Appl
	141	8	2.6	30	7	US-10-267-565-34	Sequence 34, Appl
c	142	8	2.6	32	6	US-10-079-616-13	Sequence 13, Appl
	143	8	2.6	44	6	US-10-079-616-14	Sequence 14, Appl
c	144	8	2.6	50	16	US-11-175-859-25436	Sequence 25436, A
	145	8	2.6	182	9	US-10-425-115-66404	Sequence 66404, A
c	146	8	2.6	201	9	US-10-741-600-54203	Sequence 54203, A
c	147	8	2.6	201	10	US-10-995-561-40384	Sequence 40384, A
	148	8	2.6	201	10	US-10-995-561-56659	Sequence 56659, A
	149	8	2.6	201	10	US-10-995-561-56702	Sequence 56702, A
c	150	8	2.6	201	10	US-10-995-561-56721	Sequence 56721, A
c	151	8	2.6	201	10	US-10-995-561-56753	Sequence 56753, A
c	152	8	2.6	201	16	US-11-124-367A-32612	Sequence 32612, A
c	153	8	2.6	229	8	US-10-437-963-26379	Sequence 26379, A
	154	8	2.6	280	3	US-09-560-863-932	Sequence 932, App
c	155	8	2.6	288	8	US-10-242-535A-53717	Sequence 53717, A
c	156	8	2.6	288	8	US-10-085-783A-53717	Sequence 53717, A
c	157	8	2.6	296	8	US-10-424-599-57914	Sequence 57914, A
c	158	8	2.6	369	8	US-10-424-599-118136	Sequence 118136,
c	159	8	2.6	374	3	US-09-770-791-289	Sequence 289, App
	160	8	2.6	381	8	US-10-437-963-45090	Sequence 45090, A
c	161	8	2.6	416	3	US-09-783-590-7899	Sequence 7899, Ap
c	162	8	2.6	436	7	US-10-062-674-978	Sequence 978, App
c	163	8	2.6	462	7	US-10-341-961A-368	Sequence 368, App
	164	8	2.6	467	12	US-10-301-480-28499	Sequence 28499, A
	165	8	2.6	467	12	US-10-301-480-641908	Sequence 641908,
c	166	8	2.6	474	6	US-10-027-632-48724	Sequence 48724, A
c	167	8	2.6	474	7	US-10-027-632-48724	Sequence 48724, A
c	168	8	2.6	474	12	US-10-301-480-3946	Sequence 3946, Ap
c	169	8	2.6	474	12	US-10-301-480-3947	Sequence 3947, Ap
c	170	8	2.6	474	12	US-10-301-480-617355	Sequence 617355,
c	171	8	2.6	474	12	US-10-301-480-617356	Sequence 617356,
	172	8	2.6	476	3	US-09-918-995-25870	Sequence 25870, A
	173	8	2.6	491	4	US-09-925-065A-538665	Sequence 538665,
	174	8	2.6	491	5	US-09-925-065A-538665	Sequence 538665,
c	175	8	2.6	494	6	US-10-027-632-198942	Sequence 198942,
c	176	8	2.6	494	7	US-10-027-632-198942	Sequence 198942,
c	177	8	2.6	500	4	US-09-925-065A-376272	Sequence 376272,
c	178	8	2.6	500	4	US-09-925-065A-376273	Sequence 376273,
c	179	8	2.6	500	4	US-09-925-065A-376274	Sequence 376274,
c	180	8	2.6	500	5	US-09-925-065A-376272	Sequence 376272,
c	181	8	2.6	500	5	US-09-925-065A-376273	Sequence 376273,
c	182	8	2.6	500	5	US-09-925-065A-376274	Sequence 376274,
	183	8	2.6	507	4	US-09-925-065A-511562	Sequence 511562,
	184	8	2.6	507	4	US-09-925-065A-511564	Sequence 511564,
	185	8	2.6	507	5	US-09-925-065A-511562	Sequence 511562,
	186	8	2.6	507	5	US-09-925-065A-511564	Sequence 511564,
c	187	8	2.6	515	6	US-10-027-632-58241	Sequence 58241, A
c	188	8	2.6	515	6	US-10-027-632-58242	Sequence 58242, A
c	189	8	2.6	515	6	US-10-027-632-59248	Sequence 59248, A
c	190	8	2.6	515	6	US-10-027-632-59249	Sequence 59249, A
c	191	8	2.6	515	6	US-10-027-632-309198	Sequence 309198,
c	192	8	2.6	515	6	US-10-027-632-309199	Sequence 309199,
c	193	8	2.6	515	7	US-10-027-632-58241	Sequence 58241, A
c	194	8	2.6	515	7	US-10-027-632-58242	Sequence 58242, A
c	195	8	2.6	515	7	US-10-027-632-59248	Sequence 59248, A
c	196	8	2.6	515	7	US-10-027-632-59249	Sequence 59249, A
c	197	8	2.6	515	7	US-10-027-632-309198	Sequence 309198,
c	198	8	2.6	515	7	US-10-027-632-309199	Sequence 309199,
	199	8	2.6	526	4	US-09-925-065A-188969	Sequence 188969,
	200	8	2.6	526	5	US-09-925-065A-188969	Sequence 188969,

ALIGNMENTS

RESULT 1
US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26

LENGTH: 921
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(921)
OTHER INFORMATION:
US-09-917-265-26

Alignment Scores:

Pred. No.:	3.83e-311	Length:	921
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265-26 (1-921)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 2
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-28

Alignment Scores:

Pred. No.:	3.83e-311	Length:	921
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265-28 (1-921)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442
```

```
y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
r         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b         21 TGGGCATCCGTGTCCTGCAGT 1

ESULT 3
S-10-821-670-26
 Sequence 26, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 26
   LENGTH: 921
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(921)
S-10-821-670-26

lignment Scores:
red. No.:              3.83e-311      Length:        921
core:                  307.00         Matches:       307
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-27 (1-307) x US-10-821-670-26 (1-921)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 4
US-10-821-670-28/c
; Sequence 28, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
```

SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 921
TYPE: DNA
ORGANISM: Felis catus
US-10-821-670-28

Alignment Scores:

Pred. No.:	3.83e-311	Length:	921
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-821-670-28 (1-921)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
```

RESULT 5
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:

Pred. No.:	6.1e-311	Length:	1533
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265-43 (1-1533)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
b        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b        901 TGGGCATCCGTGTCCTGCAGT 921

ESULT 6
S-09-917-265-45/c
 Sequence 45, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 45
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Felis catus
S-09-917-265-45

lignment Scores:
red. No.:              6.1e-311      Length:        1533
core:                  307.00        Matches:       307
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            100.0%        Indels:        0
B:                     3             Gaps:          0

S-10-821-670A-27 (1-307) x US-09-917-265-45 (1-1533)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 7
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
```

```
    LENGTH: 1533
    TYPE: DNA
    ORGANISM: Felis catus
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)..(1533)
US-10-821-670-43

Alignment Scores:
Pred. No.:                6.1e-311      Length:          1533
Score:                    307.00        Matches:         307
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              100.0%        Indels:          0
DB:                       9             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-821-670-43 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 8
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:
Pred. No.:                6.1e-311      Length:          1533
Score:                    307.00        Matches:         307
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              100.0%        Indels:          0
DB:                       9             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-821-670-45 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054
```

```
y       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

y       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

y       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

y       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

y       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

y       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

y       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

y       301 TrpAlaSerValSerCysSer 307
            |||||||||||||||||||||
b       633 TGGGCATCCGTGTCCTGCAGT 613
```

```
ESULT 9
S-09-917-265-38
 Sequence 38, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 38
   LENGTH: 1599
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1599)
   OTHER INFORMATION:
S-09-917-265-38

lignment Scores:
ed. No.:              6.34e-311     Length:         1599
core:                 307.00        Matches:        307
ercent Similarity:    100.0%        Conservative:   0
est Local Similarity: 100.0%        Mismatches:     0
uery Match:           100.0%        Indels:         0
B:                    3             Gaps:           0

S-10-821-670A-27 (1-307) x US-09-917-265-38 (1-1599)

y         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy       41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy       61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy       81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy      101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy      121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy      141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy      161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy      181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy      201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy      221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy      241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy      261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy      281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy      301 TrpAlaSerValSerCysSer 307
            |||||||||||||||||||||
Db      967 TGGGCATCCGTGTCCTGCAGT 987
```

```
RESULT 10
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
```

SEQ ID NO 40
LENGTH: 1599
TYPE: DNA
ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:

Pred. No.:	6.34e-311	Length:	1599
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265-40 (1-1599)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

RESULT 11
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:

Pred. No.:	6.34e-311	Length:	1599
Score:	307.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-821-670-38 (1-1599)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
```

```
y        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

y        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

y        301 TrpAlaSerValSerCysSer 307
             |||||||||||||||||||||
b        967 TGGGCATCCGTGTCCTGCAGT 987

ESULT 12
S-10-821-670-40/c
 Sequence 40, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 40
   LENGTH: 1599
   TYPE: DNA
   ORGANISM: Felis catus
S-10-821-670-40

ignment Scores:
red. No.:              6.34e-311      Length:        1599
core:                  307.00         Matches:       307
rcent Similarity:      100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            100.0%         Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-27 (1-307) x US-10-821-670-40 (1-1599)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 13
US-10-079-616-6
; Sequence 6, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
```

```
          COUNTRY: USA
          ZIP: 20004
       COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/10/079,616
          FILING DATE: 22-Feb-2002
          CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 09/011,143
          FILING DATE: 04-FEB-1998
          APPLICATION NUMBER: PCT/JP97/01824
          FILING DATE: 29-MAY-1997
          APPLICATION NUMBER: JP 165249/1996
          FILING DATE: 04-JUN-1996
       ATTORNEY/AGENT INFORMATION:
          NAME: BROWDY, Roger L.
          REGISTRATION NUMBER: 25,618
          REFERENCE/DOCKET NUMBER: IMAMURA=1
       TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
    INFORMATION FOR SEQ ID NO: 6:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 921 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
       MOLECULE TYPE: cDNA
       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

Alignment Scores:
Pred. No.:              3e-205      Length:          921
Score:                  206.00      Matches:         306
Percent Similarity:     99.7%       Conservative:    0
Best Local Similarity:  99.7%       Mismatches:      1
Query Match:            67.1%       Indels:          0
DB:                     6           Gaps:            0

US-10-821-670A-27 (1-307) x US-10-079-616-6 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 14
US-10-079-616-7
; Sequence 7, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
```

```
            REGISTRATION NUMBER: 25,618
            REFERENCE/DOCKET NUMBER: IMAMURA=1
        TELECOMMUNICATION INFORMATION:
            TELEPHONE: 202-628-5197
            TELEFAX: 202-737-3528
    INFORMATION FOR SEQ ID NO: 7:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 921 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
S-10-079-616-7

Alignment Scores:
Pred. No.:                3e-205          Length:         921
Score:                    206.00          Matches:        306
Percent Similarity:       99.7%           Conservative:   0
Best Local Similarity:    99.7%           Mismatches:     1
Query Match:              67.1%           Indels:         0
DB:                       6               Gaps:           0

S-10-821-670A-27 (1-307) x US-10-079-616-7 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 15
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-29

Alignment Scores:
Pred. No.:                3.19e-205       Length:         987
Score:                    206.00          Matches:        306
Percent Similarity:       99.7%           Conservative:   0
Best Local Similarity:    99.7%           Mismatches:     1
Query Match:              67.1%           Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265-29 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 16
US-09-917-265-31/c
  Sequence 31, Application US/09917265
  Patent No. US20020052030A1
  GENERAL INFORMATION:
   APPLICANT: Wonderling, Ramani S.
   APPLICANT:  Boroughs, Karen L.
   TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
   FILE REFERENCE: IM-5
   CURRENT APPLICATION NUMBER: US/09/917,265
   CURRENT FILING DATE:  2001-07-27
   PRIOR APPLICATION NUMBER: 60/223,016
   PRIOR FILING DATE: 2000-08-04
   NUMBER OF SEQ ID NOS: 109
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 31
    LENGTH: 987
    TYPE: DNA
    ORGANISM: Felis catus
US-09-917-265-31

Alignment Scores:
Seq. No.:                3.19e-205      Length:          987
Score:                   206.00         Matches:         306
Percent Similarity:      99.7%          Conservative:    0
Best Local Similarity:   99.7%          Mismatches:      1
Query Match:             67.1%          Indels:          0
DB:                      3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-917-265-31 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 17
US-10-821-670-29
; Sequence 29, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
```

```
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 29
   LENGTH: 987
   TYPE: DNA
   ORGANISM: Felis catus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(987)
S-10-821-670-29

Alignment Scores:
Pred. No.:              3.19e-205      Length:         987
Score:                  206.00         Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            67.1%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-27 (1-307) x US-10-821-670-29 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 18
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-31

Alignment Scores:
Pred. No.:              3.19e-205      Length:         987
Score:                  206.00         Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            67.1%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-27 (1-307) x US-10-821-670-31 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562
```

```
Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 19
US-10-041-672C-1
  Sequence 1, Application US/10041672C
  Publication No. US20030157059A1
  GENERAL INFORMATION:
   APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
   APPLICANT:  Universitat Zurich
   TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
   FILE REFERENCE: NHL-NP-36
   CURRENT APPLICATION NUMBER: US/10/041,672C
   CURRENT FILING DATE:  2002-01-08
   NUMBER OF SEQ ID NOS: 11
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 1
    LENGTH: 990
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

Alignment Scores:
Pred. No.:              3.2e-205      Length:          990
Score:                  206.00        Matches:         306
Percent Similarity:     99.7%         Conservative:    0
Best Local Similarity:  99.7%         Mismatches:      1
Query Match:            67.1%         Indels:          0
DB:                     7             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-041-672C-1 (1-990)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 20
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
```

```
      NUMBER OF SEQUENCES: 26
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: BROWDY AND NEIMARK
           STREET: 419 Seventh Street, N.W., Suite 300
           CITY: Washington
           STATE: D.C.
           COUNTRY: USA
           ZIP: 20004
      COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
           OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/10/079,616
           FILING DATE: 22-Feb-2002
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 09/011,143
           FILING DATE: 04-FEB-1998
           APPLICATION NUMBER: PCT/JP97/01824
           FILING DATE: 29-MAY-1997
           APPLICATION NUMBER: JP 165249/1996
           FILING DATE: 04-JUN-1996
      ATTORNEY/AGENT INFORMATION:
           NAME: BROWDY, Roger L.
           REGISTRATION NUMBER: 25,618
           REFERENCE/DOCKET NUMBER: IMAMURA=1
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: 202-628-5197
           TELEFAX: 202-737-3528
   INFORMATION FOR SEQ ID NO: 5:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 2193 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
S-10-079-616-5

Alignment Scores:
Pred. No.:              6.62e-205     Length:          2193
Score:                  206.00        Matches:         306
Percent Similarity:     99.7%         Conservative:    0
Best Local Similarity:  99.7%         Mismatches:      1
Query Match:            67.1%         Indels:          0
DB:                     6             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-079-616-5 (1-2193)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050

RESULT 21
US-10-041-672C-10
; Sequence 10, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 4522
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pMol-fil12p40
US-10-041-672C-10

Alignment Scores:
Pred. No.:              1.28e-204     Length:          4522
Score:                  206.00        Matches:         306
Percent Similarity:     99.7%         Conservative:    0
Best Local Similarity:  99.7%         Mismatches:      1
Query Match:            67.1%         Indels:          0
DB:                     7             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-041-672C-10 (1-4522)
```

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db       4013 TGGGCATCCGTGTCCTGCAGT 4033
```

```
RESULT 22
US-09-917-265-55
  Sequence 55, Application US/09917265
  Patent No. US20020052030A1
  GENERAL INFORMATION:
   APPLICANT: Wonderling, Ramani S.
   APPLICANT:  Boroughs, Karen L.
   TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
   FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
;   OTHER INFORMATION:
US-09-917-265-55

Alignment Scores:
Pred. No.:                3.56e-204       Length:                 985
Score:                    205.00          Matches:                305
Percent Similarity:       99.7%           Conservative:           0
Best Local Similarity:    99.7%           Mismatches:             1
Query Match:              66.8%           Indels:                 0
DB:                       3               Gaps:                   0

US-10-821-670A-27 (1-307) x US-09-917-265-55 (1-985)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
```

```
y        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

y        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

y        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

y        301 TrpAlaSerValSerCys 306
            ||||||||||||||||||
b        967 TGGGCATCCGTGTCCTGC 984

RESULT 23
S-09-917-265-57/c
 Sequence 57, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 57
   LENGTH: 985
   TYPE: DNA
   ORGANISM: Felis catus
S-09-917-265-57

Alignment Scores:
Pred. No.:              3.56e-204      Length:          985
Score:                  205.00         Matches:         305
Percent Similarity:     99.7%          Conservative:    0
Best Local Similarity:  99.7%          Mismatches:      1
Query Match:            66.8%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-27 (1-307) x US-09-917-265-57 (1-985)

y          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

y         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

y         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

y         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

y         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

y        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

y        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy       301 TrpAlaSerValSerCys 306
             ||||||||||||||||||
Db        19 TGGGCATCCGTGTCCTGC 2

RESULT 24
US-10-821-670-55
; Sequence 55, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-10-821-670-55

Alignment Scores:
Pred. No.:              3.56e-204      Length:          985
Score:                  205.00         Matches:         305
Percent Similarity:     99.7%          Conservative:    0
Best Local Similarity:  99.7%          Mismatches:      1
Query Match:            66.8%          Indels:          0
DB:                     9              Gaps:            0

US-10-821-670A-27 (1-307) x US-10-821-670-55 (1-985)
```

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCys 306
              ||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGC 984
```

RESULT 25
US-10-821-670-57/c
Sequence 57, Application US/10821670
Publication No. US20040248261A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-57

Alignment Scores:

Pred. No.:	3.56e-204	Length:	985
Score:	205.00	Matches:	305
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	66.8%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-821-670-57 (1-985)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy        301 TrpAlaSerValSerCys 306
              ||||||||||||||||||
Db         19 TGGGCATCCGTGTCCTGC 2

RESULT 26
US-09-917-265-52
 Sequence 52, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 52
   LENGTH: 921
   TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(921)
   OTHER INFORMATION:
US-09-917-265-52

Alignment Scores:
Pred. No.:              4.62e-28        Length:         921
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265-52 (1-921)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 27
US-09-917-265-54/c
 Sequence 54, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-54

Alignment Scores:
Pred. No.:              4.62e-28        Length:         921
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265-54 (1-921)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

RESULT 28
US-10-821-670-52
; Sequence 52, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-52

Alignment Scores:
Pred. No.:              4.62e-28        Length:         921
Score:                  37.00           Matches:        37
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            12.1%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-821-670-52 (1-921)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 29
US-10-821-670-54/c
; Sequence 54, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
```

APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/10/821,670
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 54
LENGTH: 921
TYPE: DNA
ORGANISM: Canis familiaris
S-10-821-670-54

lignment Scores:

ed. No.:	4.62e-28	Length:	921
core:	37.00	Matches:	37
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	12.1%	Indels:	0
B:	9	Gaps:	0

S-10-821-670A-27 (1-307) x US-10-821-670-54 (1-921)

```
y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271
```

ESULT 30
S-09-917-265-58
Sequence 58, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 987
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(987)
OTHER INFORMATION:
S-09-917-265-58

lignment Scores:

ed. No.:	4.92e-28	Length:	987
core:	37.00	Matches:	37
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	12.1%	Indels:	0
B:	3	Gaps:	0

S-10-821-670A-27 (1-307) x US-09-917-265-58 (1-987)

```
y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
```

RESULT 31
US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-60

Alignment Scores:

Pred. No.:	4.92e-28	Length:	987
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	12.1%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265-60 (1-987)

```
Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271
```

RESULT 32
US-10-821-670-58
; Sequence 58, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
US-10-821-670-58

Alignment Scores:

Pred. No.:	4.92e-28	Length:	987
Score:	37.00	Matches:	37
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0

```
uery Match:            12.1%          Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-27 (1-307) x US-10-821-670-58 (1-987)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
:        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 33
S-10-821-670-60/c
 Sequence 60, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 60
   LENGTH: 987
   TYPE: DNA
   ORGANISM: Canis familiaris
S-10-821-670-60

Lignment Scores:
red. No.:              4.92e-28       Length:        987
core:                  37.00          Matches:       37
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            12.1%          Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-27 (1-307) x US-10-821-670-60 (1-987)

         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322

         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
:        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 271

ESULT 34
S-09-917-265-66
 Sequence 66, Application US/09917265
 Patent No. US20020052030A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/09/917,265
  CURRENT FILING DATE:  2001-07-27
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 66
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(1533)
;  OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:
Pred. No.:             7.36e-28       Length:        1533
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           12.1%          Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-917-265-66 (1-1533)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 35
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

Alignment Scores:
Pred. No.:             7.36e-28       Length:        1533
Score:                 37.00          Matches:       37
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           12.1%          Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-917-265-68 (1-1533)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 36
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
```

```
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 66
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(1533)
US-10-821-670-66

Alignment Scores:
Pred. No.:              7.36e-28      Length:          1533
Score:                  37.00         Matches:         37
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            12.1%         Indels:          0
DB:                     9             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-821-670-66 (1-1533)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 651

RESULT 37
US-10-821-670-68/c
 Sequence 68, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 68
   LENGTH: 1533
   TYPE: DNA
   ORGANISM: Canis familiaris
US-10-821-670-68

Alignment Scores:
Pred. No.:              7.36e-28      Length:          1533
Score:                  37.00         Matches:         37
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            12.1%         Indels:          0
DB:                     9             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-821-670-68 (1-1533)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 38
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:
Pred. No.:              7.65e-28      Length:          1599
Score:                  37.00         Matches:         37
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            12.1%         Indels:          0
DB:                     3             Gaps:            0

US-10-821-670A-27 (1-307) x US-09-917-265-61 (1-1599)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

RESULT 39
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

Alignment Scores:
Pred. No.:              7.65e-28      Length:          1599
Score:                  37.00         Matches:         37
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            12.1%         Indels:          0
DB:                     3             Gaps:            0

US-10-821-670A-27 (1-307) x US-09-917-265-63 (1-1599)
```

```
y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

ESULT 40
S-10-821-670-61
 Sequence 61, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 61
    LENGTH: 1599
    TYPE: DNA
    ORGANISM: Canis familiaris
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)..(1599)
-10-821-670-61

.ignment Scores:
:ed. No.:              7.65e-28       Length:        1599
:ore:                  37.00          Matches:       37
:rcent Similarity:     100.0%         Conservative:  0
:st Local Similarity:  100.0%         Mismatches:    0
.ery Match:            12.1%          Indels:        0
B:                     9              Gaps:          0

S-10-821-670A-27 (1-307) x US-10-821-670-61 (1-1599)

y        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

y        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
b        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717

ESULT 41
S-10-821-670-63/c
 Sequence 63, Application US/10821670
 Publication No. US20040248261A1
 GENERAL INFORMATION:
  APPLICANT: Wonderling, Ramani S.
  APPLICANT:  Boroughs, Karen L.
  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
  TITLE OF INVENTION:  THEREOF
  FILE REFERENCE: IM-5
  CURRENT APPLICATION NUMBER: US/10/821,670
  CURRENT FILING DATE:  2004-04-09
  PRIOR APPLICATION NUMBER: 60/223,016
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 63
   LENGTH: 1599
   TYPE: DNA
   ORGANISM: Canis familiaris
-10-821-670-63

Alignment Scores:
Pred. No.:              7.65e-28       Length:        1599
Score:                  37.00          Matches:       37
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            12.1%          Indels:        0
DB:                     9              Gaps:          0

US-10-821-670A-27 (1-307) x US-10-821-670-63 (1-1599)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 883

RESULT 42
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
;   OTHER INFORMATION:
US-09-917-265-107

Alignment Scores:
Pred. No.:              1.05e-27       Length:        2267
Score:                  37.00          Matches:       37
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            12.1%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-917-265-107 (1-2267)

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 43
US-09-917-265-109/c
; Sequence 109, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
```

```
  PRIOR FILING DATE: 2000-08-04
  NUMBER OF SEQ ID NOS: 109
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 109
   LENGTH: 2267
   TYPE: DNA
   ORGANISM: Canis familiaris
US-09-917-265-109

Alignment Scores:
Pred. No.:                1.05e-27      Length:          2267
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              12.1%         Indels:          0
DB:                       3             Gaps:            0

US-10-821-670A-27 (1-307) x US-09-917-265-109 (1-2267)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

RESULT 44
US-10-821-670-107
  Sequence 107, Application US/10821670
  Publication No. US20040248261A1
  GENERAL INFORMATION:
   APPLICANT: Wonderling, Ramani S.
   APPLICANT:  Boroughs, Karen L.
   TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
   TITLE OF INVENTION:  THEREOF
   FILE REFERENCE: IM-5
   CURRENT APPLICATION NUMBER: US/10/821,670
   CURRENT FILING DATE:  2004-04-09
   PRIOR APPLICATION NUMBER: 60/223,016
   PRIOR FILING DATE: 2000-08-04
   NUMBER OF SEQ ID NOS: 111
   SOFTWARE: PatentIn version 3.2
  SEQ ID NO 107
    LENGTH: 2267
    TYPE: DNA
    ORGANISM: Canis familiaris
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (154)..(1140)
US-10-821-670-107

Alignment Scores:
Pred. No.:                1.05e-27      Length:          2267
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              12.1%         Indels:          0
DB:                       9             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-821-670-107 (1-2267)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 819

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 870

RESULT 45
US-10-821-670-109/c
  Sequence 109, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-109

Alignment Scores:
Pred. No.:                1.05e-27      Length:          2267
Score:                    37.00         Matches:         37
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              12.1%         Indels:          0
DB:                       9             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-821-670-109 (1-2267)

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 1449

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProPro 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 1398

RESULT 46
US-09-754-014-2
; Sequence 2, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
```

```
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
   INFORMATION FOR SEQ ID NO: 2:
      SEQUENCE CHARACTERISTICS:
           LENGTH: 987 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: single
           TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
:-09-754-014-2

.ignment Scores:
:ed. No.:              6.15e-26       Length:        987
:ore:                  35.00          Matches:       35
:rcent Similarity:     100.0%         Conservative:  0
:st Local Similarity:  100.0%         Mismatches:    0
.ery Match:            11.4%          Indels:        0
B:                     3              Gaps:          0

S-10-821-670A-27 (1-307) x US-09-754-014-2 (1-987)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
:       646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
:       706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

ESULT 47
S-09-754-014-3
 Sequence 3, Application US/09754014
 Patent No. US20020119940A1
   GENERAL INFORMATION:
      APPLICANT: Jeff No. US20020119940A1dstrom
                 Bruce Freimark
                 Deepa Deshpande
      TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
                          AND USES
      NUMBER OF SEQUENCES: 12
      CORRESPONDENCE ADDRESS:
           ADDRESSEE: Lyon & Lyon
           STREET: 633 West Fifth Street
                   Suite 4700
           CITY: Los Angeles
           STATE: California
           COUNTRY: U.S.A.
           ZIP: 90071-2066
      COMPUTER READABLE FORM:
           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                        storage
           COMPUTER: IBM Compatible
           OPERATING SYSTEM: IBM P.C. DOS 5.0
           SOFTWARE: FastSEQ for Windows 2.0
      CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/754,014
           FILING DATE: 03-Jan-2001
           CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
           APPLICATION NUMBER: 08/948,958
           FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
           NAME: Berkman, Charles S.
           REGISTRATION NUMBER: 38,077
           REFERENCE/DOCKET NUMBER: 226/284
      TELECOMMUNICATION INFORMATION:
           TELEPHONE: (213) 489-1600
           TELEFAX: (213) 955-0440
           TELEX: 67-3510
   INFORMATION FOR SEQ ID NO: 3:
      SEQUENCE CHARACTERISTICS:
;           LENGTH: 987 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-754-014-3

Alignment Scores:
Pred. No.:              6.15e-26       Length:        987
Score:                  35.00          Matches:       35
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            11.4%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-754-014-3 (1-987)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCC 705

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      706 GACCCCCCCAAGAACCTGCAGCTGAAGCCCCTGAAGAACAGCCGC 750

RESULT 48
US-09-754-014-4
; Sequence 4, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;      APPLICANT: Jeff No. US20020119940A1dstrom
;                 Bruce Freimark
;                 Deepa Deshpande
;      TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                          AND USES
;      NUMBER OF SEQUENCES: 12
;      CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Lyon & Lyon
;           STREET: 633 West Fifth Street
;                   Suite 4700
;           CITY: Los Angeles
;           STATE: California
;           COUNTRY: U.S.A.
;           ZIP: 90071-2066
;      COMPUTER READABLE FORM:
;           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                        storage
;           COMPUTER: IBM Compatible
;           OPERATING SYSTEM: IBM P.C. DOS 5.0
;           SOFTWARE: FastSEQ for Windows 2.0
;      CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/754,014
;           FILING DATE: 03-Jan-2001
;           CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/948,958
;           FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;           NAME: Berkman, Charles S.
;           REGISTRATION NUMBER: 38,077
;           REFERENCE/DOCKET NUMBER: 226/284
;      TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (213) 489-1600
;           TELEFAX: (213) 955-0440
;           TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 4:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 987 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-754-014-4
```

Alignment Scores:
Pred. No.: 6.15e-26 Length: 987
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-27 (1-307) x US-09-754-014-4 (1-987)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 646 CACAAGCTGAAGTACGAGAACTACACCAGCAGCTTCTTCATCCGCGACATCATCAAGCCT 705

Qy 215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
|||||||||||||||||||||||||||||||||||||||||||||
Db 706 GACCCACCCAAGAACCTCCAGCTGAAGCCCCTCAAGAACTCCCGC 750

RESULT 49
US-09-836-866-2
Sequence 2, Application US/09836866
Patent No. US20020123473A1
GENERAL INFORMATION:
APPLICANT: No. US20020123473A1dstrom, Jeff
Freimark, Bruce
Deshpande, Deepa
TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
DELIVERY SYTEMS AND USES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,866
FILING DATE: 16-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/949,160
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 226/285
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-836-866-2

Alignment Scores:
Pred. No.: 6.15e-26 Length: 987
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.4% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-27 (1-307) x US-09-836-866-2 (1-987)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy 215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
|||||||||||||||||||||||||||||||||||||||||||||
Db 706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 50
US-10-221-975A-1
; Sequence 1, Application US/10221975A
; Publication No. US20040023332A1
; GENERAL INFORMATION:
; APPLICANT: Pohang University of Science and Technology
; APPLICANT: Progen Co., Ltd.
; APPLICANT: Sung, Young Chul
; APPLICANT: Lee, Sung Hee
; APPLICANT: Ha, Sang Jun
; APPLICANT: Song, Man Ki
; APPLICANT: Chang, Jun
; TITLE OF INVENTION: Genes of IL-12p40 Subunit Mutated for Improving the Activity of
; TITLE OF INVENTION: IL-12 and Use Thereof for DNA Vaccine Adjuvant
; FILE REFERENCE: 59520-00005
; CURRENT APPLICATION NUMBER: US/10/221,975A
; CURRENT FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1007
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-975A-1

Alignment Scores:
Pred. No.: 6.27e-26 Length: 1007
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.4% Indels: 0
DB: 8 Gaps: 0

US-10-821-670A-27 (1-307) x US-10-221-975A-1 (1-1007)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 711

Qy 215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
|||||||||||||||||||||||||||||||||||||||||||||
Db 712 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 756

RESULT 51
US-10-267-384-194
; Sequence 194, Application US/10267384
; Publication No. US20030198623A1
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; Tartaglia, James
; Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,384
FILING DATE: 09-Oct-2002
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 194:

-10-267-384-194

ignment Scores:
ed. No.: 6.33e-26 Length: 1018
ore: 35.00 Matches: 35
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 11.4% Indels: 0
B: 7 Gaps: 0

-10-821-670A-27 (1-307) x US-10-267-384-194 (1-1018)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPheIleArgAspIleIleLysPro 214
Db 677 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 736

Qy 215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
Db 737 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 781

RESULT 52
S-10-603-064-4
Sequence 4, Application US/10603064
Publication No. US20040072299A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/10/603,064
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/634,368
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1389
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human
OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
-10-603-064-4

ignment Scores:
ed. No.: 8.41e-26 Length: 1389
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.4% Indels: 0
DB: 8 Gaps: 0

US-10-821-670A-27 (1-307) x US-10-603-064-4 (1-1389)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPheIleArgAspIleIleLysPro 214
Db 646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy 215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
Db 706 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 750

RESULT 53
US-10-349-507-2
; Sequence 2, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
; APPLICANT: Hekimi , Siegfried
; APPLICANT: Jiang , Ning
; APPLICANT: Benard, Claire
; APPLICANT: Kebir , Hania
; APPLICANT: McCright, Brenton
; APPLICANT: Lakowski , Bernard
; TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: 11202-006-999
; CURRENT APPLICATION NUMBER: US/10/349,507
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 10/312,187
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/CA01/00913
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/213,174
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/254,932
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1397
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)...(1024)
US-10-349-507-2

Alignment Scores:
Pred. No.: 8.45e-26 Length: 1397
Score: 35.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.4% Indels: 0
DB: 7 Gaps: 0

US-10-821-670A-27 (1-307) x US-10-349-507-2 (1-1397)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPheIleArgAspIleIleLysPro 214
Db 686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy 215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
Db 746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790

RESULT 54
US-10-267-565-2
; Sequence 2, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:

APPLICANT: Gately, Maurice
APPLICANT: Gubler, Ulrich
APPLICANT: Hulmes, Jeffery
APPLICANT: Podlaski, Frank
APPLICANT: Stern, Alvin
TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
TITLE OF INVENTION: ANTIBODIES THERETO
FILE REFERENCE: 11126-005
CURRENT APPLICATION NUMBER: US/10/267,565
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: 09/401,839
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 08/459,151
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 08/205,011
PRIOR FILING DATE: 1994-03-02
PRIOR APPLICATION NUMBER: 07/857,023
PRIOR FILING DATE: 1992-03-24
PRIOR APPLICATION NUMBER: 07/572,284
PRIOR FILING DATE: 1990-08-27
PRIOR APPLICATION NUMBER: 07/520,935
PRIOR FILING DATE: 1990-05-09
PRIOR APPLICATION NUMBER: 07/455,708
PRIOR FILING DATE: 1989-12-22
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1397
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (41)...(1024)
US-10-267-565-2

Alignment Scores:

Pred. No.:	8.45e-26	Length:	1397
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.4%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-267-565-2 (1-1397)

```
Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 745

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        746 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 790
```

RESULT 55
US-10-929-182-22
Sequence 22, Application US/10929182
Publication No. US20050064483A1
GENERAL INFORMATION:
APPLICANT: Zang, Jingwu
APPLICANT: Hong, Jian
TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
TITLE OF INVENTION: Multiple Sclerosis
FILE REFERENCE: HO-P02859US1
CURRENT APPLICATION NUMBER: US/10/929,182
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: US 60/498,731
PRIOR FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 1399
TYPE: DNA
ORGANISM: HUMAN
US-10-929-182-22

Alignment Scores:

Pred. No.:	8.46e-26	Length:	1399
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.4%	Indels:	0
DB:	10	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-929-182-22 (1-1399)

```
Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

RESULT 56
US-10-429-802-44
; Sequence 44, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: WONG, KA YIN
; APPLICANT: ZOU, YIYU
; TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
; FILE REFERENCE: UTSC:752US
; CURRENT APPLICATION NUMBER: US/10/429,802
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/377,672
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 2347
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-429-802-44

Alignment Scores:

Pred. No.:	1.36e-25	Length:	2347
Score:	35.00	Matches:	35
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.4%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-429-802-44 (1-2347)

```
Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db        748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792
```

RESULT 57
US-10-430-503-35
; Sequence 35, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LAN, KENG-LI
; APPLICANT: OU-YANG, FU
; APPLICANT: LIU, JAW-CHING
; APPLICANT: LAN, KENG-HSIN
; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS

```
  FILE REFERENCE: UTSC:797US
  CURRENT APPLICATION NUMBER: US/10/430,503
  CURRENT FILING DATE:  2003-05-06
  PRIOR APPLICATION NUMBER: 60/383,063
  PRIOR FILING DATE: 2002-05-06
  NUMBER OF SEQ ID NOS: 42
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 35
   LENGTH: 2347
   TYPE: DNA
   ORGANISM: Homo sapiens
S-10-430-503-35

lignment Scores:
red. No.:              1.36e-25       Length:        2347
core:                  35.00          Matches:       35
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            11.4%          Indels:        0
B:                     7              Gaps:          0

S-10-821-670A-27 (1-307) x US-10-430-503-35 (1-2347)

y       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       688 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 747

y       215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
b       748 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 792

ESULT 58
S-09-924-703-3
 Sequence 3, Application US/09924703
 Patent No. US20020137898A1
 GENERAL INFORMATION:
  APPLICANT: TRINCHIERI, GIORGIO
  APPLICANT:  PERUSSIA, BICE
  APPLICANT:  CLARK, STEVEN C.
  APPLICANT:  WONG, GORDON G.
  APPLICANT:  HEWICK, RODNEY
  APPLICANT:  KOBAYASHI, MICHIKO
  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
  FILE REFERENCE: 01142.0142.0100
  CURRENT APPLICATION NUMBER: US/09/924,703
  CURRENT FILING DATE:  2001-08-09
  PRIOR APPLICATION NUMBER: 09/325,958
  PRIOR FILING DATE: 1999-06-04
  PRIOR APPLICATION NUMBER: 08/858,000
  PRIOR FILING DATE: 1997-05-16
  PRIOR APPLICATION NUMBER: 08/403,013
  PRIOR FILING DATE: 1995-03-13
  PRIOR APPLICATION NUMBER: 07/584,941
  PRIOR FILING DATE: 1990-09-18
  PRIOR APPLICATION NUMBER: 07/307,817
  PRIOR FILING DATE: 1989-02-07
  PRIOR APPLICATION NUMBER: 07/269,945
  PRIOR FILING DATE: 1988-11-10
  NUMBER OF SEQ ID NOS: 19
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
   LENGTH: 2362
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
   NAME/KEY: CDS
   LOCATION: (33)..(1016)
S-09-924-703-3

lignment Scores:
red. No.:              1.37e-25       Length:        2362
```

```
Score:                 35.00          Matches:       35
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           11.4%          Indels:        0
DB:                    3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-924-703-3 (1-2362)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737

Qy      215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
            |||||||||||||||||||||||||||||||||||||||||||||
Db      738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 59
US-10-358-395-3
; Sequence 3, Application US/10358395
; Publication No. US20040044186A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/10/358,395
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US/09/924,703
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-10-358-395-3

Alignment Scores:
Pred. No.:             1.37e-25       Length:        2362
Score:                 35.00          Matches:       35
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           11.4%          Indels:        0
DB:                    8              Gaps:          0

US-10-821-670A-27 (1-307) x US-10-358-395-3 (1-2362)

Qy      195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 737
```

```
Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        738 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 782

RESULT 60
US-10-136-837-1
  Sequence 1, Application US/10136837
  Publication No. US20030181405A1
  GENERAL INFORMATION:
   APPLICANT: NORDSTROM, Jeffrey L
   APPLICANT:  PERICLE, Federica
   APPLICANT:  ROLLAND, Alain
   APPLICANT:  RALSTON, Robert
   TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
   TITLE OF INVENTION:  Using the Same
   FILE REFERENCE: 273/082 (GM15-1USC1)
   CURRENT APPLICATION NUMBER: US/10/136,837
   CURRENT FILING DATE:  2002-04-29
   PRIOR APPLICATION NUMBER: US 09/268,135
   PRIOR FILING DATE: 1999-03-12
   NUMBER OF SEQ ID NOS: 5
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 1
    LENGTH: 5686
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Human IL-12 Plasmid pIN1143
US-10-136-837-1

Alignment Scores:
Pred. No.:                3.05e-25       Length:          5686
Score:                    35.00          Matches:         35
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              11.4%          Indels:          0
DB:                       7              Gaps:            0

US-10-821-670A-27 (1-307) x US-10-136-837-1 (1-5686)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3864 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3923

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db       3924 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3968

RESULT 61
US-10-511-237-1
  Sequence 1, Application US/10511237
  Publication No. US20050233457A1
  GENERAL INFORMATION:
   APPLICANT: Block, Andreas
   TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
   TITLE OF INVENTION:  Genes
   FILE REFERENCE: 66741-043
   CURRENT APPLICATION NUMBER: US/10/511,237
   CURRENT FILING DATE:  2004-10-12
   NUMBER OF SEQ ID NOS: 5
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 1
    LENGTH: 11569
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.hscIL-12 for regulated expre
    OTHER INFORMATION: human IL-12
    FEATURE:
    NAME/KEY: gene
    LOCATION: (327)..(713)
    OTHER INFORMATION: VP16
    FEATURE:
    NAME/KEY: gene
    LOCATION: (714)..(1352)
    OTHER INFORMATION: TetR
    FEATURE:
    NAME/KEY: Intron
    LOCATION: (1353)..(1912)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: promoter
    LOCATION: (1864)..(1902)
    OTHER INFORMATION: TK-min
    FEATURE:
    NAME/KEY: protein_bind
    LOCATION: (1913)..(2212)
    OTHER INFORMATION: TetO7
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: (2213)..(2709)
    OTHER INFORMATION: CMV-min + Intron
    FEATURE:
    NAME/KEY: promoter
    LOCATION: (2226)..(2264)
    OTHER INFORMATION: CMV-min
    FEATURE:
    NAME/KEY: gene
    LOCATION: (2710)..(4308)
    OTHER INFORMATION: Human single-chain IL-12
    FEATURE:
    NAME/KEY: mutation
    LOCATION: (4020)..(4023)
    OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-1

Alignment Scores:
Pred. No.:                5.84e-25       Length:          11569
Score:                    35.00          Matches:         35
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              11.4%          Indels:          0
DB:                       10             Gaps:            0

US-10-821-670A-27 (1-307) x US-10-511-237-1 (1-11569)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3355 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3414

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||||||||||||||||||||||||
Db       3415 GACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 3459

RESULT 62
US-10-528-644A-53
; Sequence 53, Application US/10528644A
; Publication No. US20050287117A1
; GENERAL INFORMATION:
;  APPLICANT: SUNG, Young Chul
;  APPLICANT:  YOUN, Jin-Won
;  APPLICANT:  YANG, Se-Hwan
;  APPLICANT:  PARK, Su-Hwan
;  APPLICANT:  LEE, Chang Geun
;  TITLE OF INVENTION: A VACCINE ENHANCING THE PROTECTIVE IMMUNITY TO
;  TITLE OF INVENTION:  HEPATITIS C VIRUS USING PLASMID DNA AND RECOMBINANT ADENOVIRUS
;  FILE REFERENCE: 428.1049
;  CURRENT APPLICATION NUMBER: US/10/528,644A
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: PCT/KR03/01951
;  PRIOR FILING DATE: 2003-11-19
;  PRIOR APPLICATION NUMBER: KR 2002-0058712
;  PRIOR FILING DATE: 2002-09-27
;  PRIOR APPLICATION NUMBER: KR 2002-68496
;  PRIOR FILING DATE: 2002-11-06
;  NUMBER OF SEQ ID NOS: 54
```

```
  SOFTWARE: KopatentIn 1.71
 SEQ ID NO 53
   LENGTH: 2390
   TYPE: DNA
   ORGANISM: Homo sapiens (hIL-12m)
S-10-528-644A-53

Alignment Scores:
Pred. No.:              3.01e-18        Length:         2390
Score:                  28.00           Matches:        28
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            9.1%            Indels:         0
DB:                     10              Gaps:           0

S-10-821-670A-27 (1-307) x US-10-528-644A-53 (1-2390)

Qy        202 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2070 TACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAG 2129

Qy        222 LeuLysProLeuLysAsnSerArg 229
              |||||||||||||||||||||||
Db       2130 CTGAAGCCATTAAAGAATTCTCGG 2153

RESULT 63
S-09-826-025-24
Sequence 24, Application US/09826025
Patent No. US20020162123A1
  GENERAL INFORMATION:
       APPLICANT: Chang, Lung-Ji
       TITLE OF INVENTION: Combination Immunogene Therapy
       NUMBER OF SEQUENCES: 25
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: Medlen & Carroll, LLP
            STREET: 220 Montgomery Street, Suite 2200
            CITY: San Francisco
            STATE: California
            COUNTRY: United States of America
            ZIP: 94104
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/826,025
            FILING DATE: 04-Apr-2001
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/838,702
            FILING DATE: <Unknown>
       ATTORNEY/AGENT INFORMATION:
            NAME: Ingolia, Diane E.
            REGISTRATION NUMBER: 40,027
            REFERENCE/DOCKET NUMBER: CHANG-02687
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: (415) 705-8410
            TELEFAX: (415) 397-8338
  INFORMATION FOR SEQ ID NO: 24:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 987 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: double
            TOPOLOGY: linear
       MOLECULE TYPE: other nucleic acid
            DESCRIPTION: /desc = "DNA"
       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
S-09-826-025-24

Alignment Scores:
Pred. No.:              2.35e-13        Length:         987
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.5%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-826-025-24 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705

Qy        215 AspProPro 217
              |||||||||
Db        706 GACCCACCC 714

RESULT 64
US-10-785-577-24
; Sequence 24, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/785,577
;             FILING DATE: 23-Feb-2004
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/838,702
;             FILING DATE: 9-Apr-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-785-577-24

Alignment Scores:
Pred. No.:              2.35e-13        Length:         987
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.5%            Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-785-577-24 (1-987)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 705
```

Qy 215 AspProPro 217
Db 706 GACCCACCC 714

RESULT 65
US-10-373-456-18
Sequence 18, Application US/10373456
Publication No. US20040009146A1
GENERAL INFORMATION:
APPLICANT: Podhajcer, Osvaldo
TITLE OF INVENTION: Anti-Tumor Vaccine and Method
FILE REFERENCE: 1423P-US/101141-14
CURRENT APPLICATION NUMBER: US/10/373,456
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/359,836
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 1005
TYPE: DNA
ORGANISM: Homo sapiens
US-10-373-456-18

Alignment Scores:

Pred. No.:	2.39e-13	Length:	1005
Score:	23.00	Matches:	23
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.5%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-373-456-18 (1-1005)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
Db 654 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 713

Qy 215 AspProPro 217
Db 714 GACCCACCC 722

RESULT 66
US-10-373-456-20
Sequence 20, Application US/10373456
Publication No. US20040009146A1
GENERAL INFORMATION:
APPLICANT: Podhajcer, Osvaldo
TITLE OF INVENTION: Anti-Tumor Vaccine and Method
FILE REFERENCE: 1423P-US/101141-14
CURRENT APPLICATION NUMBER: US/10/373,456
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/359,836
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 1017
TYPE: DNA
ORGANISM: Homo sapiens
US-10-373-456-20

Alignment Scores:

Pred. No.:	2.41e-13	Length:	1017
Score:	23.00	Matches:	23
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.5%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-373-456-20 (1-1017)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
Db 658 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 717

Qy 215 AspProPro 217
Db 718 GACCCACCC 726

RESULT 67
US-10-742-405-7
; Sequence 7, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Edward P.
; APPLICANT: Chan, Jason R.
; APPLICANT: Moore, Kevin
; APPLICANT: Nguyen, Nhung
; APPLICANT: Churakova, Tatyana
; APPLICANT: Chen, Shi-Juan
; APPLICANT: Cua, Daniel J.
; TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
; FILE REFERENCE: DX01578K
; CURRENT APPLICATION NUMBER: US/10/742,405
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1569)
US-10-742-405-7

Alignment Scores:

Pred. No.:	3.61e-13	Length:	1580
Score:	23.00	Matches:	23
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.5%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-742-405-7 (1-1580)

Qy 195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
Db 658 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 717

Qy 215 AspProPro 217
Db 718 GACCCACCC 726

RESULT 68
US-10-373-456-2
; Sequence 2, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
; APPLICANT: Podhajcer, Osvaldo
; TITLE OF INVENTION: Anti-Tumor Vaccine and Method
; FILE REFERENCE: 1423P-US/101141-14
; CURRENT APPLICATION NUMBER: US/10/373,456
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,836
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: p40-linker-p35 fragment cloned into MVL-hIL12lig vector (Fig. 11)

-10-373-456-2

ignment Scores:
ed. No.: 4.12e-13 Length: 1828
ore: 23.00 Matches: 23
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 7.5% Indels: 0
: 7 Gaps: 0

-10-821-670A-27 (1-307) x US-10-373-456-2 (1-1828)

195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
658 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 717

215 AspProPro 217
718 GACCCACCC 726

SULT 69
-10-228-811-4
Sequence 4, Application US/10228811
Publication No. US20030054392A1
GENERAL INFORMATION:
APPLICANT: Wittig, Prof. Burghardt
APPLICANT: Junghans, Claas
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
TITLE OF INVENTION: Therapy
FILE REFERENCE: XI 597/99
CURRENT APPLICATION NUMBER: US/10/228,811
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: DE 196 48 625.4
PRIOR FILING DATE: 1996-11-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 1870
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1870)
OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1)..(2)
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
OTHER INFORMATION: 2 can be modified with amino or caroxy features
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1869)..(1870)
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
OTHER INFORMATION: to 1870 can be modified with amino or caroxy features
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No
-10-228-811-4

ignment Scores:
ed. No.: 4.21e-13 Length: 1870
ore: 23.00 Matches: 23
rcent Similarity: 100.0% Conservative: 0
st Local Similarity: 100.0% Mismatches: 0
ery Match: 7.5% Indels: 0
: 6 Gaps: 0

-10-821-670A-27 (1-307) x US-10-228-811-4 (1-1870)

195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
1278 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 1337

215 AspProPro 217
1338 GACCCACCC 1346

RESULT 70
US-10-172-399-7
; Sequence 7, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
; APPLICANT: Li, Chuan-Yuan
; APPLICANT: Dewhirst, Mark
; APPLICANT: Huang, Qian
; TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTHE
; FILE REFERENCE: 180-129
; CURRENT APPLICATION NUMBER: US/10/172,399
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 2318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(1000)
US-10-172-399-7

Alignment Scores:
Pred. No.: 5.12e-13 Length: 2318
Score: 23.00 Matches: 23
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 7.5% Indels: 0
DB: 6 Gaps: 0

US-10-821-670A-27 (1-307) x US-10-172-399-7 (1-2318)

195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
659 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 718

215 AspProPro 217
719 GACCCACCC 727

RESULT 71
US-10-476-961-3
; Sequence 3, Application US/10476961
; Publication No. US20040241843A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
; FILE REFERENCE: RTSP-0393
; CURRENT APPLICATION NUMBER: US/10/476,961
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 2001-05-07
; PRIOR FILING DATE: 09/851,062
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
; LENGTH: 2318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)...(1000)
US-10-476-961-3

Alignment Scores:
Pred. No.: 5.12e-13 Length: 2318
Score: 23.00 Matches: 23
Percent Similarity: 100.0% Conservative: 0

```
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            7.5%          Indels:        0
B:                     9             Gaps:          0

S-10-821-670A-27 (1-307) x US-10-476-961-3 (1-2318)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        659 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 718

y        215 AspProPro 217
             |||||||||
b        719 GACCCACCC 727

ESULT 72
S-10-373-456-1
  Sequence 1, Application US/10373456
  Publication No. US20040009146A1
  GENERAL INFORMATION:
   APPLICANT: Podhajcer, Osvaldo
   TITLE OF INVENTION: Anti-Tumor Vaccine and Method
   FILE REFERENCE: 1423P-US/101141-14
   CURRENT APPLICATION NUMBER: US/10/373,456
   CURRENT FILING DATE:  2003-02-25
   PRIOR APPLICATION NUMBER: US 60/359,836
   PRIOR FILING DATE: 2002-02-26
   NUMBER OF SEQ ID NOS: 20
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 1
    LENGTH: 2466
    TYPE: DNA
    ORGANISM: Artificial
    FEATURE:
    OTHER INFORMATION: p35-IRES-p40 fragment cloned into MVL-hIL-12 and MVL-hIL-12-hIL-1
    OTHER INFORMATION: 0 vectors (Fig 11)
S-10-373-456-1

lignment Scores:
ed. No.:               5.42e-13      Length:        2466
core:                  23.00         Matches:       23
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            7.5%          Indels:        0
B:                     7             Gaps:          0

S-10-821-670A-27 (1-307) x US-10-373-456-1 (1-2466)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       2115 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 2174

y        215 AspProPro 217
             |||||||||
b       2175 GACCCACCC 2183

ESULT 73
S-09-828-825-1
  Sequence 1, Application US/09828825
  Patent No. US20020018767A1
  GENERAL INFORMATION:
   APPLICANT: Lee, Seewoo
   APPLICANT:  Kim, Han-soo
   TITLE OF INVENTION: Anti-cancer Cellular Vaccine
   FILE REFERENCE: 84906-102
   CURRENT APPLICATION NUMBER: US/09/828,825
   CURRENT FILING DATE:  2001-04-10
   PRIOR APPLICATION NUMBER: KR00-43498
   PRIOR FILING DATE: 2000-07-27
   NUMBER OF SEQ ID NOS: 16
   SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 1
    LENGTH: 8578
    TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV  IE
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA Promoter
;   NAME/KEY: mRNA
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: mRNA
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
;   OTHER INFORMATION: linker at 3624-3629)
;   NAME/KEY: promoter
;   LOCATION: (4352)..(4431)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4362)..(4583)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4678)..(5133)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5197)..(6564)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6975)..(7835)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4223)
;   OTHER INFORMATION: IL 12.0 coding sequence - 2 amino acid linker at
;   OTHER INFORMATION: 3624
US-09-828-825-1

Alignment Scores:
Pred. No.:             1.69e-12      Length:        8578
Score:                 23.00         Matches:       23
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           7.5%          Indels:        0
DB:                    3             Gaps:          0

US-10-821-670A-27 (1-307) x US-09-828-825-1 (1-8578)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3285 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3344

Qy        215 AspProPro 217
              |||||||||
Db       3345 GACCCACCC 3353

RESULT 74
US-09-828-825-3
; Sequence 3, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
```

```
 PRIOR FILING DATE: 2000-07-27
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
  LENGTH: 8578
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: plasmid
  NAME/KEY: enhancer
  LOCATION: (1)..(659)
  OTHER INFORMATION: CMV IE Enhancer
  NAME/KEY: promoter
  LOCATION: (669)..(750)
  OTHER INFORMATION: CMV IE Promoter
  NAME/KEY: misc_feature
  LOCATION: (890)..(1002)
  OTHER INFORMATION: InTervening Sequence
  NAME/KEY: promoter
  LOCATION: (1067)..(1085)
  OTHER INFORMATION: T7 RNA polymerase promoter
  NAME/KEY: misc_feature
  LOCATION: (1090)..(1984)
  OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
  NAME/KEY: RBS
  LOCATION: (2013)..(2593)
  OTHER INFORMATION: IRES sequence
  NAME/KEY: misc_feature
  LOCATION: (2627)..(4263)
  OTHER INFORMATION: Human IL12.0 sequence (2640-4217 is coding
  OTHER INFORMATION: sequence)
  NAME/KEY: promoter
  LOCATION: (4346)..(4425)
  OTHER INFORMATION: T3 RNA polymerase promoter
  NAME/KEY: polyA_signal
  LOCATION: (4356)..(4577)
  OTHER INFORMATION: SV40 fragment containing polyadenylation signal
  NAME/KEY: rep_origin
  LOCATION: (4672)..(5127)
  OTHER INFORMATION: f1 origin of replication
  NAME/KEY: misc_feature
  LOCATION: (5191)..(6558)
  OTHER INFORMATION: Neo r expression cassette
  NAME/KEY: misc_feature
  LOCATION: (6969)..(7829)
  OTHER INFORMATION: Ampicillin resistance
  NAME/KEY: CDS
  LOCATION: (2640)..(4217)
  OTHER INFORMATION: IL12.0 coding sequence - no linker
-09-828-825-3

ignment Scores:
ed. No.:                1.69e-12        Length:         8578
ore:                    23.00           Matches:        23
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              7.5%            Indels:         0
:                       3               Gaps:           0

-10-821-670A-27 (1-307) x US-09-828-825-3 (1-8578)

        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3285 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3344

        215 AspProPro 217
            |||||||||
       3345 GACCCACCC 3353

SULT 75
-09-828-825-7
 Sequence 7, Application US/09828825
 Patent No. US20020018767A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
;   OTHER INFORMATION: sequence, 13 amino acid flexible linker at
;   OTHER INFORMATION: 3606-3676)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4253)
;   OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4362)..(4383)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4393)..(4614)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4709)..(5164)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5228)..(6595)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7006)..(7866)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-7

Alignment Scores:
Pred. No.:              1.7e-12         Length:         8608
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.5%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-828-825-7 (1-8608)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3285 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3344

Qy        215 AspProPro 217
              |||||||||
```

```
Db       3345 GACCCACCC 3353

RESULT 76
US-09-828-825-5
 Sequence 5, Application US/09828825
 Patent No. US20020018767A1
 GENERAL INFORMATION:
  APPLICANT: Lee, Seewoo
  APPLICANT:  Kim, Han-soo
  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
  FILE REFERENCE: 84906-102
  CURRENT APPLICATION NUMBER: US/09/828,825
  CURRENT FILING DATE:  2001-04-10
  PRIOR APPLICATION NUMBER: KR00-43498
  PRIOR FILING DATE: 2000-07-27
  NUMBER OF SEQ ID NOS: 16
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 5
    LENGTH: 8623
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: (1)..(750)
    OTHER INFORMATION: CMV enhancer and promoter
    NAME/KEY: misc_feature
    LOCATION: (890)..(1002)
    OTHER INFORMATION: Intervening sequence
    NAME/KEY: promoter
    LOCATION: (1067)..(1085)
    OTHER INFORMATION: T7 RNA polymerase promoter
    NAME/KEY: misc_feature
    LOCATION: (1090)..(1984)
    OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
    NAME/KEY: RBS
    LOCATION: (2013)..(2593)
    OTHER INFORMATION: IRES sequence
    NAME/KEY: misc_feature
    LOCATION: (2627)..(4278)
    OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
    OTHER INFORMATION: flexible linker from 3606-3690
    NAME/KEY: CDS
    LOCATION: (2640)..(4268)
    OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
    OTHER INFORMATION: sequence
    NAME/KEY: promoter
    LOCATION: (4398)..(4407)
    OTHER INFORMATION: T3 RNA polymerase promoter
    NAME/KEY: polyA_signal
    LOCATION: (4408)..(4629)
    OTHER INFORMATION: SV40 fragment containing polyadenylation signal
    NAME/KEY: rep_origin
    LOCATION: (4724)..(5179)
    OTHER INFORMATION: f1 origin of replication
    NAME/KEY: misc_feature
    LOCATION: (5243)..(6610)
    OTHER INFORMATION: Neo r expression cassette
    NAME/KEY: misc_feature
    LOCATION: (7021)..(7881)
    OTHER INFORMATION: Ampicillin resistance
    OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

Alignment Scores:
Pred. No.:              1.7e-12       Length:         8623
Score:                  23.00         Matches:        23
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            7.5%          Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-27 (1-307) x US-09-828-825-5 (1-8623)
```

```
Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3285 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3344

Qy        215 AspProPro 217
              |||||||||
Db       3345 GACCCACCC 3353

RESULT 77
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 8629
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2726)
;   OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
;   OTHER INFORMATION: amino acid linker at 2087-2116)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2716)
;   OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2752)..(3332)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3369)..(4263)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4383)..(4404)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4414)..(4635)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4730)..(5185)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5249)..(6616)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7027)..(7887)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

Alignment Scores:
Pred. No.:              1.7e-12       Length:         8629
Score:                  23.00         Matches:        23
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            7.5%          Indels:         0
DB:                     3             Gaps:           0
```

```
-10-821-670A-27 (1-307) x US-09-828-825-15 (1-8629)

        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1748 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 1807

        215 AspProPro 217
            |||||||||
       1808 GACCCACCC 1816

ESULT 78
-09-828-825-9
 Sequence 9, Application US/09828825
 Patent No. US20020018767A1
 GENERAL INFORMATION:
  APPLICANT: Lee, Seewoo
  APPLICANT:  Kim, Han-soo
  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
  FILE REFERENCE: 84906-102
  CURRENT APPLICATION NUMBER: US/09/828,825
  CURRENT FILING DATE:  2001-04-10
  PRIOR APPLICATION NUMBER: KR00-43498
  PRIOR FILING DATE: 2000-07-27
  NUMBER OF SEQ ID NOS: 16
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
    LENGTH: 8638
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Description of Artificial Sequence: plasmid
    NAME/KEY: misc_feature
    LOCATION: (1)..(750)
    OTHER INFORMATION: CMV enhancer and promoter
    NAME/KEY: misc_feature
    LOCATION: (890)..(1002)
    OTHER INFORMATION: Intervening sequence
    NAME/KEY: promoter
    LOCATION: (1067)..(1085)
    OTHER INFORMATION: T7 RNA polymerase promoter
    NAME/KEY: misc_feature
    LOCATION: (1090)..(1984)
    OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
    NAME/KEY: RBS
    LOCATION: (2013)..(2593)
    OTHER INFORMATION: IRES sequence
    NAME/KEY: misc_feature
    LOCATION: (2627)..(4293)
    OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
    OTHER INFORMATION: amino acid linker at 3606-3706)
    NAME/KEY: CDS
    LOCATION: (2640)..(4283)
    OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
    NAME/KEY: promoter
    LOCATION: (4392)..(4413)
    OTHER INFORMATION: T3 RNA Polymerase promoter
    NAME/KEY: polyA_signal
    LOCATION: (4423)..(4644)
    OTHER INFORMATION: SV40 fragment containing polyadenylation signal
    NAME/KEY: rep_origin
    LOCATION: (4739)..(5194)
    OTHER INFORMATION: f1 origin of replication
    NAME/KEY: misc_feature
    LOCATION: (5258)..(6625)
    OTHER INFORMATION: Neo r expression cassette
    NAME/KEY: misc_feature
    LOCATION: (7036)..(7896)
    OTHER INFORMATION: Ampicillin resistance
-09-828-825-9

 ignment Scores:
 ed. No.:              1.7e-12        Length:       8638
 ore:                  23.00          Matches:      23
```

```
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            7.5%          Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-27 (1-307) x US-09-828-825-9 (1-8638)

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3285 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3344

Qy        215 AspProPro 217
              |||||||||
Db       3345 GACCCACCC 3353

RESULT 79
US-09-828-825-13
; Sequence 13, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 8644
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2731)
;   OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
;   OTHER INFORMATION: amino acid linker at 2087-2131)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2731)
;   OTHER INFORMATION: IL12.3 (15 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2767)..(3347)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3384)..(4278)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4419)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4429)..(4650)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4745)..(5200)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5264)..(5681)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7042)..(7902)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-13

Alignment Scores:
```

```
ed. No.:              1.71e-12        Length:         8644
core:                 23.00           Matches:        23
ercent Similarity:    100.0%          Conservative:   0
est Local Similarity: 100.0%          Mismatches:     0
uery Match:           7.5%            Indels:         0
B:                    3               Gaps:           0

S-10-821-670A-27 (1-307) x US-09-828-825-13 (1-8644)

y        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b       1748 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 1807

y        215 AspProPro 217
             |||||||||
b       1808 GACCCACCC 1816

ESULT 80
3-09-828-825-11
 Sequence 11, Application US/09828825
 Patent No. US20020018767A1
 GENERAL INFORMATION:
  APPLICANT: Lee, Seewoo
  APPLICANT:  Kim, Han-soo
  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
  FILE REFERENCE: 84906-102
  CURRENT APPLICATION NUMBER: US/09/828,825
  CURRENT FILING DATE:  2001-04-10
  PRIOR APPLICATION NUMBER: KR00-43498
  PRIOR FILING DATE: 2000-07-27
  NUMBER OF SEQ ID NOS: 16
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 11
    LENGTH: 8659
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: (1)..(750)
    OTHER INFORMATION: CMV enhancer and promoter
    NAME/KEY: promoter
    LOCATION: (1067)..(1085)
    OTHER INFORMATION: T7 RNA polymerase promoter
    NAME/KEY: misc_feature
    LOCATION: (1090)..(2756)
    OTHER INFORMATION: Human IL12.4 (coding sequence 1103-2746, 19 amino
    OTHER INFORMATION: acid linker at 2087-2146)
    NAME/KEY: CDS
    LOCATION: (1103)..(2746)
    OTHER INFORMATION: Human IL12.4 (19 amino acid linker)
    NAME/KEY: RBS
    LOCATION: (2782)..(3362)
    OTHER INFORMATION: IRES sequence
    NAME/KEY: misc_feature
    LOCATION: (3399)..(4293)
    OTHER INFORMATION: Human B7.1 sequence
    NAME/KEY: promoter
    LOCATION: (4413)..(4434)
    OTHER INFORMATION: T3 RNA polymerase promoter
    NAME/KEY: polyA_signal
    LOCATION: (4444)..(4665)
    OTHER INFORMATION: SV40 fragment containing polyadenylation signal
    NAME/KEY: rep_origin
    LOCATION: (4760)..(5215)
    OTHER INFORMATION: f1 origin of replication
    NAME/KEY: misc_feature
    LOCATION: (5279)..(6646)
    OTHER INFORMATION: Neo r expression cassette
    NAME/KEY: misc_feature
    LOCATION: (7057)..(7917)
    OTHER INFORMATION: Ampicillin resistance gene
    OTHER INFORMATION: Description of Artificial Sequence: plasmid
B-09-828-825-11

Alignment Scores:
Pred. No.:              1.71e-12        Length:         8659
Score:                  23.00           Matches:        23
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.5%            Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-828-825-11 (1-8659)

Qy       195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1748 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 1807

Qy       215 AspProPro 217
             |||||||||
Db      1808 GACCCACCC 1816

RESULT 81
US-10-511-237-3
; Sequence 3, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 11453
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pShuttle.3r.hscIL-12 for regulated
;   OTHER INFORMATION: expression of human IL-12 following virus generation using AdEasy
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2709)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2710)..(4308)
;   OTHER INFORMATION: Human singe-chain IL-12
;   FEATURE:
;   NAME/KEY: mutation
```

```
   LOCATION: (4020)..(4023)
   OTHER INFORMATION: T/C, A/T, G/C, T/G
-10-511-237-3

ignment Scores:
ed. No.:              2.21e-12        Length:         11453
ore:                  23.00           Matches:        23
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            7.5%            Indels:         0
:                     10              Gaps:           0

-10-821-670A-27 (1-307) x US-10-511-237-3 (1-11453)

        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       3355 CACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCT 3414

        215 AspProPro 217
            |||||||||
       3415 GACCCACCC 3423

SULT 82
-10-240-376A-130
 Sequence 130, Application US/10240376A
 Publication No. US20040161747A1
 GENERAL INFORMATION:
  APPLICANT: Morahan, Grant
  TITLE OF INVENTION: A METHOD FOR SCREENING FOR AUTOIMMUNE
  TITLE OF INVENTION:  DISEASE BY IDENTIFYING POLYMORPHISMS IN IL-12 p40
  FILE REFERENCE: DAVI186.001APC
  CURRENT APPLICATION NUMBER: US/10/240,376A
  CURRENT FILING DATE:  2002-09-27
  PRIOR APPLICATION NUMBER: PCT/AU01/00340
  PRIOR FILING DATE: 2001-03-27
  PRIOR APPLICATION NUMBER: PQ 6466
  PRIOR FILING DATE: 2000-03-27
  PRIOR APPLICATION NUMBER: US 60/204,366
  PRIOR FILING DATE: 2000-05-15
  NUMBER OF SEQ ID NOS: 140
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 130
   LENGTH: 18340
   TYPE: DNA
   ORGANISM: mammalian
-10-240-376A-130

ignment Scores:
ed. No.:              3.79e-11        Length:         18340
ore:                  22.00           Matches:        22
rcent Similarity:     100.0%          Conservative:   0
st Local Similarity:  100.0%          Mismatches:     0
ery Match:            7.2%            Indels:         0
:                     8               Gaps:           0

-10-821-670A-27 (1-307) x US-10-240-376A-130 (1-18340)

        231 ValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeu 250
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      14078 GTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCCCTG 14137

        251 ThrPhe 252
            ||||||
      14138 ACATTC 14143

ESULT 83
S-10-029-386-16833/c
 Sequence 16833, Application US/10029386
 Publication No. US20030194704A1
 GENERAL INFORMATION:
  APPLICANT: Penn, Sharron G.
  APPLICANT:  Rank, David R.
  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16833
;   LENGTH: 270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR5.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;   OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BF204907.1, EVALUE 9.20e-02
;   OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 4.00e-41
US-10-029-386-16833

Alignment Scores:
Pred. No.:            1e-10           Length:         270
Score:                20.00           Matches:        20
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          6.5%            Indels:         0
DB:                   7               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-029-386-16833 (1-270)

Qy          41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         167 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 108

RESULT 84
US-11-128-061-661
; Sequence 661, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
;  TITLE OF INVENTION:  TO MONITOR GENE EXPRESSION
;  FILE REFERENCE: 01997.027701
;  CURRENT APPLICATION NUMBER: US/11/128,061
;  CURRENT FILING DATE:  2005-05-11
;  PRIOR APPLICATION NUMBER: US 60/570,425
;  PRIOR FILING DATE: 2004-05-11
;  NUMBER OF SEQ ID NOS: 7285
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 661
;   LENGTH: 399
;   TYPE: DNA
;   ORGANISM: Mesocricetus auratus
US-11-128-061-661

Alignment Scores:
Pred. No.:            1.43e-10        Length:         399
Score:                20.00           Matches:        20
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          6.5%            Indels:         0
DB:                   16              Gaps:           0

US-10-821-670A-27 (1-307) x US-11-128-061-661 (1-399)
```

```
Qy        113 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182

RESULT 85
US-11-128-061-4303
  Sequence 4303, Application US/11128061
  Publication No. US20060003958A1
  GENERAL INFORMATION:
   APPLICANT: Melville, Mark W.
   APPLICANT:  Charlebois, Timothy S.
   APPLICANT:  Mounts, William M.
   APPLICANT:  Hann, Louane E.
   APPLICANT:  Sinacore, Martin S.
   APPLICANT:  Leonard, Mark W.
   APPLICANT:  Brown, Eugene L.
   APPLICANT:  Miller, Christopher P.
   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
   TITLE OF INVENTION:  TO MONITOR GENE EXPRESSION
   FILE REFERENCE: 01997.027701
   CURRENT APPLICATION NUMBER: US/11/128,061
   CURRENT FILING DATE:  2005-05-11
   PRIOR APPLICATION NUMBER: US 60/570,425
   PRIOR FILING DATE: 2004-05-11
   NUMBER OF SEQ ID NOS: 7285
   SOFTWARE: PatentIn version 3.3
  SEQ ID NO 4303
    LENGTH: 399
    TYPE: DNA
    ORGANISM: Mesocricetus auratus
US-11-128-061-4303

Alignment Scores:
Pred. No.:                1.43e-10        Length:         399
Score:                    20.00           Matches:        20
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              6.5%            Indels:         0
DB:                       16              Gaps:           0

US-10-821-670A-27 (1-307) x US-11-128-061-4303 (1-399)

Qy        113 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182

RESULT 86
US-11-128-049-661
  Sequence 661, Application US/11128049
  Publication No. US20060010513A1
  GENERAL INFORMATION:
   APPLICANT: Melville, Mark W.
   APPLICANT:  Charlebois, Timothy S.
   APPLICANT:  Mounts, William M.
   APPLICANT:  Hann, Louane E.
   APPLICANT:  Sinacore, Martin S.
   APPLICANT:  Leonard, Mark W.
   APPLICANT:  Brown, Eugene L.
   APPLICANT:  Miller, Christopher P.
   TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
   TITLE OF INVENTION:  MAKING AND USING SAME
   FILE REFERENCE: 01997.027700
   CURRENT APPLICATION NUMBER: US/11/128,049
   CURRENT FILING DATE:  2005-05-11
   PRIOR APPLICATION NUMBER: US 60/570,425
   PRIOR FILING DATE: 2004-05-11
   NUMBER OF SEQ ID NOS: 7285
   SOFTWARE: PatentIn version 3.3
  SEQ ID NO 661
    LENGTH: 399
    TYPE: DNA
    ORGANISM: Mesocricetus auratus
US-11-128-049-661

Alignment Scores:
Pred. No.:                1.43e-10        Length:         399
Score:                    20.00           Matches:        20
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              6.5%            Indels:         0
DB:                       16              Gaps:           0

US-10-821-670A-27 (1-307) x US-11-128-049-661 (1-399)

Qy        113 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182

RESULT 87
US-11-128-049-4303
; Sequence 4303, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
;  APPLICANT: Melville, Mark W.
;  APPLICANT:  Charlebois, Timothy S.
;  APPLICANT:  Mounts, William M.
;  APPLICANT:  Hann, Louane E.
;  APPLICANT:  Sinacore, Martin S.
;  APPLICANT:  Leonard, Mark W.
;  APPLICANT:  Brown, Eugene L.
;  APPLICANT:  Miller, Christopher P.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
;  TITLE OF INVENTION:  MAKING AND USING SAME
;  FILE REFERENCE: 01997.027700
;  CURRENT APPLICATION NUMBER: US/11/128,049
;  CURRENT FILING DATE:  2005-05-11
;  PRIOR APPLICATION NUMBER: US 60/570,425
;  PRIOR FILING DATE: 2004-05-11
;  NUMBER OF SEQ ID NOS: 7285
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4303
;   LENGTH: 399
;   TYPE: DNA
;   ORGANISM: Mesocricetus auratus
US-11-128-049-4303

Alignment Scores:
Pred. No.:                1.43e-10        Length:         399
Score:                    20.00           Matches:        20
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              6.5%            Indels:         0
DB:                       16              Gaps:           0

US-10-821-670A-27 (1-307) x US-11-128-049-4303 (1-399)

Qy        113 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 AATTACTCTGGACGGTTCACCTGCTGGTGGCTGACTGCAATCAGCACTGACTTGAAGTTC 182

RESULT 88
US-10-029-386-3133/c
; Sequence 3133, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
```

```
SEQ ID NO 3133
  LENGTH: 556
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  OTHER INFORMATION: MAP TO CHR5.1
  OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
  OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
  OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
  OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
  OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
  OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 5.00e-43
  OTHER INFORMATION: EST_HUMAN HIT: BG389008.1, EVALUE 2.00e-01
-10-029-386-3133

ignment Scores:
ed. No.:                1.94e-10        Length:         556
ore:                    20.00           Matches:        20
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              6.5%            Indels:         0
:                       7               Gaps:           0

-10-821-670A-27 (1-307) x US-10-029-386-3133 (1-556)

          41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         362 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 303

SULT 89
-09-823-549-77
Sequence 77, Application US/09823549
Publication No. US20020147998A1
GENERAL INFORMATION:
 APPLICANT: McConlogue, Lisa  C
 APPLICANT:  Games, Kate D.
 APPLICANT:  Yednock, Theodore A.
 APPLICANT:  Hua, Tan
 APPLICANT:  Messersmith, Elizabeth
 APPLICANT:  Bard, Frederique
 TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
 FILE REFERENCE: 015270-009110US
 CURRENT APPLICATION NUMBER: US/09/823,549
 CURRENT FILING DATE:  2001-03-30
 PRIOR APPLICATION NUMBER: US 60/193,847
 PRIOR FILING DATE: 2000-03-30
 NUMBER OF SEQ ID NOS: 85
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 77
  LENGTH: 73
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: IL-12 p40, #1 marker
-09-823-549-77

ignment Scores:
ed. No.:                4.24e-08        Length:         73
ore:                    17.00           Matches:        17
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              5.5%            Indels:         0
:                       3               Gaps:           0

-10-821-670A-27 (1-307) x US-09-823-549-77 (1-73)

        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
          9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59

SULT 90
-10-685-992-77
Sequence 77, Application US/10685992
; Publication No. US20040213739A1
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/10/685,992
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US/09/823,549
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-10-685-992-77

Alignment Scores:
Pred. No.:              4.24e-08        Length:         73
Score:                  17.00           Matches:        17
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.5%            Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-685-992-77 (1-73)

Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 59

RESULT 91
US-11-136-527-4408
; Sequence 4408, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4408
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-4408

Alignment Scores:
Pred. No.:              2.91e-07        Length:         600
Score:                  17.00           Matches:        17
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            5.5%            Indels:         0
DB:                     16              Gaps:           0

US-10-821-670A-27 (1-307) x US-11-136-527-4408 (1-600)

Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

)b 262 AGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAG 312

ESULT 92
S-11-136-527-312
Sequence 312, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 312
LENGTH: 1024
TYPE: DNA
ORGANISM: Rattus norvegicus
S-11-136-527-312

lignment Scores:

ed. No.:	4.74e-07	Length:	1024
core:	17.00	Matches:	17
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	5.5%	Indels:	0
B:	16	Gaps:	0

S-10-821-670A-27 (1-307) x US-11-136-527-312 (1-1024)

y 205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
)b 686 AGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAG 736

ESULT 93
S-10-603-064-3
Sequence 3, Application US/10603064
Publication No. US20040072299A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin Ming
TITLE OF INVENTION: Multiple Cytokine Protein Complexes
FILE REFERENCE: LEX-010
CURRENT APPLICATION NUMBER: US/10/603,064
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/634,368
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,924
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1409
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
S-10-603-064-3

lignment Scores:

ed. No.:	6.34e-07	Length:	1409
core:	17.00	Matches:	17
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	5.5%	Indels:	0
B:	8	Gaps:	0

S-10-821-670A-27 (1-307) x US-10-603-064-3 (1-1409)

Qy 205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740

RESULT 94
US-10-603-064-2
; Sequence 2, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-2

Alignment Scores:

Pred. No.:	6.6e-07	Length:	1472
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.5%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-603-064-2 (1-1472)

Qy 205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 690 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 740

RESULT 95
US-10-603-064-12
; Sequence 12, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-10-603-064-12

Alignment Scores:

Pred. No.:	7e-07	Length:	1569
Score:	17.00	Matches:	17

```
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            5.5%            Indels:        0
:                     8               Gaps:          0

-10-821-670A-27 (1-307) x US-10-603-064-12 (1-1569)

        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
       1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

SULT 96
-10-742-405-5
 Sequence 5, Application US/10742405
 Publication No. US20040213761A1
 GENERAL INFORMATION:
  APPLICANT: Bowman, Edward P.
  APPLICANT:  Chan, Jason R.
  APPLICANT:  Moore, Kevin
  APPLICANT:  Nguyen, Nhung
  APPLICANT:  Churakova, Tatyana
  APPLICANT:  Chen, Shi-Juan
  APPLICANT:  Cua, Daniel J.
  TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
  FILE REFERENCE: DX01578K
  CURRENT APPLICATION NUMBER: US/10/742,405
  CURRENT FILING DATE:  2003-12-18
  NUMBER OF SEQ ID NOS: 12
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 5
    LENGTH: 1610
    TYPE: DNA
    ORGANISM: Mus musculus
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (7)..(1599)
-10-742-405-5

ignment Scores:
ed. No.:              7.17e-07        Length:        1610
ore:                  17.00           Matches:       17
rcent Similarity:     100.0%          Conservative:  0
st Local Similarity:  100.0%          Mismatches:    0
ery Match:            5.5%            Indels:        0
:                     9               Gaps:          0

-10-821-670A-27 (1-307) x US-10-742-405-5 (1-1610)

        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
        682 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 732

SULT 97
-10-172-399-3
 Sequence 3, Application US/10172399
 Publication No. US20030045495A1
 GENERAL INFORMATION:
  APPLICANT: Li, Chuan-Yuan
  APPLICANT:  Dewhirst, Mark
  APPLICANT:  Huang, Qian
  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
  FILE REFERENCE: 180-129
  CURRENT APPLICATION NUMBER: US/10/172,399
  CURRENT FILING DATE:  2002-06-14
  NUMBER OF SEQ ID NOS: 13
  SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3
    LENGTH: 1840
    TYPE: DNA
    ORGANISM: Mus musculus
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (35)..(1042)

US-10-172-399-3

Alignment Scores:
Pred. No.:            8.1e-07         Length:        1840
Score:                17.00           Matches:       17
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          5.5%            Indels:        0
DB:                   6               Gaps:          0

US-10-821-670A-27 (1-307) x US-10-172-399-3 (1-1840)

Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 754

RESULT 98
US-10-603-064-11
; Sequence 11, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-10-603-064-11

Alignment Scores:
Pred. No.:            8.79e-07        Length:        2013
Score:                17.00           Matches:       17
Percent Similarity:   100.0%          Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:          5.5%            Indels:        0
DB:                   8               Gaps:          0

US-10-821-670A-27 (1-307) x US-10-603-064-11 (1-2013)

Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1281

RESULT 99
US-10-603-064-13
; Sequence 13, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
```

SEQ ID NO 13
LENGTH: 2709
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: murine
OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
OTHER INFORMATION: sequence
US-10-603-064-13

Alignment Scores:

Seq. No.:	1.15e-06	Length:	2709
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.5%	Indels:	0
DB:	8	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-603-064-13 (1-2709)

```
Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 1977
```

RESULT 100
US-10-136-837-3
Sequence 3, Application US/10136837
Publication No. US20030181405A1
GENERAL INFORMATION:
APPLICANT: NORDSTROM, Jeffrey L
APPLICANT: PERICLE, Federica
APPLICANT: ROLLAND, Alain
APPLICANT: RALSTON, Robert
TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 273/082 (GM15-1USC1)
CURRENT APPLICATION NUMBER: US/10/136,837
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 09/268,135
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 5966
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Mouse IL-12 pIN0961
US-10-136-837-3

Alignment Scores:

Seq. No.:	2.37e-06	Length:	5966
Score:	17.00	Matches:	17
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.5%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-136-837-3 (1-5966)

```
Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5343 AGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTGCAG 5393
```

Search completed: June 12, 2006, 17:16:02
Job time : 1510.59 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

M protein - nucleic search, using frame_plus_p2n model

un on: June 10, 2006, 02:09:37 ; Search time 20.9229 Seconds
(without alignments)
2793.504 Million cell updates/sec

itle: US-10-821-670A-27
erfect score: 307
equence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

coring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

earched: 253354 seqs, 63461778 residues

ord size: 1

otal number of hits satisfying chosen parameters: 506227

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Listing first 200 summaries

ommand line parameters:
MODEL=frame+_p2n.model -DEV=xlh
Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110508_27905/app_query.fasta_1
DB=Published_Applications_NA_New -QFMT=fastap
SUFFIX=oligo.p2n.200scores.rnpbn -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=200
DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=pto
NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
USER=US10821670_@CGN_1_1_62_@runat_07062006_110508_27905 -NCPU=6 -ICPU=3
NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

atabase : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.		Score	% Query Match	Length	DB	ID	Description
c	1	9	2.9	3284	7	US-11-293-697-630	Sequence 630, App
	2	8	2.6	2115	7	US-11-217-529-76502	Sequence 76502, A
	3	7	2.3	334	6	US-10-560-723-28	Sequence 28, Appl
c	4	7	2.3	595	6	US-10-953-349-6086	Sequence 6086, Ap
c	5	7	2.3	819	6	US-10-471-571A-635	Sequence 635, App
	6	7	2.3	849	6	US-10-471-571A-5423	Sequence 5423, Ap
c	7	7	2.3	939	6	US-10-953-349-32992	Sequence 32992, A
	8	7	2.3	1005	6	US-10-953-349-802	Sequence 802, App
	9	7	2.3	1035	6	US-10-953-349-8097	Sequence 8097, Ap
c	10	7	2.3	1092	7	US-11-217-529-4663	Sequence 4663, Ap
c	11	7	2.3	1158	7	US-11-217-529-77622	Sequence 77622, A
	12	7	2.3	1161	7	US-11-297-134-9	Sequence 9, Appli
c	13	7	2.3	1176	6	US-10-953-349-8850	Sequence 8850, Ap
c	14	7	2.3	1184	6	US-10-953-349-20842	Sequence 20842, A
c	15	7	2.3	1209	7	US-11-217-529-4209	Sequence 4209, Ap
	16	7	2.3	1237	6	US-10-953-349-21311	Sequence 21311, A
	17	7	2.3	1584	7	US-11-217-529-75662	Sequence 75662, A
c	18	7	2.3	1636	6	US-10-953-349-17465	Sequence 17465, A
	19	7	2.3	1651	7	US-11-145-307A-256	Sequence 256, App
c	20	7	2.3	1690	6	US-10-953-349-18501	Sequence 18501, A
	21	7	2.3	1717	6	US-10-953-349-33266	Sequence 33266, A
c	22	7	2.3	1737	7	US-11-217-529-81980	Sequence 81980, A
	23	7	2.3	2121	7	US-11-217-529-78482	Sequence 78482, A
	24	7	2.3	2148	7	US-11-217-529-2300	Sequence 2300, Ap
	25	7	2.3	2240	6	US-10-953-349-11671	Sequence 11671, A
c	26	7	2.3	2259	7	US-11-293-697-1478	Sequence 1478, Ap
	27	7	2.3	2304	7	US-11-121-154-64	Sequence 64, Appl
c	28	7	2.3	2507	6	US-10-953-349-9838	Sequence 9838, Ap
c	29	7	2.3	2508	7	US-11-293-697-1575	Sequence 1575, Ap
c	30	7	2.3	2616	6	US-10-471-571A-4673	Sequence 4673, Ap
	31	7	2.3	2787	6	US-10-471-571A-2597	Sequence 2597, Ap
c	32	7	2.3	2825	7	US-11-293-697-1497	Sequence 1497, Ap
	33	7	2.3	2857	6	US-10-196-749-105	Sequence 105, App
c	34	7	2.3	3226	7	US-11-293-697-723	Sequence 723, App
c	35	7	2.3	3624	7	US-11-217-529-3816	Sequence 3816, Ap
c	36	7	2.3	5934	7	US-11-313-450-13	Sequence 13, Appl
c	37	7	2.3	6371	7	US-11-251-465-8	Sequence 8, Appli
c	38	7	2.3	56580	6	US-10-553-298-1	Sequence 1, Appli
c	39	7	2.3	394191	6	US-10-506-549-3	Sequence 3, Appli
c	40	6	2.0	20	7	US-11-266-409-12	Sequence 12, Appl
	41	6	2.0	25	7	US-11-217-529-9246	Sequence 9246, Ap
	42	6	2.0	25	7	US-11-217-529-18480	Sequence 18480, A
c	43	6	2.0	25	7	US-11-217-529-31190	Sequence 31190, A
	44	6	2.0	25	7	US-11-217-529-36523	Sequence 36523, A
c	45	6	2.0	25	7	US-11-217-529-36968	Sequence 36968, A
c	46	6	2.0	25	7	US-11-217-529-43878	Sequence 43878, A
	47	6	2.0	25	7	US-11-217-529-48094	Sequence 48094, A
	48	6	2.0	25	7	US-11-217-529-50534	Sequence 50534, A
c	49	6	2.0	25	7	US-11-217-529-71800	Sequence 71800, A
c	50	6	2.0	25	7	US-11-217-529-82993	Sequence 82993, A
	51	6	2.0	25	7	US-11-217-529-88008	Sequence 88008, A
	52	6	2.0	25	7	US-11-217-529-106446	Sequence 106446,
c	53	6	2.0	25	7	US-11-217-529-107708	Sequence 107708,
c	54	6	2.0	25	7	US-11-217-529-112662	Sequence 112662,
c	55	6	2.0	25	7	US-11-217-529-123888	Sequence 123888,
	56	6	2.0	25	7	US-11-217-529-142444	Sequence 142444,
	57	6	2.0	25	7	US-11-217-529-144453	Sequence 144453,
c	58	6	2.0	25	7	US-11-217-529-152420	Sequence 152420,
	59	6	2.0	72	7	US-11-267-871-456	Sequence 456, App
c	60	6	2.0	72	7	US-11-267-871-456	Sequence 456, App
c	61	6	2.0	177	7	US-11-217-529-79352	Sequence 79352, A
c	62	6	2.0	198	6	US-10-471-571A-5615	Sequence 5615, Ap
	63	6	2.0	240	7	US-11-244-678-7	Sequence 7, Appli
c	64	6	2.0	243	7	US-11-217-529-147	Sequence 147, App
	65	6	2.0	243	7	US-11-217-529-80845	Sequence 80845, A
	66	6	2.0	267	7	US-11-217-529-166793	Sequence 166793,
c	67	6	2.0	279	6	US-10-512-190-1	Sequence 1, Appli
c	68	6	2.0	294	6	US-10-511-814-9	Sequence 9, Appli
c	69	6	2.0	294	6	US-10-511-814-10	Sequence 10, Appl
c	70	6	2.0	294	6	US-10-511-814-12	Sequence 12, Appl
c	71	6	2.0	294	6	US-10-511-814-13	Sequence 13, Appl
	72	6	2.0	297	7	US-11-217-529-81028	Sequence 81028, A
	73	6	2.0	306	7	US-11-217-529-190938	Sequence 190938,
	74	6	2.0	306	7	US-11-321-421-87	Sequence 87, Appl
	75	6	2.0	324	7	US-11-217-529-76199	Sequence 76199, A
c	76	6	2.0	339	7	US-11-217-529-166940	Sequence 166940,
c	77	6	2.0	348	6	US-10-488-619-499	Sequence 499, App
	78	6	2.0	348	7	US-11-217-529-77235	Sequence 77235, A
c	79	6	2.0	357	7	US-11-217-529-6132	Sequence 6132, Ap
c	80	6	2.0	369	6	US-10-499-266-11	Sequence 11, Appl
c	81	6	2.0	379	6	US-10-994-679-63	Sequence 63, Appl
c	82	6	2.0	387	7	US-11-217-529-78662	Sequence 78662, A

	83	6	2.0	387	7	US-11-217-529-80425	Sequence 80425, A
::	84	6	2.0	393	7	US-11-217-529-76946	Sequence 76946, A
::	85	6	2.0	396	7	US-11-217-529-82136	Sequence 82136, A
::	86	6	2.0	402	7	US-11-217-529-75995	Sequence 75995, A
	87	6	2.0	420	7	US-11-255-980-6	Sequence 6, Appli
	88	6	2.0	423	7	US-11-217-529-3397	Sequence 3397, Ap
	89	6	2.0	427	6	US-10-488-619-1587	Sequence 1587, Ap
	90	6	2.0	436	6	US-10-488-619-552	Sequence 552, App
:	91	6	2.0	438	6	US-10-488-619-1590	Sequence 1590, Ap
	92	6	2.0	441	6	US-10-468-193-6	Sequence 6, Appli
:	93	6	2.0	444	7	US-11-217-529-82599	Sequence 82599, A
:	94	6	2.0	447	7	US-11-217-529-166970	Sequence 166970,
:	95	6	2.0	450	6	US-10-471-571A-3305	Sequence 3305, Ap
:	96	6	2.0	461	7	US-11-301-554-965	Sequence 965, App
:	97	6	2.0	462	6	US-10-473-173-248	Sequence 248, App
	98	6	2.0	471	6	US-10-488-619-417	Sequence 417, App
:	99	6	2.0	471	7	US-11-217-529-5788	Sequence 5788, Ap
	100	6	2.0	474	7	US-11-217-529-3216	Sequence 3216, Ap
	101	6	2.0	478	6	US-10-505-928-542	Sequence 542, App
	102	6	2.0	483	7	US-11-219-563-141	Sequence 141, App
	103	6	2.0	483	7	US-11-301-554-1239	Sequence 1239, Ap
::	104	6	2.0	492	7	US-11-301-554-928	Sequence 928, App
	105	6	2.0	498	6	US-10-488-619-564	Sequence 564, App
	106	6	2.0	498	7	US-11-217-529-5867	Sequence 5867, Ap
	107	6	2.0	499	6	US-10-953-349-15009	Sequence 15009, A
::	108	6	2.0	500	7	US-11-249-305-1	Sequence 1, Appli
	109	6	2.0	500	7	US-11-249-305-2	Sequence 2, Appli
::	110	6	2.0	500	7	US-11-249-305-3	Sequence 3, Appli
	111	6	2.0	500	7	US-11-249-305-4	Sequence 4, Appli
	112	6	2.0	501	7	US-11-136-524-79	Sequence 79, Appl
::	113	6	2.0	509	6	US-10-953-349-217	Sequence 217, App
::	114	6	2.0	510	7	US-11-217-529-2274	Sequence 2274, Ap
::	115	6	2.0	510	7	US-11-217-529-78451	Sequence 78451, A
::	116	6	2.0	513	7	US-11-217-529-79024	Sequence 79024, A
	117	6	2.0	518	7	US-11-301-554-371	Sequence 371, App
	118	6	2.0	518	7	US-11-301-554-1203	Sequence 1203, Ap
:	119	6	2.0	526	7	US-11-301-554-1218	Sequence 1218, Ap
:	120	6	2.0	537	6	US-10-471-571A-2883	Sequence 2883, Ap
::	121	6	2.0	541	6	US-10-560-723-113	Sequence 113, App
	122	6	2.0	543	7	US-11-301-554-956	Sequence 956, App
	123	6	2.0	543	7	US-11-217-529-5827	Sequence 5827, Ap
	124	6	2.0	549	7	US-11-301-554-359	Sequence 359, App
:	125	6	2.0	555	6	US-10-471-571A-4635	Sequence 4635, Ap
	126	6	2.0	557	7	US-11-301-554-848	Sequence 848, App
:	127	6	2.0	562	6	US-10-488-619-1255	Sequence 1255, Ap
:	128	6	2.0	564	6	US-10-488-619-1992	Sequence 1992, Ap
:	129	6	2.0	574	6	US-10-488-619-1021	Sequence 1021, Ap
	130	6	2.0	581	7	US-11-301-951-7	Sequence 7, Appli
	131	6	2.0	584	6	US-10-953-349-1733	Sequence 1733, Ap
	132	6	2.0	591	6	US-10-488-619-1230	Sequence 1230, Ap
	133	6	2.0	596	6	US-10-488-619-2778	Sequence 2778, Ap
	134	6	2.0	597	6	US-10-488-619-1332	Sequence 1332, Ap
:	135	6	2.0	597	6	US-10-488-619-2832	Sequence 2832, Ap
	136	6	2.0	597	6	US-10-471-571A-2843	Sequence 2843, Ap
	137	6	2.0	597	7	US-11-217-529-77932	Sequence 77932, A
	138	6	2.0	602	6	US-10-488-619-1740	Sequence 1740, Ap
::	139	6	2.0	607	6	US-10-488-619-1738	Sequence 1738, Ap
	140	6	2.0	615	7	US-11-217-529-2766	Sequence 2766, Ap
	141	6	2.0	618	6	US-10-953-349-5623	Sequence 5623, Ap
	142	6	2.0	621	7	US-11-217-529-76434	Sequence 76434, A
	143	6	2.0	625	6	US-10-953-349-2892	Sequence 2892, Ap
::	144	6	2.0	627	6	US-10-471-571A-3259	Sequence 3259, Ap
	145	6	2.0	633	6	US-10-953-349-8180	Sequence 8180, Ap
	146	6	2.0	633	6	US-10-953-349-28624	Sequence 28624, A
	147	6	2.0	634	7	US-11-301-554-23	Sequence 23, Appl
	148	6	2.0	635	6	US-10-488-619-2164	Sequence 2164, Ap
::	149	6	2.0	636	6	US-10-953-349-6142	Sequence 6142, Ap
::	150	6	2.0	640	6	US-10-953-349-31246	Sequence 31246, A
::	151	6	2.0	641	6	US-10-488-619-1891	Sequence 1891, Ap
	152	6	2.0	642	7	US-11-217-529-2277	Sequence 2277, Ap
	153	6	2.0	657	7	US-11-217-529-173805	Sequence 173805,
	154	6	2.0	660	7	US-11-217-529-80548	Sequence 80548, A
::	155	6	2.0	663	6	US-10-953-349-3111	Sequence 3111, Ap
c	156	6	2.0	668	6	US-10-953-349-39726	Sequence 39726, A
	157	6	2.0	669	6	US-10-488-619-1764	Sequence 1764, Ap
	158	6	2.0	669	7	US-11-257-062-37	Sequence 37, Appl
c	159	6	2.0	674	6	US-10-953-349-15213	Sequence 15213, A
	160	6	2.0	678	7	US-11-217-529-1478	Sequence 1478, Ap
	161	6	2.0	678	7	US-11-217-529-75809	Sequence 75809, A
c	162	6	2.0	679	6	US-10-509-131-2	Sequence 2, Appli
c	163	6	2.0	681	6	US-10-953-349-14260	Sequence 14260, A
c	164	6	2.0	686	6	US-10-953-349-14808	Sequence 14808, A
	165	6	2.0	693	6	US-10-953-349-28950	Sequence 28950, A
	166	6	2.0	696	7	US-11-217-529-1815	Sequence 1815, Ap
	167	6	2.0	701	6	US-10-953-349-30459	Sequence 30459, A
c	168	6	2.0	701	6	US-10-953-349-36866	Sequence 36866, A
	169	6	2.0	708	6	US-10-196-749-211	Sequence 211, App
	170	6	2.0	710	6	US-10-953-349-2939	Sequence 2939, Ap
c	171	6	2.0	714	6	US-10-471-571A-2469	Sequence 2469, Ap
c	172	6	2.0	716	6	US-10-953-349-27854	Sequence 27854, A
c	173	6	2.0	729	7	US-11-217-529-5921	Sequence 5921, Ap
	174	6	2.0	733	1	US-09-949-925-1	Sequence 1, Appli
	175	6	2.0	733	6	US-10-994-679-10	Sequence 10, Appl
	176	6	2.0	733	7	US-11-246-999-1	Sequence 1, Appli
	177	6	2.0	733	7	US-11-313-356-29	Sequence 29, Appl
c	178	6	2.0	735	7	US-11-217-529-778	Sequence 778, App
c	179	6	2.0	735	7	US-11-217-529-81004	Sequence 81004, A
c	180	6	2.0	742	6	US-10-953-349-35385	Sequence 35385, A
c	181	6	2.0	744	7	US-11-217-529-190943	Sequence 190943,
	182	6	2.0	747	7	US-11-217-529-4546	Sequence 4546, Ap
c	183	6	2.0	752	6	US-10-953-349-26573	Sequence 26573, A
	184	6	2.0	756	7	US-11-217-529-4019	Sequence 4019, Ap
	185	6	2.0	756	7	US-11-217-529-81839	Sequence 81839, A
	186	6	2.0	757	6	US-10-505-928-558	Sequence 558, App
c	187	6	2.0	759	7	US-11-217-529-937	Sequence 937, App
c	188	6	2.0	770	6	US-10-953-349-29904	Sequence 29904, A
	189	6	2.0	777	7	US-11-257-851A-59	Sequence 59, Appl
c	190	6	2.0	778	6	US-10-953-349-27093	Sequence 27093, A
c	191	6	2.0	780	6	US-10-488-619-1454	Sequence 1454, Ap
	192	6	2.0	781	6	US-10-953-349-691	Sequence 691, App
c	193	6	2.0	783	6	US-10-471-571A-2759	Sequence 2759, Ap
c	194	6	2.0	786	7	US-11-217-529-2419	Sequence 2419, Ap
c	195	6	2.0	786	7	US-11-217-529-78645	Sequence 78645, A
c	196	6	2.0	795	7	US-11-217-529-77108	Sequence 77108, A
	197	6	2.0	803	6	US-10-953-349-25047	Sequence 25047, A
c	198	6	2.0	807	6	US-10-488-619-2354	Sequence 2354, Ap
	199	6	2.0	809	6	US-10-953-349-36747	Sequence 36747, A
	200	6	2.0	810	6	US-10-488-619-870	Sequence 870, App

ALIGNMENTS

```
RESULT 1
US-11-293-697-630/c
; Sequence 630, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 630
;   LENGTH: 3284
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-630

Alignment Scores:
Pred. No.:              8.28          Length:          3284
Score:                  9.00          Matches:         9
Percent Similarity:     100.0%        Conservative:    0
```

```
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.9%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-27 (1-307) x US-11-293-697-630 (1-3284)

Qy         79 PheLeuLeuIleHisLysLysGluAsp 87
              |||||||||||||||||||||||||||||
Db       1053 TTTTTACTGATTCACAAAAAGGAAGAC 1027

RESULT 2
US-11-217-529-76502
  Sequence 76502, Application US/11217529
  Publication No. US20060099612A1
  GENERAL INFORMATION:
   APPLICANT: SUNTORY LIMITED
   APPLICANT:  NAKAO, YOSHIHIRO
   APPLICANT:  NAKAMURA, NORIHISA
   APPLICANT:  KODAMA, YUKIKO
   APPLICANT:  FUJIMURA, TOMOKO
   APPLICANT:  ASHIKARI, TOSHIHIKO
   TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
   FILE REFERENCE: S-38-285
   CURRENT APPLICATION NUMBER: US/11/217,529
   CURRENT FILING DATE:  2005-09-02
   PRIOR APPLICATION NUMBER: US 10/932,182
   PRIOR FILING DATE: 2004-09-02
   NUMBER OF SEQ ID NOS: 197023
   SOFTWARE: PatentIn version 3.3
  SEQ ID NO 76502
    LENGTH: 2115
    TYPE: DNA
    ORGANISM: Saccharomyces pastorianus
US-11-217-529-76502

Alignment Scores:
Pred. No.:              55.8            Length:         2115
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.6%            Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-27 (1-307) x US-11-217-529-76502 (1-2115)

Qy         219 AsnLeuGlnLeuLysProLeuLys 226
               |||||||||||||||||||||||||
Db         136 AATTTGCAACTTAAACCACTGAAA 159

RESULT 3
US-10-560-723-28
  Sequence 28, Application US/10560723
  Publication No. US20060115821A1
  GENERAL INFORMATION:
   APPLICANT: EXONHIT THERAPEUTICALS
   TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
   TITLE OF INVENTION:  CANCER THERAPY AND DIAGNOSIS
   FILE REFERENCE: B0213WO
   CURRENT APPLICATION NUMBER: US/10/560,723
   CURRENT FILING DATE:  2005-12-15
   NUMBER OF SEQ ID NOS: 185
   SOFTWARE: PatentIn version 3.1
  SEQ ID NO 28
    LENGTH: 334
    TYPE: DNA
    ORGANISM: Homo sapiens
US-10-560-723-28

Alignment Scores:
Pred. No.:              102             Length:         334
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.3%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-560-723-28 (1-334)

Qy         122 TrpLeuThrAlaIleSerThr 128
               |||||||||||||||||||||
Db          27 TGGCTCACTGCAATCTCCACC 47

RESULT 4
US-10-953-349-6086/c
; Sequence 6086, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6086
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-6086

Alignment Scores:
Pred. No.:              175             Length:         595
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.3%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-953-349-6086 (1-595)

Qy         132 PheThrValLysSerSerArg 138
               |||||||||||||||||||||
Db         354 TTTACTGTGAAGTCTAGTCGT 334

RESULT 5
US-10-471-571A-635/c
; Sequence 635, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 635
;   LENGTH: 819
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-635

Alignment Scores:
Pred. No.:              235             Length:         819
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.3%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-471-571A-635 (1-819)

Qy         135 LysSerSerArgGlySerSer 141
```

```
                    ||||||||||||||||||||
Db        359 AAATCTTCCCGTGGGTCATCA 339

ESULT 6
S-10-471-571A-5423
 Sequence 5423, Application US/10471571A
 Publication No. US20060115490A1
 GENERAL INFORMATION:
  APPLICANT: CHIRON SpA
  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
  FILE REFERENCE: P026927WO
  CURRENT APPLICATION NUMBER: US/10/471,571A
  CURRENT FILING DATE:  2003-09-12
  PRIOR APPLICATION NUMBER: GB-0107661.1
  PRIOR FILING DATE: 2001-03-27
  NUMBER OF SEQ ID NOS: 5642
  SOFTWARE: SeqWin99, version 1.03
 SEQ ID NO 5423
   LENGTH: 849
   TYPE: DNA
   ORGANISM: Staphylococcus aureus
S-10-471-571A-5423

lignment Scores:
ed. No.:              243           Length:        849
core:                 7.00          Matches:       7
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            2.3%          Indels:        0
B:                    6             Gaps:          0

S-10-821-670A-27 (1-307) x US-10-471-571A-5423 (1-849)

y          99 LysGluSerLysAsnLysIle 105
              ||||||||||||||||||||
Db        223 AAAGAATCTAAAAATAAGATT 243

ESULT 7
S-10-953-349-32992/c
 Sequence 32992, Application US/10953349
 Publication No. US20060107345A1
 GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION:  ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE:  2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 32992
   LENGTH: 939
   TYPE: DNA
   ORGANISM: Zea mays subsp. mays
S-10-953-349-32992

ignment Scores:
ed. No.:              267           Length:        939
ore:                  7.00          Matches:       7
rcent Similarity:     100.0%        Conservative:  0
st Local Similarity:  100.0%        Mismatches:    0
ery Match:            2.3%          Indels:        0
B:                    6             Gaps:          0

S-10-821-670A-27 (1-307) x US-10-953-349-32992 (1-939)

y         180 AlaAlaGluGluSerLeuPro 186
              ||||||||||||||||||||
Db        141 GCGGCTGAAGAGAGCCTGCCT 121

ESULT 8
S-10-953-349-802
 Sequence 802, Application US/10953349
 Publication No. US20060107345A1
 GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION:  ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE:  2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 802
   LENGTH: 1005
   TYPE: DNA
   ORGANISM: Arabidopsis thaliana
US-10-953-349-802

Alignment Scores:
Pred. No.:            284           Length:        1005
Score:                7.00          Matches:       7
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          2.3%          Indels:        0
DB:                   6             Gaps:          0

US-10-821-670A-27 (1-307) x US-10-953-349-802 (1-1005)

Qy         74 ValLeuSerHisSerPheLeu 80
              |||||||||||||||||||||
Db        920 GTGTTATCACACTCTTTTCTT 940

RESULT 9
US-10-953-349-8097
; Sequence 8097, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8097
;   LENGTH: 1035
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-8097

Alignment Scores:
Pred. No.:            292           Length:        1035
Score:                7.00          Matches:       7
Percent Similarity:   100.0%        Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:          2.3%          Indels:        0
DB:                   6             Gaps:          0

US-10-821-670A-27 (1-307) x US-10-953-349-8097 (1-1035)

Qy         44 SerGluValLeuGlySerGly 50
              ||||||||||||||||||||
Db        142 TCTGAAGTCCTTGGAAGCGGC 162

RESULT 10
US-11-217-529-4663/c
; Sequence 4663, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
```

APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4663
LENGTH: 1092
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-4663

Alignment Scores:

Pred. No.:	307	Length:	1092
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.3%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-4663 (1-1092)

Qy 295 SerSerSerTrpSerAsnTrp 301
||||||||||||||||||||
Db 323 TCCTCCTCTTGGTCAAACTGG 303

RESULT 11
US-11-217-529-77622/c
Sequence 77622, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 77622
LENGTH: 1158
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-77622

Alignment Scores:

Pred. No.:	324	Length:	1158
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.3%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-77622 (1-1158)

Qy 295 SerSerSerTrpSerAsnTrp 301
||||||||||||||||||||
Db 398 TCCTCTTCTTGGTCGAATTGG 378

RESULT 12
US-11-297-134-9
Sequence 9, Application US/11297134
Publication No. US20060111297A1
GENERAL INFORMATION:
APPLICANT: Genzyme Corporation
APPLICANT: Roberts, Bruce
TITLE OF INVENTION: BLOOD FACTOR DOMAINS
FILE REFERENCE: 5270C
CURRENT APPLICATION NUMBER: US/11/297,134
CURRENT FILING DATE: 2005-12-08
PRIOR APPLICATION NUMBER: PCT/US2005/018461
PRIOR FILING DATE: 2004-06-09
PRIOR APPLICATION NUMBER: US 60/477,291
PRIOR FILING DATE: 2003-06-09
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
US-11-297-134-9

Alignment Scores:

Pred. No.:	325	Length:	1161
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.3%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-297-134-9 (1-1161)

Qy 211 IleIleLysProAspProPro 217
||||||||||||||||||||
Db 389 ATCATCAAGCCCGACCCTCCA 409

RESULT 13
US-10-953-349-8850/c
Sequence 8850, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8850
LENGTH: 1176
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-953-349-8850

Alignment Scores:

Pred. No.:	329	Length:	1176
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-953-349-8850 (1-1176)

Qy 261 AsnArgGluLysLysAspArg 267
||||||||||||||||||||
Db 801 AATCGAGAAAAGAAAGATCGA 781

RESULT 14
US-10-953-349-20842/c
Sequence 20842, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY

```
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE:  2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 20842
   LENGTH: 1184
   TYPE: DNA
   ORGANISM: Glycine max
S-10-953-349-20842

Alignment Scores:
Pred. No.:              331          Length:        1184
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.3%         Indels:        0
DB:                     6            Gaps:          0

US-10-821-670A-27 (1-307) x US-10-953-349-20842 (1-1184)

Qy        262 ArgGluLysLysAspArgLeu 268
              |||||||||||||||||||
Db        585 AGAGAGAAAAAGGATAGGTTG 565

RESULT 15
S-11-217-529-4209/c
 Sequence 4209, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 4209
   LENGTH: 1209
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-4209

Alignment Scores:
Pred. No.:              337          Length:        1209
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.3%         Indels:        0
DB:                     7            Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-4209 (1-1209)

Qy        262 ArgGluLysLysAspArgLeu 268
              |||||||||||||||||||
Db        822 AGAGAAAAAAAAGACCGCCTT 802

RESULT 16
S-10-953-349-21311
 Sequence 21311, Application US/10953349
 Publication No. US20060107345A1
 GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION:  ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE:  2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 21311
   LENGTH: 1237
   TYPE: DNA
   ORGANISM: Glycine max
US-10-953-349-21311

Alignment Scores:
Pred. No.:              344          Length:        1237
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.3%         Indels:        0
DB:                     6            Gaps:          0

US-10-821-670A-27 (1-307) x US-10-953-349-21311 (1-1237)

Qy         75 LeuSerHisSerPheLeuLeu 81
              |||||||||||||||||||
Db         52 CTTTCTCATTCATTCTTATTA 72

RESULT 17
US-11-217-529-75662
 Sequence 75662, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 75662
   LENGTH: 1584
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
US-11-217-529-75662

Alignment Scores:
Pred. No.:              433          Length:        1584
Score:                  7.00         Matches:       7
Percent Similarity:     100.0%       Conservative:  0
Best Local Similarity:  100.0%       Mismatches:    0
Query Match:            2.3%         Indels:        0
DB:                     7            Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-75662 (1-1584)

Qy        191 ValAspAlaIleHisLysLeu 197
              |||||||||||||||||||
Db       1140 GTGGACGCAATTCATAAGCTA 1160

RESULT 18
US-10-953-349-17465/c
 Sequence 17465, Application US/10953349
 Publication No. US20060107345A1
 GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION:  ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
```

CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17465
LENGTH: 1636
TYPE: DNA
ORGANISM: Glycine max
S-10-953-349-17465

lignment Scores:

ed. No.:	446	Length:	1636
core:	7.00	Matches:	7
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.3%	Indels:	0
B:	6	Gaps:	0

S-10-821-670A-27 (1-307) x US-10-953-349-17465 (1-1636)

```
Qy        204 SerSerPhePheIleArgAsp 210
              |||||||||||||||||||||
Db       1352 TCATCTTTCTTCATAAGAGAT 1332
```

ESULT 19
S-11-145-307A-256
Sequence 256, Application US/11145307A
Publication No. US20060094035A1
GENERAL INFORMATION:
APPLICANT: Arcturus Bioscience, Inc.
APPLICANT: Erlander, Mark G.
APPLICANT: Ma, Xiao-Jun
TITLE OF INVENTION: Identification of Tumors
FILE REFERENCE: 022041-002020US
CURRENT APPLICATION NUMBER: US/11/145,307A
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 60/577,084
PRIOR FILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn version 3.1
SEQ ID NO 256
LENGTH: 1651
TYPE: DNA
ORGANISM: Homo sapiens
S-11-145-307A-256

lignment Scores:

ed. No.:	450	Length:	1651
core:	7.00	Matches:	7
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.3%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-27 (1-307) x US-11-145-307A-256 (1-1651)

```
Qy        196 LysLeuLysTyrGluAsnTyr 202
              |||||||||||||||||||||
Db       1616 AAGTTGAAATATGAAAATTAT 1636
```

ESULT 20
S-10-953-349-18501/c
Sequence 18501, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18501
; LENGTH: 1690
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-18501

Alignment Scores:

Pred. No.:	460	Length:	1690
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-953-349-18501 (1-1690)

```
Qy        216 ProProLysAsnLeuGlnLeu 222
              |||||||||||||||||||||
Db       1257 CCACCTAAAAATCTACAGTTG 1237
```

RESULT 21
US-10-953-349-33266
; Sequence 33266, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33266
; LENGTH: 1717
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33266

Alignment Scores:

Pred. No.:	467	Length:	1717
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.3%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-953-349-33266 (1-1717)

```
Qy        211 IleIleLysProAspProPro 217
              |||||||||||||||||||||
Db        205 ATCATCAAGCCCGACCCTCCC 225
```

RESULT 22
US-11-217-529-81980/c
; Sequence 81980, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81980
; LENGTH: 1737

```
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
   FEATURE:
   NAME/KEY: modified_base
   LOCATION: (1678)..(1715)
   OTHER INFORMATION: a, c, g, t, unknown, or other
S-11-217-529-81980

lignment Scores:
red. No.:              472          Length:        1737
core:                  7.00         Matches:       7
ercent Similarity:     100.0%       Conservative:  0
est Local Similarity:  100.0%       Mismatches:    0
uery Match:            2.3%         Indels:        0
B:                     7            Gaps:          0

S-10-821-670A-27 (1-307) x US-11-217-529-81980 (1-1737)

y         44 SerGluValLeuGlySerGly 50
             ||||||||||||||||||||
c         30 AGCGAAGTGTTGGGTAGCGGT 10

ESULT 23
S-11-217-529-78482
 Sequence 78482, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 78482
   LENGTH: 2121
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-78482

lignment Scores:
red. No.:              568          Length:        2121
core:                  7.00         Matches:       7
ercent Similarity:     100.0%       Conservative:  0
est Local Similarity:  100.0%       Mismatches:    0
uery Match:            2.3%         Indels:        0
B:                     7            Gaps:          0

S-10-821-670A-27 (1-307) x US-11-217-529-78482 (1-2121)

y         48 GlySerGlyLysThrLeuThr 54
             ||||||||||||||||||||
b         85 GGCTCAGGAAAAACGCTAACG 105

ESULT 24
S-11-217-529-2300
 Sequence 2300, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 2300
   LENGTH: 2148
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
US-11-217-529-2300

Alignment Scores:
Pred. No.:             574          Length:        2148
Score:                 7.00         Matches:       7
Percent Similarity:    100.0%       Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:           2.3%         Indels:        0
DB:                    7            Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-2300 (1-2148)

Qy         48 GlySerGlyLysThrLeuThr 54
              ||||||||||||||||||||
Db         85 GGTTCAGGAAAAACGTTGACG 105

RESULT 25
US-10-953-349-11671
; Sequence 11671, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11671
;   LENGTH: 2240
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-11671

Alignment Scores:
Pred. No.:             597          Length:        2240
Score:                 7.00         Matches:       7
Percent Similarity:    100.0%       Conservative:  0
Best Local Similarity: 100.0%       Mismatches:    0
Query Match:           2.3%         Indels:        0
DB:                    6            Gaps:          0

US-10-821-670A-27 (1-307) x US-10-953-349-11671 (1-2240)

Qy         82 IleHisLysLysGluAspGly 88
              ||||||||||||||||||||
Db       1054 ATTCATAAGAAAGAAGATGGG 1074

RESULT 26
US-11-293-697-1478/c
; Sequence 1478, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
```

```
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1478
   LENGTH: 2259
   TYPE: DNA
   ORGANISM: Homo sapiens
US-11-293-697-1478

Alignment Scores:
Pred. No.:                602           Length:        2259
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.3%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-293-697-1478 (1-2259)

Qy          78 SerPheLeuLeuIleHisLys 84
               ||||||||||||||||||||
Db        1074 AGTTTCCTTTTAATCCATAAG 1054

RESULT 27
US-11-121-154-64
 Sequence 64, Application US/11121154
 Publication No. US20060105914A1
 GENERAL INFORMATION:
  APPLICANT: TAYLOR, LARRY EDMUND
  APPLICANT:  WEINER, RONALD M.
  APPLICANT:  HUTCHESON, STEVEN WAYNE
  APPLICANT:  EKBORG, NATHAN A.
  APPLICANT:  HOWARD, MICHAEL
  TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
  FILE REFERENCE: 108172-00121
  CURRENT APPLICATION NUMBER: US/11/121,154
  CURRENT FILING DATE:  2005-05-04
  PRIOR APPLICATION NUMBER: 60/567,971
  PRIOR FILING DATE: 2004-05-04
  NUMBER OF SEQ ID NOS: 214
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 64
   LENGTH: 2304
   TYPE: DNA
   ORGANISM: Microbulbifer degradans
US-11-121-154-64

Alignment Scores:
Pred. No.:                613           Length:        2304
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.3%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-121-154-64 (1-2304)

Qy         294 TyrSerSerSerTrpSerAsn 300
               ||||||||||||||||||||
Db         202 TACAGTTCATCGTGGAGCAAT 222

RESULT 28
US-10-953-349-9838/c
 Sequence 9838, Application US/10953349
 Publication No. US20060107345A1
 GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION:  ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE:  2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 9838
;   LENGTH: 2507
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9838

Alignment Scores:
Pred. No.:                663           Length:        2507
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.3%          Indels:        0
DB:                       6             Gaps:          0

US-10-821-670A-27 (1-307) x US-10-953-349-9838 (1-2507)

Qy          75 LeuSerHisSerPheLeuLeu 81
               |||||||||||||||||||||
Db        261 CTTAGCCACAGCTTCCTTCTG 241

RESULT 29
US-11-293-697-1575/c
; Sequence 1575, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1575
;   LENGTH: 2508
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1575

Alignment Scores:
Pred. No.:                663           Length:        2508
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.3%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-293-697-1575 (1-2508)

Qy         203 ThrSerSerPhePheIleArg 209
               |||||||||||||||||||||
Db        1322 ACCTCGTCATTTTTCATCAGA 1302

RESULT 30
US-10-471-571A-4673/c
; Sequence 4673, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4673
;   LENGTH: 2616
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-4673
```

```
lignment Scores:
red. No.:                689              Length:          2616
core:                    7.00             Matches:         7
ercent Similarity:       100.0%           Conservative:    0
est Local Similarity:    100.0%           Mismatches:      0
uery Match:              2.3%             Indels:          0
B:                       6                Gaps:            0

S-10-821-670A-27 (1-307) x US-10-471-571A-4673 (1-2616)

y         135 LysSerSerArgGlySerSer 141
              ||||||||||||||||||||
c        1160 AAATCATCAAGGGGTTCTAGT 1140

ESULT 31
S-10-471-571A-2597
 Sequence 2597, Application US/10471571A
 Publication No. US20060115490A1
 GENERAL INFORMATION:
  APPLICANT: CHIRON SpA
  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
  FILE REFERENCE: P026927WO
  CURRENT APPLICATION NUMBER: US/10/471,571A
  CURRENT FILING DATE:  2003-09-12
  PRIOR APPLICATION NUMBER: GB-0107661.1
  PRIOR FILING DATE: 2001-03-27
  NUMBER OF SEQ ID NOS: 5642
  SOFTWARE: SeqWin99, version 1.03
 SEQ ID NO 2597
   LENGTH: 2787
   TYPE: DNA
   ORGANISM: Staphylococcus aureus
S-10-471-571A-2597

lignment Scores:
red. No.:                731              Length:          2787
core:                    7.00             Matches:         7
ercent Similarity:       100.0%           Conservative:    0
est Local Similarity:    100.0%           Mismatches:      0
uery Match:              2.3%             Indels:          0
B:                       6                Gaps:            0

S-10-821-670A-27 (1-307) x US-10-471-571A-2597 (1-2787)

y          48 GlySerGlyLysThrLeuThr 54
              ||||||||||||||||||||
c         808 GGAAGTGGTAAGACGTTGACT 828

ESULT 32
S-11-293-697-1497/c
 Sequence 1497, Application US/11293697
 Publication No. US20060105376A1
 GENERAL INFORMATION:
  APPLICANT: HELIX RESEARCH INSTITUTE
  TITLE OF INVENTION: Novel full length cDNA
  FILE REFERENCE: H1-A0106
  CURRENT APPLICATION NUMBER: US/11/293,697
  CURRENT FILING DATE:  2005-12-05
  PRIOR APPLICATION NUMBER: US/10/108,260
  PRIOR FILING DATE: 2002-03-28
  NUMBER OF SEQ ID NOS: 5458
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1497
   LENGTH: 2825
   TYPE: DNA
   ORGANISM: Homo sapiens
S-11-293-697-1497

lignment Scores:
red. No.:                740              Length:          2825
core:                    7.00             Matches:         7
ercent Similarity:       100.0%           Conservative:    0
est Local Similarity:    100.0%           Mismatches:      0
Query Match:             2.3%             Indels:          0
DB:                      7                Gaps:            0

US-10-821-670A-27 (1-307) x US-11-293-697-1497 (1-2825)

Qy        133 ThrValLysSerSerArgGly 139
              |||||||||||||||||||||
Db       1956 ACAGTGAAAAGCTCCCGTGGC 1936

RESULT 33
US-10-196-749-105
; Sequence 105, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C340
;  CURRENT APPLICATION NUMBER: US/10/196,749
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 105
;   LENGTH: 2857
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-196-749-105

Alignment Scores:
Pred. No.:               748              Length:          2857
Score:                   7.00             Matches:         7
Percent Similarity:      100.0%           Conservative:    0
Best Local Similarity:   100.0%           Mismatches:      0
Query Match:             2.3%             Indels:          0
DB:                      6                Gaps:            0

US-10-821-670A-27 (1-307) x US-10-196-749-105 (1-2857)

Qy         51 LysThrLeuThrIleGlnVal 57
              |||||||||||||||||||||
Db       1571 AAGACACTAACAATTCAAGTT 1591

RESULT 34
```

```
US-11-293-697-723/c
  Sequence 723, Application US/11293697
  Publication No. US20060105376A1
  GENERAL INFORMATION:
   APPLICANT: HELIX RESEARCH INSTITUTE
   TITLE OF INVENTION: Novel full length cDNA
   FILE REFERENCE: H1-A0106
   CURRENT APPLICATION NUMBER: US/11/293,697
   CURRENT FILING DATE:  2005-12-05
   PRIOR APPLICATION NUMBER: US/10/108,260
   PRIOR FILING DATE: 2002-03-28
   NUMBER OF SEQ ID NOS: 5458
   SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 723
    LENGTH: 3226
    TYPE: DNA
    ORGANISM: Homo sapiens
US-11-293-697-723

Alignment Scores:
Pred. No.:                837           Length:        3226
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.3%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-293-697-723 (1-3226)

Qy          80 LeuLeuIleHisLysLysGlu 86
               |||||||||||||||||||
Db        2295 CTACTTATCCATAAAAAGGAA 2275

RESULT 35
US-11-217-529-3816/c
  Sequence 3816, Application US/11217529
  Publication No. US20060099612A1
  GENERAL INFORMATION:
   APPLICANT: SUNTORY LIMITED
   APPLICANT:  NAKAO, YOSHIHIRO
   APPLICANT:  NAKAMURA, NORIHISA
   APPLICANT:  KODAMA, YUKIKO
   APPLICANT:  FUJIMURA, TOMOKO
   APPLICANT:  ASHIKARI, TOSHIHIKO
   TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
   FILE REFERENCE: S-38-285
   CURRENT APPLICATION NUMBER: US/11/217,529
   CURRENT FILING DATE:  2005-09-02
   PRIOR APPLICATION NUMBER: US 10/932,182
   PRIOR FILING DATE: 2004-09-02
   NUMBER OF SEQ ID NOS: 197023
   SOFTWARE: PatentIn version 3.3
  SEQ ID NO 3816
    LENGTH: 3624
    TYPE: DNA
    ORGANISM: Saccharomyces pastorianus
US-11-217-529-3816

Alignment Scores:
Pred. No.:                932           Length:        3624
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.3%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-3816 (1-3624)

Qy         262 ArgGluLysLysAspArgLeu 268
               |||||||||||||||||||
Db        2190 AGAGAAAAGAAAGACCGTCTT 2170

RESULT 36
```

```
US-11-313-450-13/c
; Sequence 13, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 5934
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-13

Alignment Scores:
Pred. No.:                1.47e+03      Length:        5934
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.3%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-313-450-13 (1-5934)

Qy          42 GlnSerSerGluValLeuGly 48
               ||||||||||||||||||||
Db          37 CAAAGCTCTGAGGTCCTGGGG 17

RESULT 37
US-11-251-465-8/c
; Sequence 8, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
;  APPLICANT: Brys, Reginald
;  APPLICANT:  Vandeghinste, Nick
;  APPLICANT:  Tomme, Peter
;  APPLICANT:  Klaassen, Hubertus
;  TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
;  TITLE OF INVENTION:  Same, Useful In The Treatment Of Joint Degenerative And
;  TITLE OF INVENTION:  Inflammatory Diseases
;  FILE REFERENCE: P30,172-A USA
;  CURRENT APPLICATION NUMBER: US/11/251,465
;  CURRENT FILING DATE:  2005-10-14
;  PRIOR APPLICATION NUMBER: 60/619,384
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 880
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
;   LENGTH: 6371
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-251-465-8

Alignment Scores:
Pred. No.:                1.57e+03      Length:        6371
Score:                    7.00          Matches:       7
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.3%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-251-465-8 (1-6371)

Qy          42 GlnSerSerGluValLeuGly 48
```

```
                    ||||||||||||||||||||
c          85 CAAAGCTCTGAGGTCCTGGGG 65

ESULT 38
S-10-553-298-1/c
 Sequence 1, Application US/10553298
 Publication No. US20060110385A1
 GENERAL INFORMATION:
  APPLICANT: NeuroNova AG
  TITLE OF INVENTION: A Method for Diagnosing and Treating Affective Disorders
  FILE REFERENCE: XXX
  CURRENT APPLICATION NUMBER: US/10/553,298
  CURRENT FILING DATE:  2005-10-14
  NUMBER OF SEQ ID NOS: 111
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
    LENGTH: 56580
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: exon1
    LOCATION: (3000)..(3124)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon2
    LOCATION: (24841)..(25009)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon3
    LOCATION: (26134)..(26202)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon4
    LOCATION: (30958)..(31030)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon5
    LOCATION: (32481)..(32577)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon6
    LOCATION: (35416)..(35496)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon7
    LOCATION: (36113)..(36242)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon8
    LOCATION: (37541)..(37677)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon9
    LOCATION: (45470)..(45560)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon10
    LOCATION: (47229)..(47295)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon11
    LOCATION: (47380)..(47529)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon12
    LOCATION: (50438)..(50539)
    OTHER INFORMATION:
    FEATURE:
    NAME/KEY: exon13
    LOCATION: (54392)..(54889)
    OTHER INFORMATION:
S-10-553-298-1
```

```
Alignment Scores:
Pred. No.:              1.18e+04        Length:         56580
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.3%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-553-298-1 (1-56580)

Qy          43 SerSerGluValLeuGlySer 49
               |||||||||||||||||||||
Db       21521 TCATCTGAGGTCCTGGGTTCG 21501

RESULT 39
US-10-506-549-3/c
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
;  APPLICANT: APPLERA CORPORATION
;  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL001361-US
;  CURRENT APPLICATION NUMBER: US/10/506,549
;  CURRENT FILING DATE:  2004-09-03
;  PRIOR APPLICATION NUMBER: 60/361,343
;  PRIOR FILING DATE: 2002-03-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 394191
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(394191)
;   OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Alignment Scores:
Pred. No.:              6.7e+04         Length:         394191
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            2.3%            Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-506-549-3 (1-394191)

Qy         122 TrpLeuThrAlaIleSerThr 128
               ||||||||||||||||||||
Db      331384 TGGCTCACTGCAATCTCCACC 331364

RESULT 40
US-11-266-409-12/c
; Sequence 12, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
;  APPLICANT: SUZUMURA, AKIO
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
;  FILE REFERENCE: 279847US40
;  CURRENT APPLICATION NUMBER: US/11/266,409
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: US 60/624,851
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

OTHER INFORMATION: Synthetic DNA
US-11-266-409-12

Alignment Scores:

Pred. No.:	76.4	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-266-409-12 (1-20)

```
Qy        244 ProHisSerTyrPheSer 249
              |||||||||||||||||
Db         20 CCCCATTCCTACTTCTCC 3
```

RESULT 41
US-11-217-529-9246
Sequence 9246, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9246
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-9246

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-9246 (1-25)

```
Qy        136 SerSerArgGlySerSer 141
              |||||||||||||||||
Db          8 TCATCGAGAGGCAGCAGT 25
```

RESULT 42
US-11-217-529-18480
Sequence 18480, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18480
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-18480

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-18480 (1-25)

```
Qy        182 GluGluSerLeuProIle 187
              |||||||||||||||||
Db          2 GAGGAATCGTTGCCTATC 19
```

RESULT 43
US-11-217-529-31190/c
Sequence 31190, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31190
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-31190

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-31190 (1-25)

```
Qy         45 GluValLeuGlySerGly 50
              |||||||||||||||||
Db         22 GAAGTATTAGGTTCAGGG 5
```

RESULT 44
US-11-217-529-36523
Sequence 36523, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

```
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 36523
   LENGTH: 25
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-36523

lignment Scores:
red. No.:                93.9          Length:        25
core:                    6.00          Matches:       6
ercent Similarity:       100.0%        Conservative:  0
est Local Similarity:    100.0%        Mismatches:    0
uery Match:              2.0%          Indels:        0
B:                       7             Gaps:          0

S-10-821-670A-27 (1-307) x US-11-217-529-36523 (1-25)

y          9 TyrValValGluLeuAsp 14
             ||||||||||||||||||
c          2 TACGTCGTGGAGTTAGAT 19

ESULT 45
S-11-217-529-36968/c
 Sequence 36968, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 36968
   LENGTH: 25
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-36968

lignment Scores:
red. No.:                93.9          Length:        25
core:                    6.00          Matches:       6
ercent Similarity:       100.0%        Conservative:  0
est Local Similarity:    100.0%        Mismatches:    0
uery Match:              2.0%          Indels:        0
B:                       7             Gaps:          0

S-10-821-670A-27 (1-307) x US-11-217-529-36968 (1-25)

y        125 AlaIleSerThrAspLeu 130
             ||||||||||||||||||
c         22 GCTATTAGTACAGATCTG 5

ESULT 46
S-11-217-529-43878/c
 Sequence 43878, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43878
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-43878

Alignment Scores:
Pred. No.:                93.9          Length:        25
Score:                    6.00          Matches:       6
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.0%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-43878 (1-25)

Qy         136 SerSerArgGlySerSer 141
               ||||||||||||||||||
Db          21 TCTTCAAGAGGTTCGTCT 4

RESULT 47
US-11-217-529-48094
; Sequence 48094, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48094
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-48094

Alignment Scores:
Pred. No.:                93.9          Length:        25
Score:                    6.00          Matches:       6
Percent Similarity:       100.0%        Conservative:  0
Best Local Similarity:    100.0%        Mismatches:    0
Query Match:              2.0%          Indels:        0
DB:                       7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-48094 (1-25)

Qy          91 SerThrAspIleLeuArg 96
               ||||||||||||||||||
Db           2 AGTACGGATATTTTAAGG 19

RESULT 48
US-11-217-529-50534
```

Sequence 50534, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 50534
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-50534

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-50534 (1-25)

```
Qy         58 LysGluPheAlaAspAla 63
              |||||||||||||||||||
Db          6 AAGGAGTTCGCGGACGCA 23
```

RESULT 49
US-11-217-529-71800/c
Sequence 71800, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 71800
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-71800

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-71800 (1-25)

```
Qy         22 GluMetValValLeuThr 27
              ||||||||||||||||||
Db         18 GAGATGGTGGTACTGACC 1
```

RESULT 50
US-11-217-529-82993/c
; Sequence 82993, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82993
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82993

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-82993 (1-25)

```
Qy         71 GlyGlyGluValLeuSer 76
              ||||||||||||||||||
Db         20 GGTGGAGAAGTGCTATCT 3
```

RESULT 51
US-11-217-529-88008
; Sequence 88008, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-88008

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0

```
B:                    7             Gaps:          0

S-10-821-670A-27 (1-307) x US-11-217-529-88008 (1-25)

y        220 LeuGlnLeuLysProLeu 225
             |||||||||||||||||
b          2 CTGCAGCTCAAACCTCTG 19

ESULT 52
S-11-217-529-106446
 Sequence 106446, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 106446
   LENGTH: 25
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
-11-217-529-106446

lignment Scores:
red. No.:              93.9          Length:        25
core:                  6.00          Matches:       6
rcent Similarity:      100.0%        Conservative:  0
st Local Similarity:   100.0%        Mismatches:    0
ery Match:             2.0%          Indels:        0
B:                     7             Gaps:          0

S-10-821-670A-27 (1-307) x US-11-217-529-106446 (1-25)

y         51 LysThrLeuThrIleGln 56
             ||||||||||||||||||
b          3 AAGACGCTAACGATCCAG 20

ESULT 53
S-11-217-529-107708/c
 Sequence 107708, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 107708
   LENGTH: 25
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
-11-217-529-107708

lignment Scores:
Pred. No.:             93.9          Length:        25
Score:                 6.00          Matches:       6
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           2.0%          Indels:        0
DB:                    7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-107708 (1-25)

Qy       273 ThrSerAlaLysValVal 278
             |||||||||||||||||
Db        22 ACGTCGGCAAAAGTTGTC 5

RESULT 54
US-11-217-529-112662/c
; Sequence 112662, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112662
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-112662

Alignment Scores:
Pred. No.:             93.9          Length:        25
Score:                 6.00          Matches:       6
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           2.0%          Indels:        0
DB:                    7             Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-112662 (1-25)

Qy       270 ValAspLysThrSerAla 275
             |||||||||||||||||
Db        24 GTCGACAAAACCAGCGCA 7

RESULT 55
US-11-217-529-123888/c
; Sequence 123888, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123888
;   LENGTH: 25
```

TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-123888

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-123888 (1-25)

```
Qy        257 GlnGlyLysAsnAsnArg 262
              |||||||||||||||||
Db         24 CAAGGAAAGAACAATCGA 7
```

RESULT 56
US-11-217-529-142444
Sequence 142444, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 142444
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-142444

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-142444 (1-25)

```
Qy         43 SerSerGluValLeuGly 48
              |||||||||||||||||
Db          3 TCTTCGGAAGTACTGGGC 20
```

RESULT 57
US-11-217-529-144453
Sequence 144453, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 144453
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-144453

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-144453 (1-25)

```
Qy        136 SerSerArgGlySerSer 141
              |||||||||||||||||
Db          5 TCTAGTCGAGGGTCTTCA 22
```

RESULT 58
US-11-217-529-152420/c
Sequence 152420, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 152420
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-152420

Alignment Scores:

Pred. No.:	93.9	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-152420 (1-25)

```
Qy        302 AlaSerValSerCysSer 307
              |||||||||||||||||
Db         20 GCTAGCGTATCCTGTTCC 3
```

RESULT 59
US-11-267-871-456
Sequence 456, Application US/11267871
Publication No. US20060094655A1
GENERAL INFORMATION:
APPLICANT: Guyon, Thierry
APPLICANT: Borrelly, Gilles
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: MODIFIED GROWTH HORMONES
FILE REFERENCE: 17109-015001/925

CURRENT APPLICATION NUMBER: US/11/267,871
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: 60/706,697
PRIOR FILING DATE: 2005-08-08
PRIOR APPLICATION NUMBER: 60/625,652
PRIOR FILING DATE: 2004-11-04
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 456
LENGTH: 72
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
S-11-267-871-456

Alignment Scores:

Pred. No.:	250	Length:	72
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-267-871-456 (1-72)

```
Qy        136 SerSerArgGlySerSer 141
              ||||||||||||||||||
Db         13 TCCAGTCGTGGATCGAGC 30
```

RESULT 60
US-11-267-871-456/c
Sequence 456, Application US/11267871
Publication No. US20060094655A1
GENERAL INFORMATION:
APPLICANT: Guyon, Thierry
APPLICANT: Borrelly, Gilles
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: MODIFIED GROWTH HORMONES
FILE REFERENCE: 17109-015001/925
CURRENT APPLICATION NUMBER: US/11/267,871
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: 60/706,697
PRIOR FILING DATE: 2005-08-08
PRIOR APPLICATION NUMBER: 60/625,652
PRIOR FILING DATE: 2004-11-04
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 456
LENGTH: 72
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
S-11-267-871-456

Alignment Scores:

Pred. No.:	250	Length:	72
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-267-871-456 (1-72)

```
Qy        136 SerSerArgGlySerSer 141
              ||||||||||||||||||
Db         60 TCCAGTCGTGGATCGAGC 43
```

RESULT 61
S-11-217-529-79352/c

; Sequence 79352, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79352
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79352

Alignment Scores:

Pred. No.:	576	Length:	177
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-79352 (1-177)

```
Qy        224 ProLeuLysAsnSerArg 229
              ||||||||||||||||||
Db        119 CCCTTGAAAAATTCTAGA 102
```

RESULT 62
US-10-471-571A-5615/c
; Sequence 5615, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5615
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-5615

Alignment Scores:

Pred. No.:	639	Length:	198
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-27 (1-307) x US-10-471-571A-5615 (1-198)

```
Qy         80 LeuLeuIleHisLysLys 85
              ||||||||||||||||||
Db        154 TTACTAATACATAAAAAA 137
```

RESULT 63
US-11-244-678-7

Sequence 7, Application US/11244678
Publication No. US20060099206A1
GENERAL INFORMATION:
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark
APPLICANT: Laken, Haley A.
APPLICANT: Rouse, Jason
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMPROVING
TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION
FILE REFERENCE: 16158-052001
CURRENT APPLICATION NUMBER: US/11/244,678
CURRENT FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/616,474
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 240
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated oligonucleotide
US-11-244-678-7

Alignment Scores:

Pred. No.:	764	Length:	240
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-244-678-7 (1-240)

```
Qy        253 GlyValGlnValGlnGly 258
              |||||||||||||||||
Db          6 GGAGTACAAGTGCAAGGT 23
```

RESULT 64
US-11-217-529-147/c
Sequence 147, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 147
LENGTH: 243
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-147

Alignment Scores:

Pred. No.:	773	Length:	243
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-147 (1-243)

```
Qy        261 AsnArgGluLysLysAsp 266
              |||||||||||||||||
Db        198 AATCGTGAGAAAAAAGAC 181
```

RESULT 65
US-11-217-529-80845
; Sequence 80845, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80845
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80845

Alignment Scores:

Pred. No.:	773	Length:	243
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-80845 (1-243)

```
Qy        136 SerSerArgGlySerSer 141
              |||||||||||||||||
Db         37 TCTAGTCGAGGGTCTTCA 54
```

RESULT 66
US-11-217-529-166793
; Sequence 166793, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166793
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166793

Alignment Scores:

Pred. No.:	843	Length:	267
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0

```
uery Match:            2.0%          Indels:        0
B:                     7             Gaps:          0

S-10-821-670A-27 (1-307) x US-11-217-529-166793 (1-267)

y        149 GlyAlaAlaThrLeuSer 154
             |||||||||||||||||
c        241 GGTGCTGCAACTTTATCC 258

ESULT 67
S-10-512-190-1/c
 Sequence 1, Application US/10512190
 Publication No. US20060099219A1
 GENERAL INFORMATION:
  APPLICANT: Hallez, Sophie
  APPLICANT:  Burny, Arsene
  APPLICANT:  Jacquet, Alain
  APPLICANT:  Bollen, Alex
  TITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION
  TITLE OF INVENTION:  COMPRISING IT AND ITS PREPARATION PROCESS
  FILE REFERENCE: 9997.50USWO
  CURRENT APPLICATION NUMBER: US/10/512,190
  CURRENT FILING DATE:  2004-10-22
  PRIOR APPLICATION NUMBER: PCT/BE03/000073
  PRIOR FILING DATE: 2003-04-24
  PRIOR APPLICATION NUMBER: US 60/410,461
  PRIOR FILING DATE: 2002-09-13
  PRIOR APPLICATION NUMBER: FR 0205173
  PRIOR FILING DATE: 2002-04-24
  PRIOR APPLICATION NUMBER: FR 0304170
  PRIOR FILING DATE: 2003-04-03
  NUMBER OF SEQ ID NOS: 9
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 1
   LENGTH: 279
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Mutated (recombinant) HPV-16 E7
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(279)
S-10-512-190-1

lignment Scores:
red. No.:              878           Length:        279
core:                  6.00          Matches:       6
ercent Similarity:     100.0%        Conservative:  0
est Local Similarity:  100.0%        Mismatches:    0
uery Match:            2.0%          Indels:        0
B:                     6             Gaps:          0

S-10-821-670A-27 (1-307) x US-10-512-190-1 (1-279)

y        175 GlySerAlaCysProAla 180
             ||||||||||||||||||
c        122 GGTTCTGCTTGTCCAGCT 105

ESULT 68
S-10-511-814-9/c
 Sequence 9, Application US/10511814
 Publication No. US20060088472A1
 GENERAL INFORMATION:
  APPLICANT: McCance, Dennis
  APPLICANT:  Westbrook, III, Thomas F.
  TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
  FILE REFERENCE: 21108.0016U2
  CURRENT APPLICATION NUMBER: US/10/511,814
  CURRENT FILING DATE:  2004-10-19
  PRIOR APPLICATION NUMBER: PCT/US03/12667
  PRIOR FILING DATE: 2003-04-21
  PRIOR APPLICATION NUMBER: 60/374,245
  PRIOR FILING DATE: 2002-04-19
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: Synthetic Construct
US-10-511-814-9

Alignment Scores:
Pred. No.:             922           Length:        294
Score:                 6.00          Matches:       6
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           2.0%          Indels:        0
DB:                    6             Gaps:          0

US-10-821-670A-27 (1-307) x US-10-511-814-9 (1-294)

Qy       175 GlySerAlaCysProAla 180
             ||||||||||||||||||
Db       140 GGTTCTGCTTGTCCAGCT 123

RESULT 69
US-10-511-814-10/c
; Sequence 10, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
;  APPLICANT: McCance, Dennis
;  APPLICANT:  Westbrook, III, Thomas F.
;  TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
;  FILE REFERENCE: 21108.0016U2
;  CURRENT APPLICATION NUMBER: US/10/511,814
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US03/12667
;  PRIOR FILING DATE: 2003-04-21
;  PRIOR APPLICATION NUMBER: 60/374,245
;  PRIOR FILING DATE: 2002-04-19
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: Synthetic Construct
US-10-511-814-10

Alignment Scores:
Pred. No.:             922           Length:        294
Score:                 6.00          Matches:       6
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           2.0%          Indels:        0
DB:                    6             Gaps:          0

US-10-821-670A-27 (1-307) x US-10-511-814-10 (1-294)

Qy       175 GlySerAlaCysProAla 180
             ||||||||||||||||||
Db       140 GGTTCTGCTTGTCCAGCT 123

RESULT 70
US-10-511-814-12/c
; Sequence 12, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
;  APPLICANT: McCance, Dennis
;  APPLICANT:  Westbrook, III, Thomas F.
;  TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
```

FILE REFERENCE: 21108.0016U2
CURRENT APPLICATION NUMBER: US/10/511,814
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US03/12667
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,245
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 294
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =
OTHER INFORMATION: Synthetic Construct
S-10-511-814-12

Alignment Scores:

Pred. No.:	922	Length:	294
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	6	Gaps:	0

S-10-821-670A-27 (1-307) x US-10-511-814-12 (1-294)

```
Qy        175 GlySerAlaCysProAla 180
              ||||||||||||||||||
Db        140 GGTTCTGCTTGTCCAGCT 123
```

RESULT 71
S-10-511-814-13/c
Sequence 13, Application US/10511814
Publication No. US20060088472A1
GENERAL INFORMATION:
APPLICANT: McCance, Dennis
APPLICANT: Westbrook, III, Thomas F.
TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
FILE REFERENCE: 21108.0016U2
CURRENT APPLICATION NUMBER: US/10/511,814
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US03/12667
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,245
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 294
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =
OTHER INFORMATION: Synthetic Construct
S-10-511-814-13

Alignment Scores:

Pred. No.:	922	Length:	294
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	6	Gaps:	0

S-10-821-670A-27 (1-307) x US-10-511-814-13 (1-294)

```
Qy        175 GlySerAlaCysProAla 180
              ||||||||||||||||||
Db        140 GGTTCTGCTTGTCCAGCT 123
```

RESULT 72
US-11-217-529-81028
; Sequence 81028, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81028
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81028

Alignment Scores:

Pred. No.:	931	Length:	297
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-81028 (1-297)

```
Qy         95 LeuArgGluGlnLysGlu 100
              ||||||||||||||||||
Db         79 TTAAGAGAGCAGAAGGAA 96
```

RESULT 73
US-11-217-529-190938
; Sequence 190938, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190938
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-190938

Alignment Scores:

Pred. No.:	957	Length:	306
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-190938 (1-306)

```
y        259 LysAsnAsnArgGluLys 264
             ||||||||||||||||||
c        139 AAAAACAATCGTGAAAAG 156
```

```
ESULT 74
S-11-321-421-87
 Sequence 87, Application US/11321421
 Publication No. US20060115496A1
 GENERAL INFORMATION:
  APPLICANT: Milhausen, Michael James
  TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
  FILE REFERENCE: TX-1-C2-1
  CURRENT APPLICATION NUMBER: US/11/321,421
  CURRENT FILING DATE:  2005-12-29
  PRIOR APPLICATION NUMBER: 09/216,393
  PRIOR FILING DATE: 1998-12-18
  PRIOR APPLICATION NUMBER: 08/994,825
  PRIOR FILING DATE: 1997-12-19
  NUMBER OF SEQ ID NOS: 366
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 87
   LENGTH: 306
   TYPE: DNA
   ORGANISM: Toxoplasma gondii
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (1)..(306)
   OTHER INFORMATION:
S-11-321-421-87
```

```
lignment Scores:
red. No.:               957          Length:         306
core:                   6.00         Matches:        6
ercent Similarity:      100.0%       Conservative:   0
est Local Similarity:   100.0%       Mismatches:     0
uery Match:             2.0%         Indels:         0
B:                      7            Gaps:           0
```

```
S-10-821-670A-27 (1-307) x US-11-321-421-87 (1-306)
```

```
y         17 ProAspAlaProGlyGlu 22
             ||||||||||||||||||
c        204 CCTGACGCCCCAGGAGAG 221
```

```
ESULT 75
S-11-217-529-76199
 Sequence 76199, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 76199
   LENGTH: 324
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-76199
```

```
lignment Scores:
red. No.:               1.01e+03     Length:         324
core:                   6.00         Matches:        6
ercent Similarity:      100.0%       Conservative:   0
```

```
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            2.0%         Indels:         0
DB:                     7            Gaps:           0
```

```
US-10-821-670A-27 (1-307) x US-11-217-529-76199 (1-324)
```

```
Qy       150 AlaAlaThrLeuSerAla 155
             ||||||||||||||||||
Db        37 GCAGCTACGCTGAGCGCA 54
```

```
RESULT 76
US-11-217-529-166940/c
; Sequence 166940, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166940
;   LENGTH: 339
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (186)..(210)
;   OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-166940
```

```
Alignment Scores:
Pred. No.:              1.05e+03     Length:         339
Score:                  6.00         Matches:        6
Percent Similarity:     100.0%       Conservative:   0
Best Local Similarity:  100.0%       Mismatches:     0
Query Match:            2.0%         Indels:         0
DB:                     7            Gaps:           0
```

```
US-10-821-670A-27 (1-307) x US-11-217-529-166940 (1-339)
```

```
Qy        75 LeuSerHisSerPheLeu 80
             ||||||||||||||||||
Db       297 CTTAGTCATTCTTTTCTT 280
```

```
RESULT 77
US-10-488-619-499/c
; Sequence 499, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 499
;   LENGTH: 348
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-488-619-499
```

```
Alignment Scores:
```

```
ed. No.:              1.08e+03        Length:         348
core:                 6.00            Matches:        6
ercent Similarity:    100.0%          Conservative:   0
est Local Similarity: 100.0%          Mismatches:     0
uery Match:           2.0%            Indels:         0
B:                    6               Gaps:           0

S-10-821-670A-27 (1-307) x US-10-488-619-499 (1-348)

y        204 SerSerPhePheIleArg 209
             |||||||||||||||||||
b        336 TCCTCCTTCTTCATCCGA 319

ESULT 78
S-11-217-529-77235
 Sequence 77235, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 77235
   LENGTH: 348
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-77235

lignment Scores:
ed. No.:              1.08e+03        Length:         348
core:                 6.00            Matches:        6
ercent Similarity:    100.0%          Conservative:   0
est Local Similarity: 100.0%          Mismatches:     0
uery Match:           2.0%            Indels:         0
B:                    7               Gaps:           0

S-10-821-670A-27 (1-307) x US-11-217-529-77235 (1-348)

y        246 SerTyrPheSerLeuThr 251
             |||||||||||||||||||
b        113 TCTTACTTTTCTTTAACC 130

ESULT 79
S-11-217-529-6132/c
 Sequence 6132, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 6132
   LENGTH: 357
;  TYPE: DNA
;  ORGANISM: Saccharomyces pastorianus
US-11-217-529-6132

Alignment Scores:
Pred. No.:            1.1e+03         Length:         357
Score:                6.00            Matches:        6
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          2.0%            Indels:         0
DB:                   7               Gaps:           0

US-10-821-670A-27 (1-307) x US-11-217-529-6132 (1-357)

Qy       106 PheLeuLysCysGluAla 111
             |||||||||||||||||||
Db       242 TTCCTCAAGTGCGAAGCC 225

RESULT 80
US-10-499-266-11/c
; Sequence 11, Application US/10499266
; Publication No. US20060088531A1
; GENERAL INFORMATION:
;  APPLICANT: Smethurst, Peter Alexander
;  APPLICANT:  Ouwehand, Willem Hendrik
;  APPLICANT:  Farndale, Richard William
;  TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST HUMAN
;  TITLE OF INVENTION:  GLYCOPROTEIN VI AND THEIR USE
;  FILE REFERENCE: 191134.401USPC
;  CURRENT APPLICATION NUMBER: US/10/499,266
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: PCT/GB02/05755
;  PRIOR FILING DATE: 2002-12-18
;  PRIOR APPLICATION NUMBER: GB 0130543.2
;  PRIOR FILING DATE: 2001-12-20
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 369
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-499-266-11

Alignment Scores:
Pred. No.:            1.14e+03        Length:         369
Score:                6.00            Matches:        6
Percent Similarity:   100.0%          Conservative:   0
Best Local Similarity: 100.0%         Mismatches:     0
Query Match:          2.0%            Indels:         0
DB:                   6               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-499-266-11 (1-369)

Qy       153 LeuSerAlaGluLysVal 158
             |||||||||||||||||||
Db       221 TTGTCGGCTGAGAAGGTG 204

RESULT 81
US-10-994-679-63/c
; Sequence 63, Application US/10994679
; Publication No. US20060111559A2
; GENERAL INFORMATION:
;  APPLICANT: Roschke, Viktor
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000I
;  CURRENT APPLICATION NUMBER: US/10/994,679
;  CURRENT FILING DATE:  2004-11-23
;  PRIOR APPLICATION NUMBER: US/10/067,800
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: PCT/US01/04153
;  PRIOR FILING DATE: 2001-02-09
```

PRIOR APPLICATION NUMBER: 09/779,880
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/297,257
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/310,458
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/328,447
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/341,725
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 379
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(378)
OTHER INFORMATION:
S-10-994-679-63

lignment Scores:

red. No.:	1.17e+03	Length:	379
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.0%	Indels:	0
B:	6	Gaps:	0

S-10-821-670A-27 (1-307) x US-10-994-679-63 (1-379)

' 136 SerSerArgGlySerSer 141
||||||||||||||||||
: 328 AGTAGTAGGGGTAGCTCC 311

ESULT 82
S-11-217-529-78662/c
Sequence 78662, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 78662
LENGTH: 387
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
S-11-217-529-78662

lignment Scores:

red. No.:	1.19e+03	Length:	387
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.0%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-27 (1-307) x US-11-217-529-78662 (1-387)

' 256 ValGlnGlyLysAsnAsn 261
||||||||||||||||||

Db 286 GTACAAGGTAAGAATAAT 269

RESULT 83
US-11-217-529-80425
; Sequence 80425, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80425
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80425

Alignment Scores:

Pred. No.:	1.19e+03	Length:	387
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-27 (1-307) x US-11-217-529-80425 (1-387)

Qy 189 ValValValAspAlaIle 194
||||||||||||||||||
Db 103 GTTGTTGTTGACGCTATC 120

RESULT 84
US-11-217-529-76946/c
; Sequence 76946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76946
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76946

Alignment Scores:

Pred. No.:	1.21e+03	Length:	393
Score:	6.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.0%	Indels:	0
DB:	7	Gaps:	0

```
S-10-821-670A-27 (1-307) x US-11-217-529-76946 (1-393)

y        125 AlaIleSerThrAspLeu 130
             |||||||||||||||||
b        156 GCAATTTCGACCGATCTT 139

ESULT 85
S-11-217-529-82136/c
  Sequence 82136, Application US/11217529
  Publication No. US20060099612A1
  GENERAL INFORMATION:
   APPLICANT: SUNTORY LIMITED
   APPLICANT:  NAKAO, YOSHIHIRO
   APPLICANT:  NAKAMURA, NORIHISA
   APPLICANT:  KODAMA, YUKIKO
   APPLICANT:  FUJIMURA, TOMOKO
   APPLICANT:  ASHIKARI, TOSHIHIKO
   TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
   FILE REFERENCE: S-38-285
   CURRENT APPLICATION NUMBER: US/11/217,529
   CURRENT FILING DATE:  2005-09-02
   PRIOR APPLICATION NUMBER: US 10/932,182
   PRIOR FILING DATE: 2004-09-02
   NUMBER OF SEQ ID NOS: 197023
   SOFTWARE: PatentIn version 3.3
  SEQ ID NO 82136
    LENGTH: 396
    TYPE: DNA
    ORGANISM: Saccharomyces pastorianus
S-11-217-529-82136

lignment Scores:
red. No.:              1.22e+03       Length:        396
core:                  6.00           Matches:       6
ercent Similarity:     100.0%         Conservative:  0
est Local Similarity:  100.0%         Mismatches:    0
uery Match:            2.0%           Indels:        0
B:                     7              Gaps:          0

S-10-821-670A-27 (1-307) x US-11-217-529-82136 (1-396)

y         74 ValLeuSerHisSerPhe 79
             |||||||||||||||||
b        223 GTTTTATCTCATTCATTT 206

ESULT 86
S-11-217-529-75995/c
  Sequence 75995, Application US/11217529
  Publication No. US20060099612A1
  GENERAL INFORMATION:
   APPLICANT: SUNTORY LIMITED
   APPLICANT:  NAKAO, YOSHIHIRO
   APPLICANT:  NAKAMURA, NORIHISA
   APPLICANT:  KODAMA, YUKIKO
   APPLICANT:  FUJIMURA, TOMOKO
   APPLICANT:  ASHIKARI, TOSHIHIKO
   TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
   FILE REFERENCE: S-38-285
   CURRENT APPLICATION NUMBER: US/11/217,529
   CURRENT FILING DATE:  2005-09-02
   PRIOR APPLICATION NUMBER: US 10/932,182
   PRIOR FILING DATE: 2004-09-02
   NUMBER OF SEQ ID NOS: 197023
   SOFTWARE: PatentIn version 3.3
  SEQ ID NO 75995
    LENGTH: 402
    TYPE: DNA
    ORGANISM: Saccharomyces pastorianus
S-11-217-529-75995

lignment Scores:
red. No.:              1.23e+03       Length:        402
Score:                 6.00           Matches:       6
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           2.0%           Indels:        0
DB:                    7              Gaps:          0

US-10-821-670A-27 (1-307) x US-11-217-529-75995 (1-402)

Qy       247 TyrPheSerLeuThrPhe 252
             |||||||||||||||||
Db       292 TATTTTTCTCTAACATTT 275

RESULT 87
US-11-255-980-6
; Sequence 6, Application US/11255980
; Publication No. US20060115844A1
; GENERAL INFORMATION:
;  APPLICANT: FINKELSTEIN, SYDNEY DAVID
;  APPLICANT:  SWALSKY, PATRICIA
;  TITLE OF INVENTION: ENHANCED AMPLIFIABILITY OF MINUTE FIXATIVE-TREATED
;  TITLE OF INVENTION:  TISSUE SAMPLES, MINUTE STAINED CYTOLOGY SAMPLES, AND
;  TITLE OF INVENTION:  OTHER MINUTE SOURCES OF DNA
;  FILE REFERENCE: 47030.0014-01US
;  CURRENT APPLICATION NUMBER: US/11/255,980
;  CURRENT FILING DATE:  2005-10-24
;  PRIOR APPLICATION NUMBER: 60/679,969
;  PRIOR FILING DATE: 2005-05-12
;  PRIOR APPLICATION NUMBER: 60/679,968
;  PRIOR FILING DATE: 2005-05-12
;  PRIOR APPLICATION NUMBER: 60/644,568
;  PRIOR FILING DATE: 2005-01-19
;  PRIOR APPLICATION NUMBER: 60/631,240
;  PRIOR FILING DATE: 2004-11-29
;  PRIOR APPLICATION NUMBER: 60/620,926
;  PRIOR FILING DATE: 2004-10-22
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-255-980-6

Alignment Scores:
Pred. No.:             1.28e+03       Length:        420
Score:                 6.00           Matches:       6
Percent Similarity:    100.0%         Conservative:  0
Best Local Similarity: 100.0%         Mismatches:    0
Query Match:           2.0%           Indels:        0
DB:                    7              Gaps:          0

US-10-821-670A-27 (1-307) x US-11-255-980-6 (1-420)

Qy       249 SerLeuThrPheGlyVal 254
             ||||||||||||||||||
Db        62 TCCCTCACCTTCGGGGTG 79

RESULT 88
US-11-217-529-3397
; Sequence 3397, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
```

```
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 3397
   LENGTH: 423
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
S-11-217-529-3397

Alignment Scores:
Pred. No.:              1.29e+03      Length:         423
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.0%          Indels:         0
DB:                     7             Gaps:           0

S-10-821-670A-27 (1-307) x US-11-217-529-3397 (1-423)

Qy        253 GlyValGlnValGlnGly 258
              |||||||||||||||||
Db        399 GGAGTACAAGTCCAGGGC 416

RESULT 89
S-10-488-619-1587
 Sequence 1587, Application US/10488619
 Publication No. US20060099578A1
 GENERAL INFORMATION:
  APPLICANT: Greenlee, Winner and Sullivan, P.C.
  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
  FILE REFERENCE: 98-01 WO
  CURRENT APPLICATION NUMBER: US/10/488,619
  CURRENT FILING DATE:  2004-03-01
  NUMBER OF SEQ ID NOS: 3040
  SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1587
   LENGTH: 427
   TYPE: DNA
   ORGANISM: Mus musculus
   FEATURE:
   NAME/KEY: misc_feature
   LOCATION: (1)..(427)
   OTHER INFORMATION: n is a, c, g, or t
S-10-488-619-1587

Alignment Scores:
Pred. No.:              1.3e+03       Length:         427
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.0%          Indels:         0
DB:                     6             Gaps:           0

S-10-821-670A-27 (1-307) x US-10-488-619-1587 (1-427)

Qy        294 TyrSerSerSerTrpSer 299
              ||||||||||||||||||
Db        353 TACAGCTCGTCATGGTCC 370

RESULT 90
S-10-488-619-552
 Sequence 552, Application US/10488619
 Publication No. US20060099578A1
 GENERAL INFORMATION:
  APPLICANT: Greenlee, Winner and Sullivan, P.C.
  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
  FILE REFERENCE: 98-01 WO
  CURRENT APPLICATION NUMBER: US/10/488,619
  CURRENT FILING DATE:  2004-03-01
  NUMBER OF SEQ ID NOS: 3040
  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 552
;   LENGTH: 436
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-488-619-552

Alignment Scores:
Pred. No.:              1.33e+03      Length:         436
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.0%          Indels:         0
DB:                     6             Gaps:           0

US-10-821-670A-27 (1-307) x US-10-488-619-552 (1-436)

Qy         74 ValLeuSerHisSerPhe 79
              |||||||||||||||||||
Db        241 GTGTTGTCACATTCTTTC 258

RESULT 91
US-10-488-619-1590/c
; Sequence 1590, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1590
;   LENGTH: 438
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(438)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-488-619-1590

Alignment Scores:
Pred. No.:              1.33e+03      Length:         438
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.0%          Indels:         0
DB:                     6             Gaps:           0

US-10-821-670A-27 (1-307) x US-10-488-619-1590 (1-438)

Qy        139 GlySerSerAspProGln 144
              ||||||||||||||||||
Db        410 GGAAGCTCAGATCCACAA 393

RESULT 92
US-10-468-193-6
; Sequence 6, Application US/10468193
; Publication No. US20060100416A1
; GENERAL INFORMATION:
;  APPLICANT: Palli, Subba R.
;  APPLICANT:  Cress, Dean E.
;  APPLICANT:  Fujimoto, Ted T.
;  APPLICANT:  Kumar, Mohan B.
;  TITLE OF INVENTION: Novel Substitution Mutant Receptors and Their Use in A Nuclear
;  TITLE OF INVENTION:  Receptor-Based Inducible Gene Expression System
;  FILE REFERENCE: A01247-US
;  CURRENT APPLICATION NUMBER: US/10/468,193
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/313,925
;  PRIOR FILING DATE: 2001-08-21
```

```
  PRIOR APPLICATION NUMBER: PCT/US02/05090
  PRIOR FILING DATE: 2002-02-20
  NUMBER OF SEQ ID NOS: 113
  SOFTWARE: PatentIn version 3.2
 SEQ ID NO 6
   LENGTH: 441
   TYPE: DNA
   ORGANISM: Saccharomyces cerevisiae
US-10-468-193-6

Alignment Scores:
Pred. No.:              1.34e+03      Length:         441
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.0%          Indels:         0
DB:                     6             Gaps:           0

US-10-821-670A-27 (1-307) x US-10-468-193-6 (1-441)

Qy        124 ThrAlaIleSerThrAsp 129
              |||||||||||||||||
Db        195 ACAGCTATTTCTACTGAT 212

RESULT 93
US-11-217-529-82599/c
 Sequence 82599, Application US/11217529
 Publication No. US20060099612A1
 GENERAL INFORMATION:
  APPLICANT: SUNTORY LIMITED
  APPLICANT:  NAKAO, YOSHIHIRO
  APPLICANT:  NAKAMURA, NORIHISA
  APPLICANT:  KODAMA, YUKIKO
  APPLICANT:  FUJIMURA, TOMOKO
  APPLICANT:  ASHIKARI, TOSHIHIKO
  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
  FILE REFERENCE: S-38-285
  CURRENT APPLICATION NUMBER: US/11/217,529
  CURRENT FILING DATE:  2005-09-02
  PRIOR APPLICATION NUMBER: US 10/932,182
  PRIOR FILING DATE: 2004-09-02
  NUMBER OF SEQ ID NOS: 197023
  SOFTWARE: PatentIn version 3.3
 SEQ ID NO 82599
   LENGTH: 444
   TYPE: DNA
   ORGANISM: Saccharomyces pastorianus
   FEATURE:
   NAME/KEY: modified_base
   LOCATION: (123)..(147)
   OTHER INFORMATION: a, c, g, t, unknown, or other
   FEATURE:
   NAME/KEY: modified_base
   LOCATION: (278)..(372)
   OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-82599

Alignment Scores:
Pred. No.:              1.35e+03      Length:         444
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.0%          Indels:         0
DB:                     7             Gaps:           0

US-10-821-670A-27 (1-307) x US-11-217-529-82599 (1-444)

Qy         75 LeuSerHisSerPheLeu 80
              |||||||||||||||||
Db        234 CTTAGTCATTCTTTTCTT 217

RESULT 94
US-11-217-529-166970/c
; Sequence 166970, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166970
;   LENGTH: 447
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-166970

Alignment Scores:
Pred. No.:              1.36e+03      Length:         447
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.0%          Indels:         0
DB:                     7             Gaps:           0

US-10-821-670A-27 (1-307) x US-11-217-529-166970 (1-447)

Qy        123 LeuThrAlaIleSerThr 128
              ||||||||||||||||||
Db        341 CTGACTGCTATATCAACC 324

RESULT 95
US-10-471-571A-3305/c
; Sequence 3305, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3305
;   LENGTH: 450
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-3305

Alignment Scores:
Pred. No.:              1.37e+03      Length:         450
Score:                  6.00          Matches:        6
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            2.0%          Indels:         0
DB:                     6             Gaps:           0

US-10-821-670A-27 (1-307) x US-10-471-571A-3305 (1-450)

Qy        222 LeuLysProLeuLysAsn 227
              |||||||||||||||||
Db        149 TTAAAGCCGTTGAAGAAT 132

RESULT 96
US-11-301-554-965/c
```

```
Sequence 965, Application US/11301554
Publication No. US20060088527A1
GENERAL INFORMATION:
 APPLICANT: Henderson, Robert A.
 APPLICANT:  Wang, Tongtong
 APPLICANT:  Watanabe, Yoshihiro
 APPLICANT:  Kalos, Michael D.
 APPLICANT:  Sleath, Paul R.
 APPLICANT:  Johnson, Jeffrey C.
 APPLICANT:  Retter, Marc W.
 APPLICANT:  Durham, Margarita
 APPLICANT:  Carter, Darrick
 APPLICANT:  Fanger, Gary R.
 APPLICANT:  Vedvick, Thomas S.
 APPLICANT:  Bangur, Chaitanya S.
 APPLICANT:  McNabb, Andria
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121.478C21
 CURRENT APPLICATION NUMBER: US/11/301,554
 CURRENT FILING DATE:  2005-12-13
 PRIOR APPLICATION NUMBER: US 10/283,017
 PRIOR FILING DATE: 2002-10-28
 PRIOR APPLICATION NUMBER: US 10/113,872
 PRIOR FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: US 10/017,754
 PRIOR FILING DATE: 2001-10-29
 PRIOR APPLICATION NUMBER: US 09/902,941
 PRIOR FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: US 09/849,626
 PRIOR FILING DATE: 2001-05-03
 PRIOR APPLICATION NUMBER: US 09/736,457
 PRIOR FILING DATE: 2000-12-13
 PRIOR APPLICATION NUMBER: US 09/702,705
 PRIOR FILING DATE: 2000-10-30
 PRIOR APPLICATION NUMBER: US 09/677,419
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: US 09/671,325
 PRIOR FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: US 09/658,824
 PRIOR FILING DATE: 2000-09-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 2157
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 965
  LENGTH: 461
  TYPE: DNA
  ORGANISM: Homo sapiens
S-11-301-554-965

lignment Scores:
red. No.:               1.4e+03        Length:         461
core:                   6.00           Matches:        6
ercent Similarity:      100.0%         Conservative:   0
est Local Similarity:   100.0%         Mismatches:     0
uery Match:             2.0%           Indels:         0
B:                      7              Gaps:           0

S-10-821-670A-27 (1-307) x US-11-301-554-965 (1-461)

y          47 LeuGlySerGlyLysThr 52
              ||||||||||||||||||
c         428 CTGGGCTCAGGAAAAACC 411

ESULT 97
S-10-473-173-248/c
 Sequence 248, Application US/10473173
 Publication No. US20060088823A1
 GENERAL INFORMATION:
  APPLICANT: VAN ANDEL INSTITUTE
  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 248
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-473-173-248

Alignment Scores:
Pred. No.:              1.4e+03        Length:         462
Score:                  6.00           Matches:        6
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            2.0%           Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-27 (1-307) x US-10-473-173-248 (1-462)

Qy         102 LysAsnLysIlePheLeu 107
               |||||||||||||||||
Db          26 AAAAATAAAATATTTTTG 9

RESULT 98
US-10-488-619-417
; Sequence 417, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 417
;   LENGTH: 471
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(500)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-417

Alignment Scores:
Pred. No.:              1.43e+03       Length:         471
Score:                  6.00           Matches:        6
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            2.0%           Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-27 (1-307) x US-10-488-619-417 (1-471)

Qy         136 SerSerArgGlySerSer 141
               ||||||||||||||||||
Db          57 TCGTCCCGGGGCAGCAGC 74

RESULT 99
US-11-217-529-5788/c
; Sequence 5788, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
```

APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5788
LENGTH: 471
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
S-11-217-529-5788

lignment Scores:

ed. No.:	1.43e+03	Length:	471
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.0%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-27 (1-307) x US-11-217-529-5788 (1-471)

y 76 SerHisSerPheLeuLeu 81
||||||||||||||||||
b 274 AGCCACAGTTTTTTACTA 257

ESULT 100
S-11-217-529-3216
Sequence 3216, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3216
LENGTH: 474
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
S-11-217-529-3216

lignment Scores:

ed. No.:	1.44e+03	Length:	474
core:	6.00	Matches:	6
ercent Similarity:	100.0%	Conservative:	0
est Local Similarity:	100.0%	Mismatches:	0
uery Match:	2.0%	Indels:	0
B:	7	Gaps:	0

S-10-821-670A-27 (1-307) x US-11-217-529-3216 (1-474)

y 73 GluValLeuSerHisSer 78
||||||||||||||||||
b 420 GAAGTACTGTCTCACAGC 437

earch completed: June 10, 2006, 02:14:57
ob time : 139.923 secs

This Page Blank (uspto)